

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 106.506 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-2
Perfect score: 209
Sequence: 1 DAFFRHDSCYEYHOKLVFFAPEDVGSNKAIIGLWGVV 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	40	2	AAR33191 Beta-amy1
2	209	100.0	40	2	AAR60364 Beta-amy1
3	209	100.0	40	2	ADDL1651 Human bet
4	209	100.0	40	2	AAW23335 Amy1oid b
5	209	100.0	40	2	AAW37507 Amy1oid b
6	209	100.0	40	2	AAW47226 Beta-amy1
7	209	100.0	40	2	AAW14099 Human bet
8	209	100.0	40	2	AAW39804 Beta-amy1
9	209	100.0	40	2	AAW95854 Wild type
10	209	100.0	40	2	AAW81473 Synthetic
11	209	100.0	40	2	AAW39339 Beta-amy1
12	209	100.0	40	2	AAW25135 Human amy
13	209	100.0	40	2	AAW92723 Human tac
14	209	100.0	40	4	AAW84426 Partial s
15	209	100.0	40	4	AAW91813 Amy1oid b
16	209	100.0	40	4	AAW91829 Amy1oid b
17	209	100.0	40	4	AAW91802 Amy1oid b
18	209	100.0	40	4	AAW91802 Amy1oid b
19	209	100.0	40	4	AAW91802 Amy1oid b
20	209	100.0	40	5	AAW95425 Human pep
21	209	100.0	40	5	AAW22990 Human amy
22	209	100.0	40	5	AAW68313 Human bet
23	209	100.0	40	5	AAW96895 Human sel

24	209	100.0	40	5	AAW50909 Beta amy1
25	209	100.0	40	5	AAW80186 Amy1oid b
26	209	100.0	40	5	AAW26332 Human bet
27	209	100.0	40	5	AAW51863 Human amy
28	209	100.0	40	6	ABU08710 Amy1oid b
29	209	100.0	40	6	ABU08508 Human amy
30	209	100.0	40	6	AAO19885 Human amy
31	209	100.0	40	6	ABP96147 Human Abe
32	209	100.0	40	6	AAE53429 Abeta pro
33	209	100.0	40	6	ABP60626 Human A-b
34	209	100.0	40	6	ABP97883 Amino aci
35	209	100.0	40	6	ABU63706 Rat amylo
36	209	100.0	40	7	ADA37266 Human bet
37	209	100.0	40	7	ADB85563 Beta-amy1
38	209	100.0	40	7	AAE38648 Human amy
39	209	100.0	40	7	ADC66001 Human A(b
40	209	100.0	40	7	ADC35182 Beta-amy1
41	209	100.0	40	7	ADF55648 Human A b
42	209	100.0	40	7	ADK82702 Beta-amy1
43	209	100.0	40	8	ADP53270 Amy1oid A
44	209	100.0	40	8	ADN06093 A40, SEQ
45	209	100.0	40	8	ADNA1865 Amino aci
46	209	100.0	40	8	ADO10000 Human bet
47	209	100.0	40	8	ADQ26239 Human amy
48	209	100.0	40	8	ADQ37253 Vaccine a
49	209	100.0	40	8	ADR16410 Human Abe
50	209	100.0	40	8	ADSI8445 Amy1oid-b
51	209	100.0	40	8	ADU24434 Novel glu
52	209	100.0	40	8	ADU46708 Amy1oid b
53	209	100.0	40	9	ADV50991 Alzheimer
54	209	100.0	40	9	ADM38388 Human bet
55	209	100.0	40	9	ADY72249 N-termina
56	209	100.0	40	9	ADY81764 Human bet
57	209	100.0	40	9	ADY78385 Human amy
58	209	100.0	40	9	ADZ20480 Amy1oid b
59	209	100.0	40	9	ADZ59193 Human amy
60	209	100.0	40	9	ADZ71360 Human bet
61	209	100.0	40	9	AEA35393 Novel QC
62	209	100.0	40	9	AEBO9193 Human bet
63	209	100.0	40	9	AE888137 Human nep
64	209	100.0	40	9	AE892566 Glutaminyl
65	209	100.0	40	9	AE805253 Amy1oid b
66	209	100.0	40	9	AE8039344 Amy1oid b
67	209	100.0	40	9	AED21140 Amy1oid b
68	209	100.0	40	9	AED26003 Human amy
69	209	100.0	40	9	AED83058 Human amy
70	209	100.0	40	10	AER83486 Amy1oid b
71	209	100.0	40	10	AER92526 Human amy
72	209	100.0	40	10	AER87773 Human amy
73	209	100.0	41	2	AAW60365 Beta-amy1
74	209	100.0	41	2	AAW25136 Human amy
75	209	100.0	41	3	AAW11497 Human amy
76	209	100.0	41	6	ABU08507 Human amy
77	209	100.0	41	6	ABP96146 Human Abe
78	209	100.0	41	8	ADNA1883 Amino aci
79	209	100.0	41	9	ADY81765 Human bet
80	209	100.0	42	2	AAW20330 Sequence
81	209	100.0	42	2	AAW60366 Beta-amy1
82	209	100.0	42	2	AAW95248 Beta-A4-a
83	209	100.0	42	2	AAW94591 Alzheimer
84	209	100.0	42	2	AAW12828 Beta A4 p
85	209	100.0	42	2	AAW64507 Neurotoxi
86	209	100.0	42	2	AAW42989 Full leng
87	209	100.0	42	2	AAW47230 Beta-amy1
88	209	100.0	42	2	AAW49691 Human bet
89	209	100.0	42	2	AAW95585 Mutant ag
90	209	100.0	42	2	AAW81474 Synthetic
91	209	100.0	42	2	AAW08607 Human bet
92	209	100.0	42	2	AAW29093 A-beta-bi
93	209	100.0	42	2	AAW25137 Human amy
94	209	100.0	42	2	AAW92726 Human tac
95	209	100.0	42	2	AAW33407 Human amy
96	209	100.0	42	3	AAW96956 Beta-amy1

AAW50909	Beta amy1
AAW80186	Amy1oid b
AAW26332	Human bet
AAW51863	Human amy
ABU08710	Amy1oid b
ABU08508	Human amy
AAO19885	Human amy
ABP96147	Human Abe
AAE53429	Abeta pro
ABP60626	Human A-b
ABP97883	Amino aci
ABU63706	Rat amylo
ADA37266	Human bet
ADB85563	Beta-amy1
AAE38648	Human amy
ADC66001	Human A(b
ADC35182	Beta-amy1
ADF55648	Human A b
ADK82702	Beta-amy1
ADP53270	Amy1oid A
ADN06093	A40, SEQ
ADNA1865	Amino aci
ADO10000	Human bet
ADQ26239	Human amy
ADQ37253	Vaccine a
ADR16410	Human Abe
ADSI8445	Amy1oid-b
ADU24434	Novel glu
ADU46708	Amy1oid b
ADV50991	Alzheimer
ADM38388	Human bet
ADY72249	N-termina
ADY81764	Human bet
ADY78385	Human amy
ADZ20480	Amy1oid b
ADZ59193	Human amy
ADZ71360	Human bet
AEA35393	Novel QC
AEBO9193	Human bet
AE888137	Human nep
AE892566	Glutaminyl
AE805253	Amy1oid b
AE8039344	Amy1oid b
AED21140	Amy1oid b
AED26003	Human amy
AED83058	Human amy
AER83486	Amy1oid b
AER92526	Human amy
AER87773	Human amy
AAW60365	Beta-amy1
AAW25136	Human amy
AAW11497	Human amy
ABU08507	Human amy
ABP96146	Human Abe
ADNA1883	Amino aci
ADY81765	Human bet
AAW20330	Sequence
AAW60366	Beta-amy1
AAW95248	Beta-A4-a
AAW94591	Alzheimer
AAW12828	Beta A4 p
AAW64507	Neurotoxi
AAW42989	Full leng
AAW47230	Beta-amy1
AAW49691	Human bet
AAW95585	Mutant ag
AAW81474	Synthetic
AAW08607	Human bet
AAW29093	A-beta-bi
AAW25137	Human amy
AAW92726	Human tac
AAW33407	Human amy
AAW96956	Beta-amy1

97	209	100.0	42	4	AAB86134	Human Alz
98	209	100.0	42	4	AAB35589	Beta/A4-a
99	209	100.0	42	4	AAB49098	Human amy
100	209	100.0	42	4	AAB48497	Human amy

ALIGNMENTS

RESULT 1

AAR33191

ID AAR33191 standard; peptide; 40 AA.

AAR33191;

AC 25-MAR-2003 (revised)

DT 01-JUL-1993 (first entry)

XX Beta-amyloid peptide.

XX Alzheimer's disease; amyloid deposition; diagnosis; therapy.

XX Synthetic.

OS WO9304194-A1.

PN 04-MAR-1993.

PD 10-AUG-1992; 92WO-US006700.

XX 13-AUG-1991; 91US-00744767.

XX (MINU) UNIV MINNESOTA.

PA (HARD) HARVARD COLLEGE.

XX Magglio JE, Mantyh PW;

PI WPI; 1993-094020/11.

DR Detecting Alzheimer's disease using beta-amyloid peptide - includes

PT quantitating amyloid deposition onto tissue samples, and using screen

XX agents as therapeutic agents.

XX Disclosure; Page 34; Sipp; English.

XX The peptide is an internal fragment of the beta amyloid peptide (BAP)

CC precursor, which was produced synthetically. The peptide, when labelled,

CC can be used in vitro methods for the detection of Alzheimer's disease.

CC See also AAR33192. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 40 AA;

SQ Query Match

Best Local Similarity 100.0%; Score 209; DB 2; Length 40;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 2

AAR60364

ID AAR60364 standard; peptide; 40 AA.

AAR60364;

AC 25-MAR-2003 (revised)

DT 15-MAR-1995 (first entry)

XX Beta-amyloid (1-40).

XX Alzheimer's disease; beta-amyloid;

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;

KM

KW anti-beta-amyloid antibody; diagnosis.

XX Homo sapiens.

OS WO9417197-A1.

XX 04-AUG-1994.

XX 24-JAN-1994; 94WO-JP000089.

XX 25-JAN-1993; 93JP-00010132.

XX 05-FEB-1993; 93JP-00019035.

XX 16-NOV-1993; 93JP-00286985.

XX 28-DEC-1993; 93JP-00334773.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Suzuki N, Odaka A, Kitada C;

XX WPI; 1994-264110/32.

XX Antibodies recognising specific parts of beta-amyloid - can be used for

XX diagnosis of diseases implicating beta-amyloid, such as Alzheimer's

XX disease.

XX Disclosure; Page 82; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid

XX protein are claimed. Specifically, the antibodies (which are pref.

XX monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal

XX portion of beta-amyloid or they recognise residues 25-35 or 35-43 from

XX the C-terminal portion. The antibodies are useful for assaying beta-

XX amyloid and its derivatives for diagnosis of Alzheimer's disease.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 40 AA;

SQ Query Match

Best Local Similarity 100.0%; Score 209; DB 2; Length 40;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 3

ADD11651

ID ADD11651 standard; protein; 40 AA.

XX ADD11651;

XX 01-JAN-2004 (first entry)

XX Human beta-amyloid 1-40 (beta1-40).

XX neurotoxic effect; beta-amyloid peptide; neurotoxicity inhibitor;

XX amyloidogenic amylin; beta-2-microglobulin; amylin; Alzheimer's disease;

XX Down's syndrome; beta-amyloid neurotoxicity assay; human;

XX beta-amyloid 1-40; beta1-40.

XX Homo sapiens.

XX EP646792-A1.

XX 05-APR-1995.

XX 17-AUG-1994; 94EP-00306053.

XX 19-AUG-1993; 93US-00109782.

XX (ELIL) LILLY & CO ELI.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX May PC, Rydel RE;
XX WPI; 1995-132760/18.
XX Assay for effectiveness of agents used in the treatment of Alzheimer's
PT disease - by incubating potential inhibitor of neurotoxicity with amylin
or beta-2-microglobulin and measuring neurotoxic props. of mixt.
XX
PS Disclosure; SEQ ID NO 2; 14pp; English.
XX
XX The invention describes a method for assaying the effectiveness of agents
CC useful for ameliorating the neurotoxic effects of a condition associated
CC with the accumulation of a beta-amyloid peptide. The method comprises:
CC (a) incubating potential inhibitors of neurotoxicity with an
CC amyloidogenic amylin or beta-2-microglobulin; (b) measuring the
CC neurotoxic properties of each amylin or beta-2-microglobulin/potential
CC inhibitor mixture; and (c) detecting reduction in the neurotoxicity
CC relative to a control. The preferred amyloidogenic amylin is human
CC amylin. The method is especially for assessing the ability of an agent to
CC ameliorate the neurotoxic effects of Alzheimer's disease or Down's
CC syndrome. The method provides a more consistent beta-amyloid
CC neurotoxicity assay and is more sensitive and covers a broader range.
CC This is the amino acid sequence of human beta-amyloid 1-40 (beta1-40).
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 4
AAW23335
ID AAW23335 standard; peptide; 40 AA.
XX
XX AAW23335;
AC
XX
XX
DT 12-MAR-1998 (first entry)
XX

DE Amyloid beta peptide 1 used to inhibit damage to cells in Alzheimer's.
XX
XX Amyloid beta peptide; extracellular deposit; Alzheimer's disease;
KW neurite outgrowth; microglial activation; neuronal cell degeneration;
KM receptor for advanced glycosylation end product;
XX amyloid beta peptide fibril.
XX
OS Homo sapiens.
OS
XX
PN WO9726913-A1.
XX
XX 31-JUL-1997.
PD
XX 21-JAN-1997; 97WO-US000857.
PF
XX 26-JAN-1996; 96US-00592070.
PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA
XX Stern D, Schmidt AM, Yan SD;
PI
XX WPI; 1997-393374/36.
DR
XX

PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent
PT which inhibits interaction of an amyloid-beta peptide with a receptor for
XX advanced glycosylation end product.
XX
XX Claim 4; Page 10; 91pp; English.
XX

CC Peptides AAW23335-36 are portions of the the amyloid beta peptide, which
CC is the principal component of extracellular deposits in Alzheimer's
CC disease. It has been shown to promote neurite outgrowth, generate
CC reactive oxygen intermediates, induce cellular oxidant stress, lead to
CC neuronal cytotoxicity, and promote microglial activation. The present
CC peptide, which comprises amino acids 1-40 of the amyloid beta peptide, is
CC used in a pharmaceutical composition. This composition comprises an agent
CC capable of inhibiting interaction of an amyloid-beta peptide with a
CC receptor for advanced glycosylation end product and a carrier. A method
CC for inhibiting interaction of amyloid beta peptide with a receptor for
CC advanced glycosylation on the surface of a cell comprises contacting the
CC cell with e.g. present peptide. Depending on the type of cell, inhibiting
CC the interaction between the amyloid beta peptide and the receptor for
CC advanced glycosylation can be used for inhibiting degeneration of a
CC neuronal cell, inhibiting formation of an amyloid beta peptide fibril on
CC a cell, inhibiting extracellular assembly of amyloid beta peptide into a
CC fibril, inhibiting aggregation of amyloid beta peptide on the surface of
CC a cell, inhibiting infiltration of a microglial cell into senile plaques,
CC and inhibiting activation of microglial cells by amyloid beta peptide.
CC The methods can be used for treating e.g. diabetes, Alzheimer's Disease,
CC senility, renal failure, hyperlipidemic atherosclerosis, neuronal
CC cytotoxicity, Down's syndrome, dementia associated with head trauma,
CC atrophic lateral sclerosis, multiple sclerosis or neuronal
CC degeneration.
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 5
AAW37507
ID AAW37507 standard; peptide; 40 AA.
XX
XX AAW37507;
AC
XX
XX
DT 20-APR-1998 (first entry)
XX

DE Amyloid beta protein fragment (1-40) immunogen.

XX
XX Amyloid beta protein; A beta; immunogen; human; Alzheimer's disease;
KW amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.
XX
OS Synthetic.
OS
XX
XX Homo sapiens.
OS
XX

Key Location/Qualifiers
FH Cleavage-site 16..17
FT
XX
XX
PN EP783104-A1.
XX
XX 09-JUL-1997.
PD
XX 17-DEC-1996; 96EP-00120269.
PF
XX 27-DEC-1995; 95JP-00351296.
PR
XX (ORIT) ORIENTAL YEAST CO LTD.
PA
XX Taniguchi Y, Fujita T, Matuo Y;
PI
XX WPI; 1997-343989/32.
DR
XX

PT Assay for soluble amyloid precursor protein useful to diagnose
PT Alzheimer's disease - uses antibodies against amyloid beta-protein, also
XX new hybridoma producing antibodies.
XX

PS Example 1; Fig 2; 10pp; English.
 XX A novel method has been developed of assaying for soluble amyloid
 CC precursor protein (sAPP). The method uses an antibody against amyloid
 CC beta-protein (A beta; produced from sAPP) or sAPP. The present sequence
 CC represents amino acids 1 to 40 of amyloid beta-protein. sAPP can be
 CC assayed accurately, and when including a monoclonal antibody recognising
 CC the N-terminus of A beta and a monoclonal antibody recognising sAPP, the
 CC assay can be used to diagnose Alzheimer's disease. Senior plaque observed
 CC in the brain of Alzheimer's patients is primarily composed of A beta,
 CC which is generated from sAPP. Simple and accurate assay of sAPP is
 CC possible. The antibody (preferably monoclonal) preferably has an antigen
 CC recognition site which is an amino acid sequence common to A beta and
 CC sAPP, or specific to sAPP. The sAPP assayed for preferably has part of
 CC the A beta sequence at its amino terminus and is preferably solubilised
 CC through cleavage of the A beta between positions 16 (lysine) and 17
 CC (leucine) from the amino acid terminus. The preferred method comprises
 CC immobilising one antibody (especially generated by (2)) on to an
 CC insoluble carrier, capturing a substance to be assayed on to this
 CC antibody, reacting another, labelling, antibody with the assay substance
 CC and detecting the activity of the labelling substance bound to the
 CC carrier
 XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 6
 AAW47226 standard; peptide; 40 AA.
 XX
 AC AAW47226;
 XX
 DT 22-MAY-1998 (first entry)
 XX
 DE Beta-amyloid peptide residues 1-40.
 XX
 KM Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;
 KM Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS
 PN US5721106-A.
 XX
 PD 24-FEB-1998.
 XX
 PF 12-SEP-1994; 94US-00304585.
 XX
 PR 13-AUG-1991; 91US-00744767.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Mantyh PW, Maggio JE;
 PI
 DR WPI; 1998-168404/15.
 XX
 PT New in vitro screening assay for Alzheimer's disease drugs - comprises
 PT assessing binding of labelled beta-amyloid peptide to silk sample.
 XX
 PS Claim 8; Col 29-30; 36pp; English.
 XX
 CC The present sequence was used in the development of a novel in vitro
 CC screening assay for agents capable of affecting the deposition of beta-
 CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk
 CC sample with labelled BAP, optionally in the presence of a test agent,

CC detecting the amount of label bound to the silk and assessing the effect
 CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
 CC to silk are potentially useful for treating amyloidosis diseases,
 CC especially Alzheimer's disease
 XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 7
 AAY14099 standard; peptide; 40 AA.
 ID AAY14099 standard; peptide; 40 AA.
 XX
 AC AAY14099;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human beta-amyloid protein fragment.
 XX
 KM Beta-amyloid; human; amyloid plaque deposition; Alzheimer's disease;
 KM induction; AD; sleep; circadian activity; circadian rhythm disturbance.
 XX
 OS Homo sapiens.
 OS
 PN WO9921978-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1998; 98WO-US022731.
 XX
 PR 28-OCT-1997; 97US-00959148.
 XX
 PA (MIRI) MIRIAM HOSPITAL LIFESPAN PARTNER.
 XX
 PI Majocha R, Tate BA, Newton JL;
 PI
 DR WPI; 1999-326700/27.
 XX
 PT Inducing amyloid plaque deposition in a mammal, used to screen for agents
 PT against Alzheimer's disease.
 XX
 PS Claim 2; Page 30; 43pp; English.
 XX
 CC This sequence represents a fragment of the human beta-amyloid protein,
 CC and can be used in the method of the invention. The method is for
 CC inducing amyloid plaque deposition in a mammal by infusing into the brain
 CC an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque
 CC deposition has been induced are models of human Alzheimer's disease (AD)
 CC and are used to screen for agents (A) that inhibit: (a) deposition of
 CC amyloid plaque; and (b) AD-associated disruptions to sleep and circadian
 CC activity. They may also be used to study the etiology of AD. Compared
 CC with known methods for inducing plaque deposition, this process causes
 CC less mechanical damage; the vehicle used is less neurotoxic and at basic
 CC pH (I) is soluble enough for delivery by continuous infusion with
 CC effective delivery to brain tissue. The control peptide causes few, if
 CC any, plaques and does not stimulate an immune response. Most (I)-treated
 CC animals develop AD-type pathology (contrast transgenic models of the
 CC disease), including sleep and circadian rhythm disturbances
 XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 8

ID AAY39804 standard; peptide; 40 AA.

XX AAY39804;

DT 29-NOV-1999 (first entry)

DE Beta-amyloid protein, Beta/A4 amyloid (1-40).

XX Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
 KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KW Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
 KW subacute spongiform encephalopathy; therapy.

OS Homo sapiens.

XX US5958883-A.

PD 28-SEP-1999.

PF 05-JUN-1995; 95US-00461216.

XX 23-SEP-1992; 92US-00950417.

PR 23-OCT-1992; 92US-00969734.

PA (UNITV) UNIV WASHINGTON.

XX Snow AD;

DR WPI; 1999-561062/47.

PT Peptides of 6-8 amino acids useful for treating or preventing
 XX amyloidosis.

PS Disclosure; Col 67-68; 83pp; English.

CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 9
 AAW95584
 ID AAW95584 standard; peptide; 40 AA.

XX AAW95584;

XX 22-JUN-1999 (first entry)

DT Wild type aggregating amyloid-beta peptide.

XX Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KW diagnosis; Alzheimer's disease.

XX Synthetic.

OS Homo sapiens.

XX WO908695-A1.

PD 25-FEB-1999.

PF 13-AUG-1998; 98WO-US016809.

XX 14-AUG-1997; 97US-0055660P.

PA (REGC) UNIV CALIFORNIA.

XX Glabe C, Garzon-Rodriguez W;

XX WPI; 1999-190112/16.

DR New fluorescent labeled amyloid A-beta peptides.

PT Example 1; Page 21; 50pp; English.

CC This sequence corresponds to an aggregating amyloid-beta peptide which
 CC can be covalently labeled with a fluorescent group. The detection or
 CC monitoring of an amyloid aggregate in a sample can be used to diagnose or
 CC detect a predisposition to Alzheimer's disease. The screening assays can
 CC be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid-beta peptide are also useful for exploring other aspects of
 CC amyloid structure

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 10

ID AAW81473 standard; peptide; 40 AA.

XX AAW81473;

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).

XX Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.

XX Synthetic.

XX US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 96US-00609090.

XX 29-FEB-1996; 96US-00609090.

PA (KENT) UNIV KENTUCKY RES FOUND.

XX Aksenov M, Carney JM, Hensley K, Butterfield DA;
 PI WPI; 1999-034120/03.
 DR WPI; 1999-034120/03.
 XX Process for treating synthetic amyloid beta peptides - by organic solvent
 PT treatment, useful for studying neurotoxicity.
 XX Claim 5; Col 11-12; 14pp; English.
 CC Sequences AAM8166 to AAM81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic Abeta
 CC peptide that comprises dissolving the peptide in a deoxygenated solvent
 CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution
 CC at 20-65 deg C for 0.5-4 hour, and removing the solvent by "evaporative
 CC deposition" in 5-10 minutes. Synthetic amyloid beta peptides are useful
 CC as research tools for studying neurotoxicity resulting from Abeta peptide
 CC -enhanced free-radical production. The treatment increases the activity
 CC of the synthetic Abeta peptides in tests to determine free-radical
 CC generating capacity and glutamine synthetase inactivation
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
 RESULT 11
 ID AAY39339 standard; protein; 40 AA.
 XX AAY39339;
 AC AAY39339;
 DT 01-DEC-1999 (first entry)
 XX Beta-amyloid protein.
 DE Beta-amyloid protein.
 XX Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;
 KM cerebral blood vessel; sulphated macromolecule; Kuru;
 KM congoophilic malsee-cross spherical amyloid plaque;
 KM Creutzfeldt-Jacob disease; Gertsmann-Straussler syndrome.
 XX Homo sapiens.
 OS
 XX MO9945947-A1.
 PN
 PD 16-SEP-1999.
 XX 12-MAR-1999; 99WO-US005438.
 PF
 XX 13-MAR-1998; 98US-0077924P.
 PR
 XX (UNIV) UNIV WASHINGTON.
 PA
 XX Castillo G, Snow AD;
 PI WPI; 1999-571686/48.
 DR WPI; 1999-571686/48.
 XX Formation of amyloid plaques using amyloid protein and sulfated
 PT macromolecules, for, e.g. identification of agents for treating
 PT Alzheimer's disease.
 XX Claim 3; Page 87; 89pp; English.
 XX This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's
 CC disease is characterised by the accumulation of a 39-43 amino acid

CC peptide termed the beta-amyloid peptide in the form of extracellular
 CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.
 CC The invention relates to methods for the formation of congoophilic malsee
 CC -cross spherical amyloid plaques, which are characteristic of Alzheimer's
 CC disease. The amyloid plaques are formed by co-incubation of this beta-
 CC amyloid protein with sulphated macromolecules. The methods can be used to
 CC study the formation of amyloid plaques and to identify anti-plaque
 CC therapeutics. They can be used for diseases such as Alzheimer's disease,
 CC Creutzfeldt-Jacob disease, Gertsmann-Straussler syndrome and Kuru
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
 RESULT 12
 ID AAY25135 standard; peptide; 40 AA.
 XX AAY25135;
 AC AAY25135;
 DT 26-AUG-1999 (first entry)
 XX Human amyloid beta-A4 peptide 2.
 DE Human amyloid beta-A4 peptide 2.
 XX Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KM therapeutic drug; brain; Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX US5919631-A.
 PN
 PD 06-JUL-1999.
 XX 17-JUL-1996; 96US-00682245.
 PF
 XX 17-JUL-1996; 96US-00682245.
 PR
 XX 17-JUL-1996; 96US-00682245.
 PR
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 PA
 XX Sahaerabudhe SR, Paul JW, Goyal S, Riedel NG;
 PI WPI; 1999-403957/34.
 DR WPI; 1999-403957/34.
 XX Determination of degree of aggregation of a peptide, useful for
 PT identifying therapeutic drugs for treating Alzheimer's disease.
 PT
 XX Disclosure; Col 5-6; 8pp; English.
 PS
 XX This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated (I) with
 CC Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
 CC (I); (b) measuring the amount of (II) bound to (I) to obtain a value (1);
 CC (c) repeating steps (a) and (b) with a second sample at a different time
 CC to obtain a second value (11); and (d) determining the difference between
 CC (1) and (11) which is inversely related to the degree of aggregation of
 CC (I). This method may be applied to a screen for compounds that inhibit
 CC aggregation of (I). These inhibitors may be used as therapeutic drugs to
 CC inhibit the formation of these aggregates in the brains of patients
 CC suffering from Alzheimer's disease
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 |||||||
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 13

AAW92723
 ID AAW92723 standard; peptide; 40 AA.

XX AAW92723;

XX 20-MAR-2003 (revised)

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #69.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

PF 29-JUL-1991; 91US-00737371.

XX 27-JUL-1990; 90US-00559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

XX WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells.

XX Claim 1b; Col 41-42; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inherited congenital angiodopathy with cerebral haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF field.)

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 |||||||
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 14

AAW84426
 ID AAW84426 standard; peptide; 40 AA.

XX AAW84426;

XX 22-AUG-2001 (first entry)

DE Partial sequence of a human beta-amyloid precursor protein.

XX Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KW vaccine.

XX Homo sapiens.

XX WO200142306-A2.

XX 14-JUN-2001.

PF 08-DEC-2000; 2000MO-US033203.

XX 08-DEC-1999; 99US-0169687P.

XX (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

PI Chain B;

XX WPI; 2001-381648/40.

PT Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to T cell epitope.

XX Claim 3; Page 41; 47pp; English.

XX The present sequence represents a partial sequence of a human beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a N- or C-terminal end-specific B cell epitope from a naturally occurring internal peptide cleavage product of a precursor or mature protein, as a free N- or C-terminus, joined to a T cell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betaAPP peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They also block the interaction of amyloid beta peptides with other molecules that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide cleavage product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 |||||||
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 15

AAW91813
 ID AAW91813 standard; peptide; 40 AA.

XX AAW91813;

XX 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:989.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidyl; maleimido group; amino;

KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

XX Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.
 PD 17-MAY-2000; 2000MO-US013576.
 PF 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONT-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 518; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SO Sequence 40 AA;
 QY
 Query Match 100.0%; Score 209; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DAEFRHDSGYEVHOKLVFPFAEDVGSNKGAIIGLMVGVV 40
 1 DAEFRHDSGYEVHOKLVFPFAEDVGSNKGAIIGLMVGVV 40
 RESULT 16
 AAB91780
 ID AAB91780 standard; peptide: 40 AA.
 XX
 AC AAB91780;
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:956.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 PR 17-MAY-2000; 2000MO-US013576.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX
 PA (CONT-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 506; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SO Sequence 40 AA;
 QY
 Query Match 100.0%; Score 209; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DAEFRHDSGYEVHOKLVFPFAEDVGSNKGAIIGLMVGVV 40
 1 DAEFRHDSGYEVHOKLVFPFAEDVGSNKGAIIGLMVGVV 40
 RESULT 17
 AAB91829
 ID AAB91829 standard; peptide: 40 AA.
 XX
 AC AAB91829;
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:1005.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 PR 17-MAY-2000; 2000MO-US013576.
 PR 10-SEP-1999; 99US-0134406P.
 PR 15-OCT-1999; 99US-0159783P.
 PR 17-MAY-1999; 99US-0153406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 PR (CONT-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 523; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
RESULT 18
AAB91802
ID AAB91802 standard; peptide; 40 AA.
XX
AC AAB91802;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:978.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONT-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
XX WPI; 2001-112059/12.
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX

PS Disclosure; Page 514; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
RESULT 19
AAB05483
ID AAB05483 standard; peptide; 40 AA.
XX
AC AAB05483;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human peptide antigen comprising beta amyloid (Abeta) 40.
XX
XX Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive;
XX neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
XX age-related cognitive function loss; senile dementia; Wilson's disease;
XX Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;
XX cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
XX Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
XX Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
XX myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
XX Gilles de la Tourette's syndrome; nootropic; chronic seizure disorder;
XX brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
XX AIDS; dementia; alcoholism; autism; retinal ischemia; ophthalmological;
XX autonomic function disorder; Friedreich's ataxia; schizophrenia; therapy;
XX vasotrophic; neuroprotective; anti-HIV; human immunodeficiency virus;
XX anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
OS Homo sapiens.
XX
PN WO200152890-A1.
XX
XX 26-JUL-2001.
XX
PD 18-JAN-2001; 2001WO-US001825.
XX
PF 21-JAN-2000; 2000US-00489216.
XX
PR (UYCO-) UNIV CONNECTICUT HEALTH CENT.
XX
XX Srivastava PK;
XX
XX WPI; 2001-451897/48.
DR
XX
PT Heat shock protein and antigenic molecule complexes, useful for the

PT prevention and treatment of neurodegenerative disorders e.g. senile
 PT dementia, Alzheimer's disease and epilepsy.
 XX
 PS Disclosure; Page 13; 65pp; English.
 XX
 CC The present invention relates to pharmaceutical compositions comprising
 CC complexes of heat shock proteins (hsp) in association with antigenic
 CC molecules for use in treatment and prevention of neurodegenerative
 CC disorders and diseases. The complexes of hsp and antigenic peptides are
 CC used as vaccines for the treatment or prevention of neurodegenerative
 CC disorders e.g. Alzheimer's disease, age-related loss of cognitive
 CC function, senile dementia, Parkinson's disease, amyotrophic lateral
 CC sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear
 CC palsy, Guam disease, Lewy body dementia, prion diseases, spongiform
 CC encephalopathies, Creutzfeldt-Jacob disease, polyglutamine diseases,
 CC Huntington's disease, myotonic dystrophy, Friedreich's ataxia, ataxia,
 CC Gilles de la Tourette's syndrome, seizure disorders, epilepsy, chronic
 CC seizure disorder, stroke, brain trauma, spinal cord trauma, acquired
 CC immunodeficiency syndrome (AIDS) dementia, alcoholism, autism, retinal
 CC ischaemia, glaucoma, autonomic function disorder, hypertension,
 CC neuropsychiatric disorder, schizophrenia or schizoaffective disorder and
 CC for eliciting an immune response. The present sequence is human peptide
 CC antigen comprising beta amyloid (Abeta) 40
 CC
 SQ Sequence 40 AA;
 QY
 Query Match 100.0%; Score 209; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2,1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 QY
 RESULT 20
 AAU99425 standard; peptide; 40 AA.
 XX
 AC AAU99425;
 DT 07-OCT-2002 (first entry)
 XX
 DE Human amyloid beta-peptide (Abeta) fragment (residues 1-40).
 XX
 KM I-helical conformation; discordant helix; amyloid beta-peptide; I-helix;
 KM theta-strand structure; amyloidogenic disorder; Abeta; amyloidosis;
 KM Alzheimer's disease; prion disease; scrapie; BSE;
 KM bovine spongiform encephalopathy; Creutzfeldt-Jacob disease; CJD;
 KM fibrillation; aggregation; neurotropic; neuroprotective; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200241002-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-GB005117.
 XX
 PR 20-NOV-2000; 2000US-0253695P.
 PR 06-DEC-2000; 2000US-0251662P.
 XX
 PA (ALPH-) ALPHABETA AB.
 PA (WHIT/) WHITE M P.
 PI White MP, Johansson J;
 XX
 DR WPI; 2002-519389/55.
 XX
 PT Identifying compounds that stabilize I-helix of discordant helix in
 PT polypeptide, by measuring amount of I-helix in sample containing
 PT discordant helix-containing polypeptide in presence and absence of
 PT compound.

XX
 PS Example 4; Page 34; 55pp; English.
 XX
 CC The present invention relates to a method of identifying a compound that
 CC stabilises an I-helical conformation of a discordant helix in a
 CC polypeptide, particularly amyloid beta-peptide (Abeta). The method
 CC comprises providing a test sample comprising a polypeptide that contains
 CC a discordant helix in the form of an I-helix, contacting the test sample
 CC with a test compound and determining the rate of decrease in the amount
 CC of I-helix or the amount of I-helix present in the test sample. The
 CC method is useful for identifying a compound that stabilises an I-helical
 CC conformation of a discordant helix in a polypeptide. Such compounds are
 CC useful for decreasing the rate of formation of thet-strand structures
 CC between at least two discordant helix-containing polypeptides, and for
 CC treating amyloidogenic disorders such as amyloidosis in Alzheimer's
 CC disease, and prion diseases (e.g. scrapie, bovine spongiform
 CC encephalopathy (BSE), Creutzfeldt-Jacob disease (CJD)). The present
 CC sequence represents human Abeta fragment (amino acid residues 1-40)
 CC
 SQ Sequence 40 AA;
 QY
 Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2,1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 QY
 RESULT 21
 AAE22990 standard; peptide; 40 AA.
 XX
 AC AAE22990;
 DT 21-AUG-2002 (first entry)
 XX
 DE Human amyloid-beta (A-beta) peptide.
 XX
 KM Human; low-density lipoprotein receptor related protein-1; depression;
 KM Alzheimer's disease; neurodegenerative disorder; Huntington's disease;
 KM Parkinson's disease; multiple sclerosis; Creutzfeldt-Jacob disease;
 KM dementia; LRP-1; confusion; stroke; amyloid-beta peptide; A-beta.
 XX
 OS Homo sapiens.
 XX
 PN WO200190758-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016561.
 XX
 PR 23-MAY-2000; 2000US-0206428P.
 PR 06-NOV-2000; 2000US-0246268P.
 XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 PA Zlokovic BV;
 PI
 XX
 DR WPI; 2002-083127/11.
 XX
 PT Method for diagnosing Alzheimer's disease or identifying individual at
 PT risk of developing disease.
 XX
 PS Example; Page 17; 46pp; English.
 XX
 CC The invention relates to a method for diagnosing Alzheimer's disease or
 CC identifying an individual at risk of the developing the disease. The
 CC method involves measuring abundance of low-density lipoprotein receptor
 CC related protein-1 (LRP-1) abundance of transcripts thereof, or LRP-1
 CC receptor activity. The method is useful for treating neurodegenerative
 CC disorders such as dementia, depression, confusion, Creutzfeldt-Jacob

CC disease, Huntington's disease, Parkinson's disease, multiple sclerosis,
 CC loss of motor coordination, stroke and syncope. The present sequence is
 CC human amyloid-beta (A-beta) peptide used in the exemplification of the
 CC invention

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40

RESULT 22

AA68313 ID AAG68313 standard; peptide; 40 AA.

XX AAG68313;

XX 21-FEB-2002 (first entry)

DE Human beta amyloid related amino acid sequence SEQ ID NO:1.

XX Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;

KM amyloid precursor protein; APP.

XX Homo sapiens.

XX WO200182967-A1.

XX 08-NOV-2001.

XX 25-APR-2001; 2001WO-JP03555.

XX 28-APR-2000; 2000JP-00131037.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX (SUZU) SUZUKI T.

XX Suzuki T, Watanabe T, Kawabata S, Hachiya S;

XX WPI; 2002-026209/03.

XX Medicinal compositions for the treatment of dementia and Alzheimer's
 XX disease, comprise compounds that suppress beta amyloid production.

XX Example 1; Page 30; 62pp; Japanese.

XX The present invention describes medicinal compositions (I) inhibiting
 CC beta-amyloid production comprising an active component a substance that
 CC inhibits the activity of cyclin-dependent kinase (CDK). Also described
 CC are: (1) a method for screening compounds for their ability to inhibit
 CC the production of beta-amyloid by contacting with beta-amyloid producing
 CC cells; and (2) screening kits. (I) have neurotropic and neuroprotective
 CC activities. (I) suppress the phosphorylation of amyloid precursor protein
 CC (APP) which is an essential step in the production of beta-amyloid. (I)
 CC can be used in the treatment and prevention of neurodegenerative diseases
 CC such as dementia and Alzheimer's disease. The present sequence represents
 CC the A beta 1-40 amino acid sequence which is used in an example from the
 CC present invention

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40

RESULT 23

AAU96895 ID AAU96895 standard; peptide; 40 AA.

XX AAU96895;

XX 27-AUG-2002 (first entry)

DE Human self-associating Amyloid beta 1-40 peptide.

XX Human; amyloid beta; cell death; neuron death; Alzheimer's disease;

KM neurotropic; neuroprotective; apoptotic.

XX Homo sapiens.

XX JP2002105099-A.

XX 10-APR-2002.

XX 28-SEP-2000; 2000JP-00295577.

XX 28-SEP-2000; 2000JP-00295577.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 2002-458303/49.

XX A self-associating type amyloid beta protein.

XX Example 1; Page 9; 14pp; Japanese.

XX The invention relates to a self-associating type amyloid beta protein of
 CC particle form having an activity of inducing cell death in nervous system
 CC cells at a protein concentration of not higher than 1 micro g/ml. Also
 CC included are (1) a method for the preparation of a solution containing a
 CC self-associating type amyloid beta protein having high toxicity including
 CC a step of connecting aqueous solution containing the amyloid beta protein
 CC and a step of fractionating the solution containing the self-associating
 CC type amyloid beta protein in the connected aqueous solution; (2) a
 CC reagent containing the above self-associating type amyloid beta protein;
 CC (3) a method for inducing cell death in nervous system cells by using the
 CC above self-associating type amyloid beta protein; (4) a method for
 CC screening a drug having inhibiting activity on neuron death; a substance
 CC having an inhibiting activity on neuron death prepared by the above
 CC method; and (6) a drug for preventing and/or treating Alzheimer's disease
 CC containing the above substance as the active component. The drug is used
 CC for preventing and/or treating Alzheimer's disease. The present sequence
 CC is a human amyloid beta 1-40 peptide used in an example demonstrating
 CC preparation of the particle of the invention

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGVV 40

RESULT 24

AAU50909 ID AAU50909 standard; protein; 40 AA.

XX AAU50909;

XX 07-MAY-2002 (first entry)

XX Beta amyloid protein amino acid residues 1-40.

XX

KW Beta amyloid protein; beta/A4; amyloidosis; Alzheimer's disease;
 KW amyloid deposition; human; animal model.
 XX
 OS Homo sapiens.
 PN US6340783-B1.
 PD 22-JAN-2002.
 PF 03-OCT-1996; 96US-00723661.
 PR 23-SEP-1992; 92US-00950417.
 PR 23-OCT-1992; 92US-00969734.
 PR 05-JUN-1995; 95US-00461216.
 XX
 PA (UNIV) UNIV WASHINGTON.
 PI Snow AD;
 DR WPI; 2002-146857/19.
 XX
 PT Rodent models for studying amyloid deposition in Alzheimer's disease and
 PT for identifying candidate therapeutic agents.
 PS Disclosure; Col 67; 78pp; English.
 XX
 PS The present sequence is that of a protein comprising amino acids 1-40 of
 CC beta amyloid protein (or beta/A4). The invention provides a method for
 CC producing a rodent (especially rat) model of Alzheimer's disease, which
 CC involves infusing a proteoglycan and a beta-amyloid protein into the
 CC brain (preferably the hippocampus) of the rodent for a time sufficient to
 CC allow co-deposition, and detecting the amyloid deposit in the brain
 CC tissue using staining techniques (Congo Red or thioflavin S) for
 CC fibrillar amyloid. The beta amyloid protein is preferably comprised of 39
 CC -43 amino acids. The present peptide has the ability to self-aggregate
 CC and fold into a specific beta-pleated sheet. This can be observed using
 CC Congo Red staining. Inhibition of staining indicates that an inhibitor
 CC has altered the secondary structure of the amyloid protein. In an in vivo
 CC assay for selecting a candidate therapeutic for inhibiting fibrillar
 CC amyloid deposition/persistence in the brain, the candidate reagent is
 CC administered to a rodent in an infusate comprising beta/A4 peptide and
 CC perlecan by continuous infusion for at least 1 week into the hippocampus.
 CC The candidate reagent is selected as a candidate therapeutic for
 CC the amyloid and fibrillar beta/A4 amyloid deposition in the brain if the
 CC Congo Red and thioflavin S staining indicates that the candidate reagent
 CC infusate diminishes Congo Red and thioflavin S staining indicative of
 CC amyloid deposition adjacent to the infusion site as compared to a control
 CC rodent receiving an infusate not comprising the candidate reagent. The
 CC rodent model is used to study the process of amyloidosis that occurs in
 CC Alzheimer's disease, and to identify therapeutic agents (e.g. heparin,
 CC heparan sulfate glycosaminoglycans and related macromolecules and heparin
 CC binding peptides) that may be used for the treatment of Alzheimer's and
 CC other amyloidosis diseases
 XX
 SQ Sequence 40 AA;
 QY Query Match 100.0%; Score 209; DB 5; Length 40;
 DB Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 25
 AAU80186
 ID AAU80186 standard; peptide; 40 AA.
 XX
 AC AAU80186;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Amyloid beta peptide residues 1-40.

XX
 KW Amyloid beta; Alzheimer's disease; familial Alzheimer's disease;
 KW Down's syndrome; apolipoprotein E4; neurotrophic; neuroprotective;
 KW thioflavin; polycyclic compound.
 XX
 OS Unidentified.
 PN WO200216333-A2.
 PD 28-FEB-2002.
 PF 24-AUG-2001; 2001WO-US026427.
 PR 24-AUG-2000; 2000US-0227601P.
 XX
 PA (UYPI-) UNIV PITTSBURGH.
 PI Klunk WE, Machis CA, Wang Y;
 DR WPI; 2002-382815/41.
 XX
 PT New thioflavin derivatives, useful as amyloid binding agents for in vivo
 PT imaging of amyloid deposits.
 PS Disclosure; Page 51; 11pp; English.
 XX
 PS The invention relates to amyloid binding polycyclic derivatives
 CC especially thioflavin derivatives. The full structures of the compounds
 CC are given in the specification. Also included are methods for making the
 CC compounds; compositions for in vivo imaging of amyloid deposits
 CC comprising the novel compounds and an in vivo method for detecting
 CC amyloid deposits. The compounds show a KD for binding to Amyloid beta 1-
 CC 40 peptide of 0.0001 to 10mM. The compounds are useful for in vivo
 CC imaging of amyloid deposits. The compounds are also useful for treating
 CC Alzheimer's disease, familial Alzheimer's disease, Down's syndrome and
 CC conditions associated with apolipoprotein E4 alleles. The present
 CC sequence is the amyloid beta 1-40 peptide used to test the compounds of
 CC the invention
 XX
 SQ Sequence 40 AA;
 QY Query Match 100.0%; Score 209; DB 5; Length 40;
 DB Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 26
 AAU26332
 ID AAU26332 standard; peptide; 40 AA.
 XX
 AC AAU26332;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Human beta-amyloid peptide mutant (Abeta residues 1-40).
 XX
 KW Human; amyloidogenic protein; Alzheimer's disease; Huntington's disease;
 KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;
 KW Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS;
 KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytia; myeloma;
 KW C; beta-amyloid; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200242462-A2.
 XX
 PD 30-MAY-2002.
 XX

PF 27-NOV-2001; 2001WO-US044581.
 XX
 PR 27-NOV-2000; 2000US-0253302P.
 XX 29-NOV-2000; 2000US-0250198P.
 PR 20-DEC-2000; 2000US-0257186P.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Gefter ML, Israel DI, Joyal JL, Gosselin M;
 XX WPI; 2002-636427/68.
 DR
 XX Novel therapeutic agent useful for treating an amyloidogenic disorder,
 PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain
 PT constant region linked to a peptide capable of binding amyloidogenic
 PT protein.
 PS
 XX Claim 18; Page; 79pp; English.
 PS
 XX The invention relates to a compound comprising an immunoglobulin (Ig)
 CC heavy chain constant region or its fragment that retains the ability to
 CC bind an Fc receptor linked by a linker group or a direct bond to a
 CC peptide capable of binding an amyloidogenic protein. The invention is
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,
 CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide
 CC (IAPP), atrial natriuretic factor (ANP), kappa light chain, lambda light
 CC chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,
 CC gelsolin, calcitonin, fibrinogen, Huntingtin, alpha-synuclein and
 CC lysozyme from a subject and for treating an amyloidogenic disorder such
 CC as Alzheimer's disease and spongiform encephalopathy. Disorders treatable
 CC include those caused or characterised by deposits of TTR (eg. familial
 CC amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including
 CC scrapie in sheep, bovine spongiform encephalopathy in cows and
 CC Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker
 CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
 CC ANP (eg. isolated atrial amyloid), kappa or lambda light chain (eg.
 CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I
 CC (eg. hereditary non-neuropathic systemic amyloidosis), gelsolin (eg.
 CC familial amyloidosis of Finnish type), fibrinogen (eg. hereditary renal
 CC amyloidosis), lysozyme (eg. hereditary systemic amyloidosis). Other
 CC examples of amyloidogenic disorders include Huntingtin's disease and
 CC inclusion body myocytis. The present sequence is human beta-amyloid
 CC peptide mutant. Note: This sequence is not shown in the specification but
 CC is derived from human beta-amyloid peptide shown as SEQ ID NO: 1
 CC (AAE26265) in the specification
 CC
 SQ Sequence 40 AA;
 XX
 SQ
 Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 27
 AAMS1863
 ID AAMS1863 standard; protein; 40 AA.
 XX
 AC AAMS1863;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human amyloid beta protein.
 XX
 KM Human; amyloid beta; neurone death inhibition; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN JP2001255318-A.
 XX

PD 21-SEP-2001.
 XX
 XX
 PF 09-MAR-2000; 2000JP-00064984.
 XX
 PR 09-MAR-2000; 2000JP-00064984.
 XX
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 DR WPI; 2002-003272/01.
 XX
 PT Screening method for identifying drugs which inhibit neuron cell death
 PT comprises culturing the cells, exposing to high concentrations of self-
 PT associating Beta amyloid protein, and assessing the inhibitory action of
 PT the drug on cell death.
 PS
 XX Example; Page 7; 11pp; Japanese.
 XX
 CC The present invention relates to a method of screening drugs that exhibit
 CC inhibitory action on neurone death, involving culturing neuronal cells,
 CC exposing them to a self-associating type amyloid beta protein of high
 CC toxicity, and assessing if the sample has had an inhibitory action on
 CC neurone death when the cell death of said nervous system cells or nervous
 CC system organs is inhibited. The method is used for screening a drug
 CC having inhibitory action on neurone death, which can then be used to
 CC treat Alzheimer's disease. The present sequence is the human amyloid beta
 CC protein
 CC
 SQ Sequence 40 AA;
 XX
 SQ
 Query Match 100.0%; Score 209; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVV 40
 RESULT 28
 ABU08710
 ID ABU08710 standard; protein; 40 AA.
 XX
 AC ABU08710;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Amyloid beta protein 40 (Abeta 40).
 XX
 KM Amyloid beta; Abeta; amyloid beta A; nootropic; neuroprotective;
 KM gene therapy; alzheimer's disease.
 OS
 XX Unidentified.
 PN WO2003012141-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 01-FEB-2002; 2002WO-JP000836.
 XX
 PR 31-JUL-2001; 2001JP-00266510.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
 PA (KOMA/) KOMANO H.
 XX
 PI Komano H;
 XX
 DR WPI; 2003-239531/23.
 XX
 PT Screening gene controlling production of amyloid Beta, applicable in
 PT diagnosis of and developing drugs for Alzheimer's disease.
 XX
 PS Disclosure; Page 101; 115pp; Japanese.
 PS

XX
CC The invention describes a method of screening a DNA controlling the
CC production of amyloid protein (Abeta) by transferring a DNA library into
CC a cell line with enhancement of expression of a selection marker gene in
CC promoting the Abeta production from a precursor protein (betaAPP)
CC fragment of Abeta, then identifying a DNA clone for transferring into a
CC cell to enhance Abeta production. The methods are useful for screening
CC genes that control production of amyloid beta. The genes, encoded protein
CC and related DNA materials are useful in the diagnosis and development of
CC drugs for Alzheimer's disease. This is the amino acid sequence of amyloid
CC beta protein 40 (Abeta 40), a 40 residue amyloid beta protein fragment
SQ Sequence 40 AA;
Query Match 100.0%; Score 209; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db
RESULT 29
ABU08508
ID ABU08508 standard; peptide; 40 AA.
XX
XX AC ABU08508;
XX
XX 22-MAY-2003 (first entry)
XX
XX Human amyloid beta peptide (1-40).
DE
XX Human amyloid beta peptide (1-40); Alzheimer's disease; antigen; Abeta.
KM
XX Homo sapiens.
OS
XX
XX US2002182660-A1.
PN
XX
XX 05-DEC-2002.
PD
XX
XX 18-JAN-2002; 2002US-0005196.
PF
XX 18-FEB-2000; 2000US-0183407P.
PR
XX 16-FEB-2001; 2001US-00784854.
PS
XX (FONG/) FONG K L.
XX
XX Fong KL;
PI
XX WPI; 2003-328616/31.
DR
XX
XX Enabling measurement of full length beta-amyloid peptide level for
PT tracking progression of Alzheimer's disease, comprises capturing and
PT binding terminus of beta-amyloid peptide with antibodies.
XX
XX Disclosure; Fig 1d; 11pp; English.
PS
XX The invention relates to a measurement of the full length beta-amyloid
CC (Abeta) peptide level of a specific Abeta peptide in a sample containing
CC multiple types of Abeta peptide, by capturing and binding one terminus of
CC the types of Abeta peptides with a first antibody. The specific Abeta
CC peptide is captured and bound at an opposite non-overlapping terminus
CC with a second peptide. The invention is used for measuring full length
CC Abeta peptide level useful for tracking the progression of Alzheimer's
CC disease. The new method uses one specific antibody that recognizes the N-
CC terminus of all the Abeta peptides and a panel of detection antibodies
CC that distinguish each Abeta peptide (Abeta 1-43, 1-42, 1-41, 1-40 and 1-
CC 39) by their sequence difference at the C-terminus. This use of N and C-
CC terminus specific antibodies allows simultaneous quantification of
CC several Abeta peptides in a single assay. The present sequence is that of
CC Abeta (1-40), used to raise the N and C-terminal antibodies of the
CC invention

XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 209; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db
RESULT 30
AAO19885
ID AAO19885 standard; peptide; 40 AA.
XX
XX AC AAO19885;
XX
XX 11-AUG-2003 (first entry)
XX
XX Human amyloid precursor protein APP immunogenic peptide #5.
DE
XX
XX Human; APP; amyloid precursor protein; immunogen; Alzheimer's disease;
KM high-throughput screening; neuroprotective; neurotropic; antiparkinsonian.
XX
XX Homo sapiens.
OS
XX WO2003001881-A2.
PN
XX
XX 09-JAN-2003.
PD
XX
XX 26-JUN-2002; 2002WO-US020267.
PF
XX
XX 26-JUN-2001; 2001US-030959P.
PR
XX
XX (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.
PA
XX Mathews PM, Nixon RA, Schmidt SD, Jiang Y;
PI
XX WPI; 2003-210182/20.
DR
XX
XX Identifying compounds that modulates the generation of metabolites
PT associated with a disease or disorder, for treating e.g. Alzheimer's
PT disease by determining levels of a cellular component protein, or its
PT conformation state.
XX
XX Example 1; Page 29; 69pp; English.
PS
XX The present invention relates to a method of identifying compounds that
CC modulate the generation of one or more metabolites associated with a
CC disease or disorder comprising determining levels of a cellular component
CC protein or a conformation state of a cellular precursor protein. In
CC particular, the method can be used to determine levels of amyloid
CC precursor protein (APP), which is associated with Alzheimer's disease. It
CC is also useful for identifying compounds as drugs for treating diseases
CC or disorders associated with metabolic and/or proteolytic pathways, e.g.,
CC Alzheimer's disease, Parkinson's disease, Huntington's disease, lysosomal
CC storage disorders, prion diseases, the tau-based neurodegenerative
CC disorders, and other non-AD amyloidoses. The present sequence is an
CC immunogenic portion of human APP
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 209; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db
Search completed: September 28, 2006, 06:10:50

Thu Sep 28 14:21:04 2006

us-09-731-899-2.rag

Page 15

job time : 108.906 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 16.5022 Seconds
(without alignments)
233.221 Million cell updates/sec

Title: US-09-731-899-2
Perfect score: 209
Sequence: 1 DAEFRHDSGYEHQKLVFPAEDVGSNKGAIGIMVGVV 40

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	42	2	beta-amyloid prote
2	209	100.0	57	2	Alzheimer's diseas
3	209	100.0	57	2	Alzheimer's diseas
4	209	100.0	57	2	Alzheimer's diseas
5	209	100.0	57	2	Alzheimer's diseas
6	209	100.0	57	2	Alzheimer's diseas
7	209	100.0	57	2	Alzheimer's diseas
8	209	100.0	82	2	Alzheimer's diseas
9	209	100.0	695	1	Alzheimer's diseas
10	209	100.0	770	1	Alzheimer's diseas
11	190	90.9	695	2	Alzheimer's diseas
12	190	90.9	695	2	Alzheimer's diseas
13	190	90.9	747	2	Alzheimer's diseas
14	133	63.6	33	2	beta-amyloid prote
15	57	27.3	327	2	genome polyprotein
16	56.5	27.0	378	2	SG1 protein - yea
17	56	26.8	755	2	tryptophan 2-monoo
18	55.5	26.6	678	2	3-methyl-2-oxobuta
19	55	26.3	291	2	glycosyl transfera
20	55	26.3	317	2	glycosyl transfera
21	55	26.3	488	2	probable aldehyde
22	55	26.3	503	2	general amino acid
23	55	26.3	755	1	tryptophan 2-monoo
24	55	26.3	3063	2	genome polyprotein
25	54.5	26.1	832	2	3-methyl-2-oxobuta
26	54.5	26.1	832	2	phospholipase D [1
27	54	25.8	77	2	teoa-like protein,
28	54	25.8	284	2	genome polyprotein
29	54	25.8	755	1	tryptophan 2-monoo

30	53.5	25.6	708	2	T24727	hypothetical prote
31	53.5	25.6	971	2	D70128	conserved hypotet
32	53	25.4	256	2	G96774	hypothetical prote
33	53	25.4	422	2	D72302	hypothetical prote
34	53	25.4	601	2	T02581	nodulin-like prote
35	53	25.4	1555	2	UT0959	polypeptide - puta
36	52.5	25.1	678	2	C86495	hypothetical prote
37	52.5	25.1	678	2	H72128	3-methyl-2-oxobuta
38	52	24.9	272	2	F70979	hypothetical prote
39	52	24.9	417	2	F70132	conserved hypotet
40	52	24.9	527	2	T18232	conserved hypotet
41	51.5	24.6	297	2	G69525	formylmethanofuran
42	51.5	24.6	314	2	F86805	cation transporter
43	51.5	24.6	1364	2	T51920	probable xanthine
44	51	24.4	103	2	D75449	BUGE protein - Dei
45	51	24.4	257	2	AC1024	probable dimethyl
46	51	24.4	494	2	C70990	probable cobo prot
47	50.5	24.2	245	2	AH1098	a probable phospho
48	50.5	24.2	245	2	AG1461	probable phospho-b
49	50.5	24.2	519	2	PC1072	nuclear inclusion
50	50.5	24.2	763	2	AI3443	Na+/H+ antiporter
51	50.5	24.2	833	2	T01547	probable phosphol
52	50.5	24.2	1345	2	S55669	tegument protein 7
53	50	23.9	234	2	G95989	hypothetical glyci
54	50	23.9	285	1	B64105	naphthoate synthas
55	50	23.9	296	2	A69856	polysugar degradin
56	50	23.9	441	2	T31482	hypothetical prote
57	50	23.9	2178	2	S55805	alpha-toxin - C108
58	49.5	23.7	311	2	G86324	hypothetical prote
59	49	23.4	82	2	AF3441	hypothetical prote
60	49	23.4	339	2	A81351	signal transductio
61	49	23.4	469	2	C90446	permease, multidu
62	49	23.4	489	2	F82085	glutamate synthase
63	49	23.4	527	2	A43938	Pseudomonas cytoch
64	49	23.4	533	2	E84858	phosphoprotein pho
65	49	23.4	568	1	OSP5A	Pseudomonas cytoch
66	49	23.4	577	2	A84681	nodulin-like prote
67	49	23.4	611	2	S19434	probable transport
68	49	23.4	649	2	S58064	hdc protein - fru1
69	49	23.4	704	2	A34287	serge protein 2
70	49	23.4	769	1	UC1121	leukocyte adhesion
71	49	23.4	891	2	G96636	hypothetical prote
72	49	23.4	946	1	UC5667	multidrug resistan
73	49	23.4	1150	2	AB0064	probable membrane
74	48.5	23.2	144	2	AC2572	hypothetical prote
75	48.5	23.2	165	2	H90519	ABC transporter at
76	48.5	23.2	330	2	A26205	coat protein precu
77	48.5	23.2	330	2	B95954	probable membrane-
78	48.5	23.2	393	2	S59499	cellulase eg11 - s
79	48.5	23.2	510	2	S55124	probable membrane
80	48.5	23.2	547	2	AD2350	acetylacate synth
81	48.5	23.2	614	2	B71551	probable s/c prote
82	48.5	23.2	1068	2	T48756	mitochondrial nico
83	48	23.0	269	2	S70710	naphthoate synthas
84	48	23.0	311	2	AH1628	L-lactate dehydrog
85	48	23.0	362	2	B72574	hypothetical prote
86	48	23.0	390	2	C75103	na+/h+ antiporter
87	48	23.0	409	2	S29124	membrane glycoprot
88	48	23.0	523	2	UC7556	linoleoyl-CoA desa
89	48	23.0	644	2	A97268	methionyl-tRNA syn
90	48	23.0	656	2	B86289	probable serine/th
91	48	23.0	703	2	B34434	arylboron beta ch
92	48	23.0	738	2	C95936	conserved hypotet
93	48	23.0	930	2	E64098	DNA-directed DNA p
94	48	23.0	1112	2	H95964	probable outer mem
95	48	23.0	1286	2	T02187	probable ABC trans
96	48	23.0	1292	2	T48007	P-glycoprotein hom
97	48	23.0	1573	2	AF3514	glutamate synthase
98	47.5	22.7	190	2	G84182	hypothetical prote
99	47.5	22.7	293	2	C85898	probable proteinas
100	47.5	22.7	293	2	H91053	probable enzyme [1

ALIGNMENTS

RESULT 1

PN0512

beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: PN0512

R/Shimoda, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment

A:Reference number: PN0512; MUID:93290653; PMID:7685598

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH>

A:Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 209; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 2, 9e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 2

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: A60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2, 9e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: F60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PTDN:CAA39592.1; PID:

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2, 9e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 4

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: D60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2, 9e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 5

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: E60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2, 9e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 6

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: G60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
 C:Species: *Ursus maritimus* (polar bear)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 40
 DB 6 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 45

RESULT 7

B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: *Ursus maritimus* (polar bear)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Biochem. Biophys. Res. Commun. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56128; NID:92165; PIDN:
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 40
 DB 6 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 45

RESULT 8

PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: PQ0438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marcoun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A:Reference number: PQ0438; MUID:93075180; PMID:1445331
 A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>

A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83557
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 1-68 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 209; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 4.4e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 40
 DB 17 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 56

RESULT 9
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: *Macaca fascicularis* (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlasky, M.B.; Tolian, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117; PMID:1905108
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>

A:Cross-references: UNIPARC:UPI00002A2P2; GB:M58727; NID:9342062; PIDN:AAA36829.1; PID
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 209; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 4.8e-20;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 40
 DB 597 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVGV 636

RESULT 10

ORH04
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculature
 C:Species: *Homo sapiens* (man)

C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A32260; A35462; I39451; I39453; I59562; A44
 4668; A28583; A29302; A60812; J10038; S06121; A50355; A59011; A38364; S38252; S
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: UNIPARC:UPI00002A2P2; EMBL:X13466
 A:Note: alternative splice form APP(695)
 A:Reference number: UNIPARC:UPI00002A2P2; EMBL:X13466
 R:Lemaire, H.G.
 Submitted to the EMBL Data Library, November 1988

A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: UNIPARC:UPI00001A5EC; EMBL:X13466; NID:935598; PIDN:CAA11830.1; PID
 A:Note: alternative splice form APP(695)
 R:La Pauc, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-protein
 A:Reference number: A32277; MUID:89165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAP>

A:Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:9341202; PIDN:AACT
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
 A:Reference number: A32260; MUID:89392030; PMID:2675837
 A:Accession: A32260
 A:Molecule type: DNA
 A:Residues: 556-737 <JOH>

A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:9178863; PIDN:AAA51768.1; PID
 R:Prelli, F.; Levy, E.; van Duijn, S.G.; Boter, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Cross-references: UNIPARC:UPI0000148176
A:Note: 693-gln was found in DNA isolated from HCMVA-D patients
R.Yoshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90263318; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: UNIPARC:UPI00002DB1C; GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QMLPVPVAFWEAKVGR' <YOS2>
A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:
R.Yoshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R.Levy, E.; Carman, M.D.; Fernandez-Madrid, I.D.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:
A:Note: a mutation with 693-Gln is presented
R.Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92025553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: UNIPARC:UPI0000117EBA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:
R.Kamino, K.; Orr, H.T.; Payami, H.; Wijman, E.M.; Alonzo, M.B.; Pulst, S.M.; Anderson,
Arakaki, S.E.; Kornberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <RAM1>
A:Cross-references: UNIPARC:UPI0000117EBB; GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R.Kang, J.; Lemaire, H.G.; Untchbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:
R.Obakshi, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:
A:Note: the authors translated the codon GAG for residue 647 as Asp
R.Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:g178706; PIDN:AAA5540.1; PID:
A:Experimental source: brain
R.Tanz, R.E.; Gussella, J.F.; Watkins, P.C.; Brune, G.A.P.; St George-Hyslop, P.; Van K
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near c
A:Reference number: A47585; MUID:87120329; PMID:289367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:
R.Dyke, T.; Weidemann, A.; Maltshup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muehl
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
A:Cross-references: UNIPARC:UPI000035AB0
R.Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gussella, J.F.; Nev
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A:Reference number: S00707; MUID:88122640; PMID:2893280
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PI
A:Experimental source: promyelocytic leukemia cell line HL60
R.Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA
R.Kitaguchi, N.; Takehashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:
A:Experimental source: glioblastoma cell line
R.Vitek, M.P.; Raoof, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashto
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: B03020
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A;Residues: 122-288,'V',365-770 <VIT2>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
A;Cross-references: UNIPARC:UPI0000174094
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA

Query Match 100.0%; Score 209; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No.5.4e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 40
|||
Db 672-DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 711

RESULT 11

A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YMA>
A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727

A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:
C;Genetics: 16C3
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 90.9%; Score 190; DB 2; Length 695;
Best Local Similarity 92.5%; Pred. No.1.7e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 40
|||
Db 597-DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 636

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PID
R;Schubert, D.; Schroeder, R.; Lacorbiere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein

A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehra, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat bra
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820

A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is c
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 90.9%; Score 190; DB 2; Length 695;
Best Local Similarity 92.5%; Pred. No.1.7e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 40
|||
Db 597-DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGCV 636

RESULT 13

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI000007C880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 90.9%; Score 190; DB 2; Length 747;
Best Local Similarity 87.5%; Pred. No.1.9e-17;
Matches 35; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy	7	DSGYEVHHOKLVFPAEDVGSNKGAITGLMGVGV	40
Db	223	DSG-----RIGFPEPDVPRKPKVATIGAGISGLV	250
RESULT 18			
G71526			
3-methyl-2-oxobutanate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain pdha			
N:Alternate names: oxoisovalerate dehydrogenase			
C:Species: Chlamydia trachomatis			
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004			
C:Accession: G71526			
R:Stophens, R.S.; Kalman, S.; Lammell, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,			
Science 282, 754-759, 1998			
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac			
A:Reference number: A71570; MUID:99000809; PMID:9784136			
A:Accession: G71526			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1678 <ARN>			
A:Cross-references: UNIPROT:O84344; UNIPARC:UPI00000D7604; GB:AE001307; GB:AE001273; NIT			
A:Experimental source: serotype D, strain UW-3/Cx			
C:Genetics:			
A:Gene: pdhA/B			
C:Keywords: oxidoreductase			
Qy	3	EFRHDSGYEVHHOKLVFPAEDVGSNKGAITGL	34
Db	364	EMQRDPG-----VVVFGEVDVAGNKGVFQV	388
RESULT 19			
F95015			
glycosyl transferase, family 2 SP0136 [imported] - Streptococcus pneumoniae (strain TIGR			
C:Species: Streptococcus pneumoniae			
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004			
C:Accession: F95015			
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid			
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,			
neon, T.; Hickey, E.K.; Holt, I.E.			
Science 293, 488-506, 2001			
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,			
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.			
A:Reference number: A95000; MUID:21357209; PMID:11463916			
A:Accession: F95015			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1691 <KOR>			
A:Cross-references: UNIPROT:Q97273; UNIPARC:UPI00000512F6; GB:AE005672; PIDN:AAK74319.1			
A:Experimental source: strain TIGR4			
C:Genetics:			
A:Gene: SP0136			
C:Superfamily: Neisseria meningitidis glycosyl transferase A			
Qy	6	HDSDGYEVHHOKLVFPAEDVGSNKGAITGL	34
Db	58	HQFGYTHRIKTLISNEDLGAITNARNTGI	86

```

RESULT 20
H97888
glycosyl transferase, family 2 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H97888
R:Rockins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.;
e, R.; Leblang, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H97888
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-317 <KDR>
A:Cross-references: UNIPROT:Q8DRG7; UNIPARC:UP100000E33BF; GB:AE007317; PIDN:AAK98940.1
C:Genetics:
A:Gene: glycosyltransferase
A:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 26.3%; Score 55; DB 2; Length 317;
Best Local Similarity 37.9%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

07 6 HDGGEVHNOKLVFPAEDVGSNKGATIGL 34
||| ||| ||| ||| |||
58 HQFGYNNRIKYLISNEDLGATNARNIGI 86

```

RESULT 21

S27652
probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) - Pseudomonas sp.
C|Species: Pseudomonas sp.
C|Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C|Accession: C42971; S27652
R|Peterson, J.A.; Lu, J.Y.; Getselsoder, J.; Graham-Lorence, S.; Carmona, C.; Wilney,
J. Biol. Chem. 267, 14193-14203, 1992
A|Title: Cytochrome P-450etp. Isolation and purification of the protein and cloning an
A|Reference number: A42971; MUID:92332528; PMID:1629218
A|Accession: C42971
A|Status: preliminary; not compared with conceptual translation
A|Molecule type: nucleic acid; protein
A|Residues: 1-488 <p>>

A|Cross-references: UNIPROT:P33008; UNIPARC:UPI000012928E; EMBL:M91440; NID:g151584; PI
A|Note: sequence extracted from NCBI backbone (NCBI:P:108473)
C|Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C|Keywords: NAD; oxidoreductase

Query Match 26.3% Score 55; DB 2; Length 488;
Best Local Similarity 40.6%; Pred. No. 18;
Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

Cy 6 HDSCGYEHQKLVFPAEDV---GSNKGAIIIG 33
 | : | | | | | | | | | |
Db 305 HESTYEAFRDKLVAQNIVIGDSGQGVMTMG 336
 | : | | | | | | | | | |

RESULT 22

S73843
General amino acid permease GAP1 homolog F10_orf503 - Mycoplasma pneumoniae (strain ATCC
N|Alternate names: hypothetical protein F10_orf503
C|Species: Mycoplasma pneumoniae
A|Variety: ATCC 28342
C|Date: 27-Feb-1997 #sequence revision 25-Apr-1997 #text change 09-Jul-2004
C|Accession: S73843
R|Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Hermann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A|Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A|Reference number: S73327; MUID:97105885; PMID:8948633
A|Accession: S73843

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1503 <RTM>
 A:Cross-references: UNIPROT:P75462; UNIPARC:UPI00001394B1; EMBL:AE000051; GB:U00089; NID
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Gene: gap1
 A:Gene code: SGC3

Query Match 26.3%; Score 55; DB 2; Length 503;
 Best Local Similarity 64.7%; Pred. No. 18;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

24 VGSNKGATIGLVGGV 40
 Db 131 VKDNGALIGLVGGFV 147

RESULT 23
 O0AG4T
 Cryptophan 2-monooxygenase (EC 1.13.12.3) - Agrobacterium tumefaciens plasmid pTiAch5,
 C:Species: Agrobacterium tumefaciens
 C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 05-Oct-2004
 C:Accession: A04497; S28687; A20966
 R:Glehen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, M.; V
 EMBO J. 3, 835-846, 1984
 A>Title: The complete nucleotide sequence of the Tl-DNA of the Agrobacterium tumefaciens
 A:Reference number: A91001; MUID:84207942; PMID:6327292
 A:Accession: A04497
 A:Molecule type: DNA
 A:Residues: 1-755 <GIE>
 A:Cross-references: UNIPROT:P04029; UNIPARC:UPI00001372AD
 A:Genetics: G1
 R:Barker, K.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
 Plant Mol. Biol. 2, 335-350, 1983
 A>Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens oct
 A:Reference number: S28683
 A:Accession: S28687
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-362, 'H', 364-596, 'S', 598-717, 'IO', 720, 'A', 722-755 <BAR>
 A:Cross-references: UNIPARC:UPI000008759D; EMBL:X00493; NID:G39062; PIDN:CAA25167.1; PID
 A:Experimental source: strain octopine
 A:Genetics: G2
 R:Klee, H.; Montoya, A.; Horodyski, F.; Lichtenstein, C.; Garfinkel, D.; Fuller, S.; Flic
 Proc. Natl. Acad. Sci. U.S.A. 81, 1728-1732, 1984
 A>Title: Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti plasmid: two ge
 A:Reference number: A20966; MUID:84170374; PMID:6584906
 A:Accession: A20966
 A:Molecule type: DNA
 A:Residues: 1-717, 'IO', 720, 'A', 722-755 <KLE>
 A:Cross-references: UNIPARC:UPI0000170007; GB:K02554; NID:G154747; PIDN:AA92550.1; PID
 A:Experimental source: strain octopine
 A:Genetics: G3
 A:Genetics: <G1>
 A:Genome: plasmid
 A>Note: plasmid pTiAch5
 C:Genetics: <G2>
 A:Genome: plasmid
 A>Note: plasmid pTi15955
 C:Genetics: <G3>
 A:Gene: tme1
 A:Genome: plasmid
 A>Note: plasmid pTiA6NC
 C:Function:
 A:Pathway: tryptophan metabolism; auxin biosynthesis
 A>Note: catalyzes the first step in the biosynthesis of auxins from tryptophan
 C:Superfamily: tryptophan 2-monooxygenase
 C:Keywords: monooxygenase, oxidoreductase

Query Match 26.3%; Score 55; DB 1; Length 755;
 Best Local Similarity 41.2%; Pred. No. 29;
 Matches 14; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

Query 7 DSGEYVHOKLVFAEDVGSNKGATIGLVGGV 40
 Db 223 DSG-----RIGFFPEDVPRKVAIVAGISGLV 250

RESULT 24
 JS0166
 genome polyprotein - potato virus Y (strain N)
 N:Contains: 31K protein; 38K protein; capsid protein; cytoplasmic inclusion protein; ge
 lymerase (EC 2.7.7.46) core; nuclear inclusion protein A
 C:Species: potato virus Y, PVY
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
 C:Accession: JS0166; PS0317
 R:Robaglia, C.; Durand-Tardif, M.; Tronchet, M.; Boudazin, G.; Astier-Manifacier, S.; C
 J. Gen. Virol. 70, 935-947, 1989
 A>Title: Nucleotide sequence of potato virus Y (N strain) genomic RNA.
 A:Reference number: JS0166; MUID:89279275; PMID:2732709
 A:Accession: JS0166
 A:Molecule type: mRNA
 A:Residues: 1-3063 <ROB>
 A:Cross-references: UNIPARC:UPI0000178735
 A:Accession: PS0317
 A:Molecule type: protein
 A:Residues: 1158-1163; 2797-2812, 'Q', 2814-2816 <RO2>
 A:Cross-references: UNIPARC:UPI0000178735
 C:Superfamily: tobacco etch virus genome polyprotein
 C:Keywords: ATP; cysteine proteinase; genome-linked protein; glycoprotein; hydrolase; m
 F:1-275/Product: 31K protein #status predicted <31K>
 F:276-824/Product: helper component #status predicted <HPC>
 F:309-340/Region: zinc binding #status predicted <38K>
 F:825-1157/Product: 38K protein #status predicted <38K>
 F:1158-1791/Product: cytoplasmic inclusion protein #status predicted <CIP>
 F:1242-1250/Region: nucleotide-binding motif A (P-loop)
 F:1327-1332/Region: nucleotide-binding motif B
 F:1331-1334/Region: DEXH motif
 F:1792-1843/Product: genome-linked protein #status predicted <GLP>
 F:1844-2275/Product: nuclear inclusion protein b #status predicted <NIB>
 F:2276-2796/Product: nuclear inclusion protein b #status predicted <NIB>
 F:2797-3063/Product: capsid protein #status predicted <CAP>
 F:450,744/Binding site: carbhydrate (Asn) (covalent) #status predicted
 F:1807/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
 F:2182,2198/Active site: Cys, His #status predicted

Query Match 26.3%; Score 55; DB 2; Length 3063;
 Best Local Similarity 53.1%; Pred. No. 1,4e+02;
 Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

1 DAERHDGVEVHOKLVFAEDV---GSNK 28
 Db 2783 DDEFFELDS-YEVHQQ-----ANDTIDAGGSNK 2808

RESULT 25
 C81683
 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC06
 N:Alternate names: oxoalvalerate dehydrogenase
 C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: C81683
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg
 Nucleic Acids Res. 28, 1397-1406, 2000
 A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
 A:Reference number: AB1500; MUID:20150255; PMID:10684935
 A:Accession: C81683
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-678 <TEF>
 A:Cross-references: UNIPROT:Q9PK54; UNIPARC:UPI00000579C3; GB:AE002330; GB:AE002160; NI
 A:Experimental source: strain Nig9 (Mopn)
 A:Genetics:
 A:Gene: TC0618

A:Experimental source: clone T09A5

C:Genetics:

A:Gene: CESP:T09A5.12

A:Map position: 2

A:Insertions: 22/3; 49/3; 100/3; 130/2; 167/2; 269/2; 318/3; 461/3; 487/1; 540/1; 562/3; 59

C:Superfamily: Caenorhabditis elegans hypothetical protein T09A5.12

Query Match 25.6%; Score 53.5; DB 2; Length 708;

Best Local Similarity 38.2%; Pred. No. 42;

Matches 13; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

QY 6 HDSGYEVHQLVFFAEVGSNKGATIGLMVGV 39

Db 444 HHSCHSIDHTRMV-----LESNELASIGAIYDAV 472

Search completed: September 28, 2006, 06:24:35
Job time : 17.5022 secs


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RESULT 1
056J6 GRACR PRELIMINARY; PRT; 42 AA.
ID 056J6 GRACR PRELIMINARY; PRT; 42 AA.
AC 056J6;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_Taxid=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AY926589; AAX81918.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLLOID.
FT NON_TER 1
FT 42
FT NON_TER 1
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 209; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 2
056J7 TURTR PRELIMINARY; PRT; 42 AA.
ID 056J7 TURTR PRELIMINARY; PRT; 42 AA.
AC 056J7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Amyloid beta protein (Fragment).
OS Turisiope truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Turisiope.
OX NCBI_Taxid=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AY926588; AAX81917.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLLOID.
FT NON_TER 1
FT 42
FT NON_TER 1
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 209; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

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FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 209; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 3
Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognathu; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; Pubmed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.; specific biological activity of a beta-amyloid
RT "Receptor-mediated for NK-1 substance P receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
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DR PIR; P05112; PNO512.
DR HSSP; O16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLLOID.
FT NON_TER 1
FT 42
FT NON_TER 1
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 209; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 4
A4_URSWA STANDARD; PRT; 57 AA.
ID A4_URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-MAR-2006, entry version 36.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC	Ursus
OX	NCB1_TaxID=29073;
RN	(1)
RP	NUCLEOTIDE SEQUENCE [mRNA].
RC	TISSUE=Brain;
RX	MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT	"Conservation of the sequence of the Alzheimer's disease amyloid
RT	peptide in dog, polar bear and five other mammals by cross-species
RT	polymerase chain reaction analysis.";
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).
CC	-I- FUNCTION: Functional neuronal receptor which couples to
CC	intracellular signaling pathway through the GTP-binding protein
CC	G(O) (By similarity).
CC	-I- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC	protein.
CC	-I- SIMILARITY: Belongs to the APP family.
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CC	Distributed under the Creative Commons Attribution-NoDerivs license
CC	-----
DR	EMBL; X56128; CAA39593.1; -; mRNA.
DR	PIR; B60045; B60045.
DR	HSSP; P08592; INMJ.
DR	InterPro; IPR008155; A4_APP.
DR	InterPro; IPR001255; Beta-APP.
DR	PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR	Pfam; PF03494; Beta-APP; 1.
DR	PRINTS; PR00204; BETAMYL0ID.
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.
KW	Amyloid; Membrane; Transmembrane.
FT	CHAIN <1 .. 57
FT	/FTID=PRO_0000226244.
FT	Soluble APP-beta (By similarity).
FT	/FTID=PRO_0000000191.
FT	CTF-alpha (By similarity).
FT	/FTID=PRO_0000000192.
FT	Beta-amyloid protein 42 (By similarity).
FT	/FTID=PRO_0000000193.
FT	Beta-amyloid protein 40 (By similarity).
FT	/FTID=PRO_0000000194.
FT	Gamma-CTF(59) (By similarity).
FT	/FTID=PRO_0000000195.
FT	Gamma-CTF(57) (By similarity).
FT	/FTID=PRO_0000000196.
FT	Extracellular (Potential).
SO	SEQUENCE 57 AA; 6172 MW; 84209D8EBBA82DFA CRC64;
Query Match	100.0%; Score 209; DB 1; Length 57;
Best Local Similarity	100.0%; Pred. No. 2.5e+20;
Matches 40; Conservative	0; Mismatches 20; Indels 0; Gaps
Oy	1 DAEPHDSGYEVHHOKLVFPADVSNKGAITGLMWGVV 40
Db	6 DAEFRHDSGYEVHHOKLVFPADVSNKCAITGLMWGVV 45
RESULT 5	
ID_A4_CANFA	STANDARD; PRT; 58 AA.
AC Q28280;	
DT 01-NOV-1997,	integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006,	entry version 37.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4	
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;	
DE Beta-amyloid protein 42 (Beta-APP2); Beta-amyloid protein 40 (beta-	
DE APP40); Gamma-CTF (59) (Gamma-secretase C-terminal fragment 59); Gamma-	

DN	CTF(57) [Gamma-secretase C-terminal fragment 57] (Fragment).
DE	Name=APP.
OS	Canis familiaris (dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC	Canis.
OX	NCB1_TaxId=9615;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RC	TISUE=Kidney;
RX	MEDLINE=92011079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT	"Conservation of the sequence of the Alzheimer's disease amyloid
RT	peptide in dog, polar bear and five other mammals by cross-species
RT	polymerase chain reaction analysis."
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).
CC	-I- FUNCTION: Functional neuronal receptor which couples to
CC	intracellular signaling pathway through the GTP-binding protein
CC	Glo (By similarity).
CC	-I- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC	protein.
CC	-I- SIMILARITY: Belongs to the APP family.
CC	-----
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CC	-----
DR	EMBL; X56125; CA39590.1; -; mRNA.
DR	HSSP; P08592; INMU.
DR	Ensembl; ENSCAFG00000008557; Canis familiaris.
DR	InterPro; IPR008155; A4_APP.
DR	InterPro; IPR001255; Beta-APP.
DR	PANTHER; PTHR10083; SF6; Beta-APP; 1.
DR	Pfam; PF03494; Beta-APP; 1.
DR	PRINTS; PR00204; BETAAMYL0ID.
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.
KM	Amyloid; Membrane; Transmembrane.
FT	CHAIN <1> >58
FT	/FtId=PRO_0000226241.
FT	/FtId=PRO_0000226241.
FT	Soluble APP-beta (By similarity).
FT	/FtId=PRO_0000000070.
FT	CTF-alpha (By similarity).
FT	/FtId=PRO_0000000071.
FT	Beta-amyloid protein 42 (By similarity).
FT	/FtId=PRO_0000000072.
FT	Beta-amyloid protein 40 (By similarity).
FT	/FtId=PRO_0000000073.
FT	Gamma-CTF(59) (By similarity).
FT	/FtId=PRO_0000000074.
FT	Gamma-CTF(57) (By similarity).
FT	/FtId=PRO_0000000075.
FT	Extracellular (Potential).
FT	Potential.
FT	CHAIN 47 >58
FT	/FtId=PRO_0000000074.
FT	CHAIN 49 >58
FT	/FtId=PRO_0000000075.
FT	TOPO_DOM <1> 34
FT	TRANSMEM 35 58
FT	NON_TER 1 1
FT	NON_TER 58 58
FT	SEQUENCE 58 AA; 6285 MW; 8469D48BA2E12DFA CRC64;
QY	Query Match 100.0%; Score 209; DB 1; Length 58;
DB	Best local Similarity 100.0%; Pred. No. 2,5e-20;
Matches	40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 DAEFRHDSGYEVHHQKLVFEADVGSNGKAIIGLMGVGV 40
Db	7 DAEFRHDSGYEVHHQKLVFEADVGSNGKAIIGLMGVGV 46
RESULT 6	
A4_RABIT	
ID_A4_RABIT	STANDARD; PRT; 58 AA.
AC Q28748;	
DT 01-NOV-1997,	integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997,	sequence version 1.
DI 07-MAR-2006,	entry version 37.

RESULT 8
A4 BOVIN STANDARD; PRT; 59 AA.
AC 028053;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 1.
DE Amyloid beta A4 protein (APP) (Alzheimer disease amyloid A4 protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); Gamma-secretase C-terminal fragment 59]; Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F; Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
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DR EMBL: X56124; CA39589.1; -; mRNA.
DR EMBL: X56126; CA39591.1; -; mRNA.
DR HSSP: P08592; 1NMJ
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083; SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT FTID=PRO_0000000064.
FT CHAIN 7 >59 CTF-alpha (By similarity).
FT FTID=PRO_0000000065.
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT FTID=PRO_0000000066.
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT FTID=PRO_0000000067.
FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
FT FTID=PRO_0000000068.
FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
FT FTID=PRO_0000000069.
FT TOPO_DOM 35 58 Extracellular (Potential).
FT TOPO_DOM 59 >59 Potential.
FT NON_TER 1 1 Cytoplasmic (Potential).
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
Query Match 100.0%; Score 209; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2, 6e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

Db 7 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 46
|||||
RESULT 9
08JH58_CHESE PRELIMINARY; PRT; 113 AA.
ID 08JH58_CHESE
AC 08JH58;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Amyloid beta protein (Fragment).
DE Chelydra serpentina serpentina (common snapping turtle).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.; "Octylphenol (OP) alters the expression of members of the amyloid protein family in the hypothalamus of the snapping turtle, Chelydra serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275 (2002).
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DR EMBL: AF541917; AA004908.1; -; mRNA.
DR HSSP: Q16019; 1IYT.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005488; F:Binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083; SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
Query Match 100.0%; Score 209; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 5, 1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Db 15 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 54
|||||
RESULT 10
09J3296_CHICK PRELIMINARY; PRT; 534 AA.
ID 09J3296_CHICK
AC 09J3296;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W., Milligan C.E.; "Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880 (1998).
CC

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 DR EMBL: AF042098; AAC25052.1; -, mRNA.
 DR HSSP: Q16019; 11YT.
 DR SMR: O93296; 224-333.
 DR Ensembl: ENSGALG00000015770; Gallus gallus.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR PRINTS: PR00204; BETAMAMLOID.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 534 AA; 60597 MW; FB53RC2B66D4C92 CRC64;
 Query Match 100.0%; Score 209; DB 2; Length 534;
 Best Local Similarity 100.0%; Pred. No. 2.6e-19;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 475
 RESULT 11
 Q9PVL1 CHICK PRELIMINARY; PRT; 569 AA.
 ID Q9PVL1;
 AC Q9PVL1;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Amyloid protein (Fragment).
 GN Name=APP;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Coulson E.J., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 RT tells us about its function."
 RL Neurochem. Int. 0:0-0(2000).
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 DR EMBL: AF030341; AAF12698.1; -, mRNA.
 DR HSSP: Q16019; 11YT.
 DR SMR: Q9PVL1; 1-64, 260-369.
 DR Ensembl: ENSGALG00000015770; Gallus gallus.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR PRINTS: PR00204; BETAMAMLOID.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;
 Query Match 100.0%; Score 209; DB 2; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 472 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 511

RESULT 12
 Q2XQAO PIG PRELIMINARY; PRT; 695 AA.
 ID Q2XQAO;
 AC Q2XQAO;
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Amyloid protein variant 1.
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 OC NCBI_TaxID=9823;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Oerum M.A., Larsen K., Bendixen C.;
 RT "Porcine amyloid precursor protein, App: Cloning and characterization
 RT of cDNAs."
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: DQ267684; ABB82033.1; -, mRNA.
 DR SQ SEQUENCE 695 AA; 78615 MW; 825A7E4AC10E8F0B CRC64;
 Query Match 100.0%; Score 209; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 3.4e-19;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 636
 RESULT 13
 Q56UK3 CANFA PRELIMINARY; PRT; 695 AA.
 ID Q56UK3;
 AC Q56UK3;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Beta-amyloid protein 695.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OC NCBI_TaxID=9615;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
 RT "Relationship between canine dementia and Alzheimer's disease."
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: AY926582; AAX81911.1; -, mRNA.
 DR SMR: Q56UK3; 28-123, 124-189, 385-494.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.

```
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_C-R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 100.0%; Score 209; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3,4e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 636

RESULT 14
Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
AC Q5R477.
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE Hypothetical protein DKFp459D212.
GN Name=DKFp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Pongo.
OC NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Wamburt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR SRR; CR61380; CAH93439.1; -; mRNA.
DR SMR; Q5R477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_C-R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KM Hypothetical protein.
SQ SEQUENCE 695 AA; 78627 MW; 0BF5DD9BA2213E49 CRC64;
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Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 636

RESULT 15
Q6RH29_CANPA PRELIMINARY; PRT; 695 AA.
ID Q6RH29.
AC Q6RH29.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Beta amyloid protein isoform APP695.
GN Name=Beta APP;
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AY498707; AAR9727.1; -; mRNA.
DR HSSP; Q16019; IBA4.
DR SMR; Q6RH29; 28-123, 124-189, 385-494.
DR Ensembl; ENSCAG00000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 718CA42A9F96C10 CRC64;

Query Match 100.0%; Score 209; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3,4e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 636

RESULT 16
Q9DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
ID Q9DGJ8.
AC Q9DGJ8.
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP PubMed=16039787; DOI=10.1016/j.neuroscience.2005.05.020;
RA Carrodegas J.A., Rodolosee A., Garza M.V., Sanz-Clemente A.,
```


A4_SAI5C
 ID A4_SAI5C STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1997, sequence version 1.
 DT 07-MAR-2006, entry version 60.
 DE Amyloid beta A4 protein precursor (APP) (ABP) (Alzheimer disease
 DE amyloid beta A4 protein precursor) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble protein homolog) (Contains: Soluble APP-beta (S-APP-beta);
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
 OC Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
 RT amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tipe60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APEP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of APP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized into endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=App770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=App695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -1- DOMAIN: The basolateral sorting signal (Bass) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields p3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/Notch-stylin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 CC EMBL, S81024; AAD1347.1; -; mRNA.
 CC PDB, 1RM6; X-ray; A=346-551.
 CC SMR, Q95241; 28-123, 124-189, 287-342.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extn.
 CC InterPro: IPR001255; Beta_APP.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER, PTHR10083.SF6; Beta_APP; 5.
 CC Pfam, PF02177; A4_EXTRA; 1.
 CC Pfam, PF03494; Beta_APP; 1.
 CC Pfam, PF00014; Kunitz_BPTI; 1.
 CC PRINTS, PR00203; AMYLOID4.
 CC PRINTS, PR00759; BASICPTASE.
 CC PRINTS, PR00204; BETAAMYLOID.
 CC ProDom, PD000222; Prot_inh_Kunz-m; 1.
 CC SMART, SM00006; A4_EXTRA; 1.
 CC SMART, SM00131; KU; 1.
 CC PROSITE, PS00319; A4_EXTRA; 1.
 CC PROSITE, PS00320; A4_INTRA; 1.
 CC PROSITE, PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE, PS50279; BPTI_KUNITZ_2; 1.
 CC 3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion;

KM		Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
KM		Membrane; Metal-binding; Notch signaling pathway; Phosphorylation;
KW		Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
KW	Transmembrane; Zinc.	
FT	SIGNAL	1
FT	CHAIN	18
FT	CHAIN	18
FT	CHAIN	18
FT	CHAIN	18
FT	CHAIN	653
FT	CHAIN	653
FT	CHAIN	653
FT	CHAIN	653
FT	CHAIN	653
FT	PEPTIDE	669
FT	PEPTIDE	669
FT	PEPTIDE	669
FT	PEPTIDE	669
FT	CHAIN	693
FT	CHAIN	693
FT	CHAIN	693
FT	CHAIN	702
FT	CHAIN	721
FT	TOPO DOM	18
FT	TRANSMEM	681
FT	TOPO DOM	705
FT	DOMAIN	291
FT	REGION	96
FT	REGION	181
FT	REGION	316
FT	REGION	363
FT	REGION	504
FT	REGION	713
FT	MOTIF	705
FT	MOTIF	740
FT	COMBIAS	230
FT	COMBIAS	274
FT	METAL	137
FT	METAL	147
FT	METAL	149
FT	METAL	151
FT	METAL	658
FT	METAL	662
FT	METAL	665
FT	METAL	666
QY	1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAITGLMGVV	40
DB	653 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAITGLMGVV	692
RESULT 20		
ID	QGSGCO_HUMAN	PRELIMINARY; PRT; 751 AA.
AC	QGSGCO;	
DT	10-MAY-2005,	integrated into UniProtKB/TrEMBL.
DT	10-MAY-2005,	sequence version 1.
DT	07-FEB-2006,	entry version 7.
DE	Amyloid beta A4 protein,, isoform b.	

ON Name=APP.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutelesia; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max I., Wang Y., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stopleton M., Soares M.B., Donald M.F., Casavant P., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuki S., Carninci P., Prange C.,
RA Rata S.S., Loggialano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.J., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalley D.E.,
RA Scherach A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RG NIH WGC Project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPIT/Kunitz inhibitor domain.
CC CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License

CC --EMBL; BC065529; AAH65529.1; -; mRNA.
DR SMR; OGGSCD; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSG00000142192; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005468; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004867; F:pelletron-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; F:pelletron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012882; Cytochrome_c_R.
DR InterPro; IPR002223; Prot_inh_Kuniz-m.
DR PANTHER; PTHR10083.SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPIT; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPIT_KUNITZ_1; 1.
DR PROSITE; PS0279; BPIT_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84819 MW; C987C557C5A3714E CRC64;

Query Match 100.0%; Score 209; DB 2; Length 751;
Beet Local Similarity 100.0%; Pred. No. 3,7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAERPHDSGYVHHQKLVFAEDVGSNKGALIGMGGV 40

Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 692

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|||||
RESULT 21
Q4R4R8_MACFA PRELIMINARY; PRT; 751 AA.
ID Q4R4R8
AC Q4R4R8
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE Brain cDNA, clone: Q4R4R8, similar to human amyloid beta (A4)
DE protein (protease nexin-II, Alzheimer disease) (APP), transcript
DE variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:1594441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gotohori T., Shen C.-K.J., Wu C.-I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
EMBL: AB169826; BAB01907.1; -; mRNA.
DR SMR; Q4R4R8; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome c R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083; SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_APP.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYLOID.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
KM Protease.
SQ SEQUENCE 751 AA; 84817 MW; 83C1CD96AD355158 CRC64;
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Query Match 100.0%; Score 209; DB 2; Length 751;

Best Local Similarity 100.0%; Pred. NO. 3.7e-19; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40

Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 692

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RESULT 22
Q56JK5_CANFA PRELIMINARY; PRT; 751 AA.
ID Q56JK5
AC Q56JK5
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Galleo C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC
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CC
EMBL: AY926580; AAX81909.1; -; mRNA.
DR SMR; Q56JK5; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome c R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083; SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM000131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84520 MW; C1CD20377DFP8550 CRC64;
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Query Match 100.0%; Score 209; DB 2; Length 751;

Best Local Similarity 100.0%; Pred. NO. 3.7e-19; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 692

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RESULT 23
Q6RH28_CANFA PRELIMINARY; PRT; 751 AA.
ID Q6RH28
AC Q6RH28
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE Beta-amyloid protein isoform APP751.
OS Name-beta APP.
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; AY498708; AAR97728.1; -; mRNA.
DR HSSP; O16019; 1AAP.
DR SMR; O6RH28; 28-123, 124-189, 287-342, 441-550.
DR EMBL; ENSGALG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; A4_extra.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;
SQ
Query Match 100.0%; Score 209; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 692
RESULT 24
O2XQ99_PIG PRELIMINARY; PRT; 751 AA.
ID O2XQ99_PIG
AC O2XQ99_PIG
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Amyloid protein variant 2.
GN Name=APP;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
OX NCB1_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein, APP: Cloning and characterization
of cDNAs";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; DQ267685; ABB82034.1; -; mRNA.
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SQ SEQUENCE 751 AA; 84799 MW; 3786874380C369F CRC64;
Query Match 100.0%; Score 209; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 692
RESULT 25
O9DGJ7_CHICK PRELIMINARY; PRT; 751 AA.
ID O9DGJ7_CHICK
AC O9DGJ7_CHICK
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
OX NCB1_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16039787; DOI=10.1016/j.neuroscience.2005.05.020;
RA Carrodeguas J.A., Rodolosee A., Garza M.V., Sanz-Clemente A.,
RA Perez-Pe R., Lacosta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RA Sorribas V., Sarrasa M.;
RT "The chick embryo appears as a natural model for research in beta-
amyloid precursor protein processing.";
RL Neuroscience 134:1285-1300(2005).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; AF289219; AAC00594.1; -; mRNA.
DR HSSP; O16019; 1IYT.
DR SMR; O9DGJ7; 28-123, 124-189, 287-342, 441-550.
DR EMBL; ENSGALG0000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 751 AA; 84706 MW; E78B9413A8033D84 CRC64;
SQ
Query Match 100.0%; Score 209; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 692
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RESULT 26

ID	CAVPO	STANDARD	PRT	770 AA
AC	060495	060496		
DT	23-APR-2003	integrated into UniProtKB/Swiss-Prot.		
DT	07-FEB-2006	entry version 55.		
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid beta A4 protein precursor) [contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); C31].			
GN	Name=APP;			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
OC	Hystricognathi; Caviidae; Cavia.			
OX	NCBI_TaxID=10141;			
RN	[1]			
RC	NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.			
RX	TISSUE=Brain, and Liver;			
RX	MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;			
RT	Beck M., Mueller D., Bigl V.;			
RT	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing";			
RL	Biochim. Biophys. Acta 1351:17-21(1997).			
RN	[2]			
RP	INTERACTION OF BETA-APP40 WITH APOE.			
RX	MEDLINE=98007700; PubMed=9349544;			
RA	Marcel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C., Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;			
RT	"Isoform-specific effects of apolipoproteins E2, E3, and E4 on cerebral capillary sequestration and blood-brain barrier transport of circulating Alzheimer's amyloid beta.";			
RL	J. Neurochem. 69:1995-2004(1997).			
RT	[3]			
RP	PROCESSING.			
RX	MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;			
RA	Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T., Bigl V.;			
RT	"Guinea-pig primary cell cultures provide a model to study expression and amyloidogenic processing of endogenous amyloid precursor protein.";			
RL	Neuroscience 95:243-254(2000).			
RN	[4]			
RP	GAMMA-SECRETASE PROCESSING.			
RX	MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;			
RA	Pimix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C., Ziani-Cherif C., Onstead L., Sambamurti K.;			
RT	"A novel gamma-secretase assay based on detection of the putative C-terminal fragment-gamma of amyloid beta protein precursor.";			
RL	J. Biol. Chem. 276:481-487(2001).			
CC	-1- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(O) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction (By similarity). In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).			

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins and apolipoproteins E and J in the CSF and to HDL particles in plasma, inhibiting metal-catalyzed oxidation of lipoproteins. CC -1- FUNCTION: Apolipins elicit adhesion of neural cells to the extracellular matrix and may regulate neurite outgrowth in the brain (By similarity).

CC -1- Peptides: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8ip1, SHC1 and Numb and Dab1 (By similarity). Also interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2 (via its TPR domains), APPB2 (via BASS) and DDB1 (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Soluble Abeta40 binds all three isoforms of APOE, in vitro and in vivo. When lipidated, APOE3 appears to be the preferred amyloid binding isoform, while the APOE4 isoform-beta-APP40 complex is capable of being transported across the blood-brain barrier.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits (By similarity). During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sialated) (By similarity). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes (By similarity). Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface (By similarity). APP sorts to the basolateral surface in epithelial cells (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to exist. The L-isoforms, missing exon 15, are referred to as apilicaps;

CC Name=APP70;

CC IsoId=Q60495-1; Sequence=Displayed;

CC Name=APP695;

CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;

CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in brain. The longer isoforms containing the BPTI domain are predominantly expressed in peripheral organs such as muscle and liver.

CC -1- INDUCTION: Increased levels during neuronal differentiation.

CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue (By similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

CC -1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin1/nicastrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTFs).

RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LYS-501.
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
 RA Swenson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
 RT "NIH-SNPs, environmental genome project, NIHSS ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).
 RC TISSUE=Eye, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-10.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadelock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP ERRATUM, AND SEQUENCE REVISION.
 RA Schon E.A., Mita S., Sadelock J., Herbert J.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 1-75.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [14]
 RP PROTEIN SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [15]
 RP PROTEIN SEQUENCE OF 18-40.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;

RA Gevaert K., Goethals M., Matens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [16]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [17]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [18]
 RP NUCLEOTIDE SEQUENCE OF 266-366.
 RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [19]
 RP NUCLEOTIDE SEQUENCE OF 287-367.
 RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
 RT inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [20]
 RP NUCLEOTIDE SEQUENCE OF 507-770.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [21]
 RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 Query Match 100.0%; Score 209; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 3.8e-19; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
 DB 672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
 RESULT 28
 A4_MACFA STANDARD; PRT; 770 AA.
 AC PS1601; 060HH7; 095KN7;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 22-FEB-2006, entry version 55.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid beta A4 protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (beta-
 DE APP42); Beta-amyloid protein 40 (beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DE secretase C-terminal fragment 50); C311.
 GN Name=APP; ORFNames=QOCF-1594;
 OS Macaca fascicularis (Citrab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 RX [1]
 RN NCLECTIVE SEQUENCE [MRNA] (ISOFORMS APP65 AND APP770).
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; Pubmed=1905108;
 RA Podlenny M.B., Tolan D.R., Selkoe D.J.;
 RT "homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease.";
 RL Am. J. Pathol. 138:1423-1435(1991).
 RN [2]
 RN NCLECTIVE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
 RC TISSUE=Brain cortex;
 RA Kusuda J., Oseada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;
 RT "Isolation and characterization of cDNA for macaque neurological
 RT disease genes.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tipe60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBI, KNS2
 CC (via its TPR domain) (By similarity), APPBP2 (via BASS) and DDB1.
 CC In vitro, it binds MAP7 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;

CC Name=APP65;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC Name=3;
 CC IsoId=P53601-3; Sequence=VSP_013360, VSP_013361;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YNRPY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivative License
 CC
 CC EMBL; M58726; AAA36828.1; -; mRNA.
 CC EMBL; M58727; AAA36829.1; -; mRNA.
 CC EMBL; AB125150; BAD51938.1; -; mRNA.
 CC HSP; P08592; 1MKJ.
 CC DR SMK; P53601; 28-123, 124-189, 287-342, 460-569.
 CC InterPro; IPR008154; A4_APP.
 CC InterPro; IPR008154; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC InterPro; IPR002223; Prot_inh_Kunz-m.
 CC PANTHER; PTHR10083; SF6; Beta-APP; 6.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF03494; Beta-APP; 1.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA.
 CC PRINTS; PR00759; BASICTPASE.
 CC PRODOM; PD00222; Prot_inh_Kunz-m; 1.
 CC SMART; SM00131; KU; 1.
 CC SMART; SM00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 CC Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;

KM Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
 KM Metal-binding; Notch signaling pathway; Phosphorylation;
 KM Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KM Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 /FtId=PRO_0000000101.
 FT CHAIN 18 687 Soluble APP-alpha (Potential).
 FT CHAIN 18 671 /FtId=PRO_0000000102.
 FT CHAIN 672 770 Soluble APP-beta (Potential).
 FT CHAIN 672 770 /FtId=PRO_0000000103.
 FT CHAIN 672 770 C99 (Potential).
 FT CHAIN 672 713 /FtId=PRO_0000000104.
 FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
 FT CHAIN 672 711 /FtId=PRO_0000000105.
 FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
 FT CHAIN 688 770 /FtId=PRO_0000000106.
 FT CHAIN 688 770 C83 (Potential).
 FT CHAIN 688 713 /FtId=PRO_0000000107.
 FT CHAIN 688 713 P3(42) (Potential).
 FT CHAIN 688 711 /FtId=PRO_0000000108.
 FT CHAIN 688 711 P3(40) (Potential).
 FT CHAIN 712 770 /FtId=PRO_0000000109.
 FT CHAIN 712 770 Gamma-CTF(59) (Potential).
 FT CHAIN 714 770 /FtId=PRO_0000000110.
 FT CHAIN 714 770 Gamma-CTF(57) (Potential).
 FT CHAIN 721 770 /FtId=PRO_0000000111.
 FT CHAIN 721 770 Gamma-CTF(50) (Potential).
 FT CHAIN 740 770 /FtId=PRO_0000000112.
 FT CHAIN 740 770 C31 (Potential).
 FT CHAIN 740 770 /FtId=PRO_0000000113.
 FT CHAIN 740 770 Extracellular (Potential).
 FT CHAIN 740 770 Potential.
 FT CHAIN 740 770 Cytoplasmic (Potential).
 FT CHAIN 740 770 BPTI/Kunitz inhibitor.
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Zinc-binding (By similarity).
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Collagen-binding (By similarity).
 FT CHAIN 740 770 Interaction with G(o)-alpha (By similarity).
 FT CHAIN 740 770 Basolateral sorting signal (By similarity).
 FT MOTIF 724 734
 Query Match 100.0%; Score 209; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAERFHDGSGYEVHHOKLVFAEDVGSNKGATIGLMGSGV 40
 DB 672 DAERFHDGSGYEVHHOKLVFAEDVGSNKGATIGLMGSGV 711
 RESULT 29
 A4_PANTR STANDARD; PRT; 770 AA.
 AC OSIS80;
 DT 15-MAR-2005, integrated into UniProtKB/Swiss-Prot.
 DT 07-FEB-2006, entry version 16.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Pan.
 NCBI_TaxID=9598;

RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RP PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
 RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
 RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
 RT "Accelerated evolution of nervous system genes in the origin of Homo
 RT sapiens.";
 RT Cell 119:1027-1040(2004).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPB1/Tipe60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(i) and Jip (By
 CC similarity). Inhibits G(o) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPB
 CC family, MAP81P1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCG-like protein BPP, FPR1, APPP1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DBP1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via a clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized into endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- DOMAIN: The basolateral sorting signal (Bass) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated

CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: AY65248; AAV74286.1; -; mRNA.
 CC SMR: O51S80; 26-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_EXTra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR012282; Cytochrome C R.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER: PTHR10083; SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4_EXTra; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA.
 CC PRINTS: PR00759; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunz-m; 1.
 CC SMART: SM00006; A4_EXTra; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTra; 1.
 CC PROSITE: PS00320; A4_INTra; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS02079; BPTI_KUNITZ_2; 1.
 CC Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
 CC Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding;
 CC Notch signaling pathway; Phosphorylation; Protease inhibitor;
 CC Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 FT CHAIN 1 17 By similarity
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 /FTid=PRO_0000000127.
 FT CHAIN 18 671 Soluble APP-alpha (Potential).
 FT CHAIN 18 671 /FTid=PRO_0000000128.
 FT CHAIN 672 770 Soluble APP-beta (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000129.
 FT CHAIN 672 770 C99 (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000130.
 FT CHAIN 672 770 Beta-amyloid protein 42 (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000131.
 FT CHAIN 672 770 Beta-amyloid protein 40 (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000132.
 FT CHAIN 672 770 C83 (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000133.
 FT CHAIN 672 770 P3(42) (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000134.
 FT CHAIN 672 770 P3(40) (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000135.
 FT CHAIN 672 770 Gamma-CTF(59) (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000136.
 FT CHAIN 672 770 Gamma-CTF(57) (Potential).
 FT CHAIN 672 770 /FTid=PRO_0000000137.

FT CHAIN 721 770 Gamma-CTF(50) (Potential).
 FT CHAIN 740 770 /FTid=PRO_0000000138.
 FT CHAIN 740 770 C31 (Potential).
 FT CHAIN 740 770 /FTid=PRO_0000000139.
 FT CHAIN 740 770 Extracellular (Potential).
 FT CHAIN 740 770 Potential.
 FT CHAIN 740 770 Cytoplasmic (Potential).
 FT CHAIN 740 770 BPTI/Kunitz inhibitor.
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Zinc-binding (By similarity).
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Heparin-binding (By similarity).
 FT CHAIN 740 770 Collagen-binding (By similarity).
 FT CHAIN 740 770 Interaction with G(O)-alpha (By similarity).
 FT CHAIN 740 770 Basolateral sorting signal (By similarity).
 FT CHAIN 740 770 NPXY motif; contains endocytosis signal.
 FT CHAIN 740 770 Asp/Glu-rich (acidic).
 FT CHAIN 740 770 Poly-Thr.
 FT CHAIN 740 770 Copper (By similarity).
 FT CHAIN 740 770 Copper (By similarity).
 FT CHAIN 740 770 Copper (By similarity).
 FT CHAIN 740 770 Copper (By similarity).
 FT CHAIN 740 770 Copper or zinc (By similarity).
 FT CHAIN 740 770 Copper or zinc (By similarity).
 FT CHAIN 740 770 Copper or zinc (By similarity).
 FT CHAIN 740 770 Required for Cu(2+) reduction (By similarity).
 FT CHAIN 740 770 Reactive bond (By similarity).
 FT CHAIN 740 770 Cleavage (by beta-secretase) (By similarity).
 FT CHAIN 740 770 Cleavage (by caspase-6) (By similarity).
 FT CHAIN 740 770 Cleavage (by alpha-secretase) (By similarity).
 FT CHAIN 740 770 SITE 301 302
 FT CHAIN 740 770 SITE 671 672
 FT CHAIN 740 770 SITE 672 673
 FT CHAIN 740 770 SITE 687 688

Query Match 100.0%; Score 209; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 3; 8e-19;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDGVEVHOKVFFAEDVGSNKGAIIGLMGVGV 40
 DB 672 DAFFRHDGVEVHOKVFFAEDVGSNKGAIIGLMGVGV 711

RESULT 30
 ID A4_PIG STANDARD; PRT; 770 AA.
 AC P79307; Q29023; Q9TU10;
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 03-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 50.
 DE Amyloid beta A4 protein precursor (APP) (APP) (Alzheimer disease
 DE amyloid protein homologue) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31).
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 NCBI_TaxID=9623;
 RN NUCLEOTIDE SEQUENCE [mRNA].
 RP Kimura A., Takahashi T.,
 RA "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.

RC TISSUE=Small intestine;
 RA Whiteer A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC NUCLEOTIDE SEQUENCE (MRNA) OF 667-723.
 RX TISSUE=Brain;
 RA MEDLINE=9201076; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tipe0 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G1O and JIP (By
 CC similarity). Inhibits G1O alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APB5 family members, the ARBA
 CC family, MAP8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APP1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPP2 (via BASS) and DDB1.
 CC In vitro, it binds MAP7 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acid either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP

CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields p3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-729 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 CC EMBL: AB032550; BAB84580.1; -; mRNA.
 CC EMBL: Z84022; CAB06313.1; -; mRNA.
 CC EMBL: X56127; CAA39592.1; -; mRNA.
 CC HSSP: P08592; INMU.
 CC SMC: P79307; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4 APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER: PTHR10083:SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4 EXTRA; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz BPT1; 1.
 CC PRINTS: PR00203; AMYLOIDA.
 CC PRINTS: PR00759; BASICTPASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunz-m; 1.
 CC SMART: SM00006; A4 EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPT1_KUNITZ_1; 1.
 CC PROSITE: PS02279; BPT1_KUNITZ_2; 1.
 CC KMW: Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
 CC KMW: Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding;
 CC KMW: Notch signaling pathway; Phosphorylation; Protease inhibitor;
 CC KMW: Serine protease inhibitor; Signal; Transmembrane; Zinc.
 CC SIGNAL 1 17
 CC CHAIN 18 770
 CC /FtId=PRO_000000140.
 CC Soluble APP-alpha (potential).
 CC CHAIN 18 687
 CC /FtId=PRO_000000141.
 CC Soluble APP-beta (potential).
 CC CHAIN 18 671
 CC /FtId=PRO_000000142.
 CC C99 (By similarity).
 CC CHAIN 672 770
 CC /FtId=PRO_000000143.
 CC Beta-amyloid protein 42 (By similarity).
 CC CHAIN 672 713
 CC /FtId=PRO_000000144.
 CC Beta-amyloid protein 40 (By similarity).
 CC CHAIN 672 711
 CC /FtId=PRO_000000145.

FT	CHAIN	688	770	C83 (By similarity).
FT				/FtId=PRO_0000000146.
FT	PEPTIDE	688	713	P3(42) (By similarity).
FT				/FtId=PRO_0000000147.
FT	PEPTIDE	688	711	P3(40) (By similarity).
FT				/FtId=PRO_0000000148.
FT	CHAIN	712	770	Gamma-CTF(59).
FT				/FtId=PRO_0000000149.
FT	CHAIN	714	770	Gamma-CTF(57).
FT				/FtId=PRO_0000000150.
FT	CHAIN	721	770	Gamma-CTF(50) (By similarity).
FT				/FtId=PRO_0000000151.
FT	CHAIN	740	770	C31 (By similarity).
FT				/FtId=PRO_0000000152.
FT	TOPO_DOM	18	699	Extracellular (Potential).
FT				Potential.
FT	TRANSMEM	700	723	Cytoplasmic (Potential).
FT	TOPO_DOM	724	770	Bpt1/Kunitz inhibitor.
FT	DOMAIN	291	341	Heparin-binding (By similarity).
FT	REGION	96	110	Copper-binding (By similarity).
FT	REGION	135	155	Zinc-binding (By similarity).
FT	REGION	181	188	Heparin-binding (By similarity).
FT	REGION	391	423	Heparin-binding (By similarity).
FT	REGION	491	522	Collagen-binding (By similarity).
FT	REGION	523	540	Interaction with G(c)-alpha (By similarity).
FT	REGION	732	751	Basolateral sorting signal.
FT	MOTIF	724	734	NPXY motif, contains endocytosis signal.
FT	MOTIF	759	762	Asp/Glu-rich (acidic).
FT	COMPBIAS	230	260	

Query Match Best Local Similarity 100.0%; Score 209; DB 1; Length 770;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFDGSEVHHQKLVFFAEVDGSKNGAIIGLMVGCV 40
 |||||
 Db 672 DAERFDGSEVHHQKLVFFAEVDGSKNGAIIGLMVGCV 711

Search completed: September 28, 2006, 06:22:59
 Job time : 131.224 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:23:21 ; Search time 28.1614 Seconds
(without alignments)
124.327 Million cell updates/sec

Title: US-09-731-899-2

Perfect score: 209

Sequence: 1 DAFFRDSGVEVHOKLVFPAEDVGNKALIGLVGVV 40

Scoring table: BLOSUM62

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RB_COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	40	1	US-07-744-767A-1
2	209	100.0	40	1	US-08-235-400-2
3	209	100.0	40	1	US-08-476-464A-2
4	209	100.0	40	1	US-08-304-585-1
5	209	100.0	40	1	US-08-302-808-3
6	209	100.0	40	1	US-08-433-734-1
7	209	100.0	40	1	US-08-609-090-8
8	209	100.0	40	1	US-07-737-371B-69
9	209	100.0	40	1	US-08-682-345A-2
10	209	100.0	40	1	US-08-986-948-3
11	209	100.0	40	1	US-08-461-216-1
12	209	100.0	40	2	US-08-959-148-1
13	209	100.0	40	2	US-09-242-724-22
14	209	100.0	40	2	US-08-723-651B-1
15	209	100.0	40	2	US-09-062-365-3
16	209	100.0	40	2	US-09-133-866-3
17	209	100.0	40	2	US-09-988-842-3
18	209	100.0	40	2	US-10-455-218-1
19	209	100.0	40	2	US-10-151-614-1
20	209	100.0	40	2	US-09-623-548A-956
21	209	100.0	40	2	US-09-623-548A-978
22	209	100.0	40	2	US-09-623-548A-989
23	209	100.0	40	2	US-09-623-548A-1005
24	209	100.0	40	2	US-09-657-276-956
25	209	100.0	40	2	US-09-657-276-978
26	209	100.0	40	2	US-09-657-276-989

27	209	100.0	40	2	US-09-657-276-1005	Sequence 1005, App
28	209	100.0	40	2	US-09-362-955D-36	Sequence 36, App1
29	209	100.0	40	5	PCT-US92-06700-1	Sequence 1, App1
30	209	100.0	41	1	US-08-302-808-4	Sequence 4, App1
31	209	100.0	41	1	US-08-682-245A-3	Sequence 3, App1
32	209	100.0	41	1	US-08-986-948-4	Sequence 4, App1
33	209	100.0	42	1	US-07-744-767A-2	Sequence 2, App1
34	209	100.0	42	1	US-08-179-574-1	Sequence 1, App1
35	209	100.0	42	1	US-08-347-144-1	Sequence 19, App1
36	209	100.0	42	1	US-08-462-859A-19	Sequence 19, App1
37	209	100.0	42	1	US-08-123-659A-19	Sequence 19, App1
38	209	100.0	42	1	US-08-464-247A-19	Sequence 19, App1
39	209	100.0	42	1	US-08-464-248A-19	Sequence 19, App1
40	209	100.0	42	1	US-08-476-464A-1	Sequence 1, App1
41	209	100.0	42	1	US-08-304-585-2	Sequence 2, App1
42	209	100.0	42	1	US-08-302-808-5	Sequence 5, App1
43	209	100.0	42	1	US-08-268-348A-1	Sequence 1, App1
44	209	100.0	42	1	US-08-433-734-2	Sequence 2, App1
45	209	100.0	42	1	US-08-609-090-9	Sequence 9, App1
46	209	100.0	42	1	US-07-737-371B-72	Sequence 72, App1
47	209	100.0	42	1	US-08-422-333-4	Sequence 4, App1
48	209	100.0	42	1	US-08-682-245A-4	Sequence 4, App1
49	209	100.0	42	1	US-08-986-948-5	Sequence 5, App1
50	209	100.0	42	2	US-08-717-551A-2	Sequence 2, App1
51	209	100.0	42	2	US-09-388-890-1	Sequence 1, App1
52	209	100.0	42	2	US-09-005-215-20	Sequence 20, App1
53	209	100.0	42	2	US-09-242-724-23	Sequence 23, App1
54	209	100.0	42	2	US-08-922-930-2	Sequence 2, App1
55	209	100.0	42	2	US-09-660-984-1	Sequence 1, App1
56	209	100.0	42	2	US-08-923-055-2	Sequence 2, App1
57	209	100.0	42	2	US-08-922-889-2	Sequence 2, App1
58	209	100.0	42	2	US-09-731-460-1	Sequence 1, App1
59	209	100.0	42	2	US-09-133-866-2	Sequence 2, App1
60	209	100.0	42	2	US-09-724-984-1	Sequence 1, App1
61	209	100.0	42	2	US-09-724-961-42	Sequence 42, App1
62	209	100.0	42	2	US-09-724-552-1	Sequence 1, App1
63	209	100.0	42	2	US-09-580-018-42	Sequence 42, App1
64	209	100.0	42	2	US-10-455-218-2	Sequence 2, App1
65	209	100.0	42	2	US-09-723-927-1	Sequence 1, App1
66	209	100.0	42	2	US-09-724-489-1	Sequence 1, App1
67	209	100.0	42	2	US-09-724-477-1	Sequence 1, App1
68	209	100.0	42	2	US-09-723-762-1	Sequence 1, App1
69	209	100.0	42	2	US-09-201-430-1	Sequence 1, App1
70	209	100.0	42	2	US-09-724-551-42	Sequence 42, App1
71	209	100.0	42	2	US-10-815-353-1	Sequence 1, App1
72	209	100.0	42	2	US-10-278-181-1	Sequence 1, App1
73	209	100.0	42	2	US-10-816-529-1	Sequence 1, App1
74	209	100.0	42	2	US-09-623-548A-955	Sequence 955, App
75	209	100.0	42	2	US-09-623-548A-988	Sequence 988, App
76	209	100.0	42	2	US-10-816-022-1	Sequence 1, App1
77	209	100.0	42	2	US-09-724-953-34	Sequence 34, App1
78	209	100.0	42	2	US-09-657-276-985	Sequence 955, App
79	209	100.0	42	2	US-09-657-276-988	Sequence 988, App
80	209	100.0	42	2	US-09-657-276-988	Sequence 988, App
81	209	100.0	42	2	US-09-724-567-34	Sequence 34, App1
82	209	100.0	42	2	US-09-724-567-34	Sequence 34, App1
83	209	100.0	42	2	US-09-865-294A-65	Sequence 65, App1
84	209	100.0	42	2	US-09-879-952-34	Sequence 34, App1
85	209	100.0	42	2	US-09-885-817-34	Sequence 34, App1
86	209	100.0	42	2	US-09-962-955D-37	Sequence 37, App1
87	209	100.0	42	2	US-09-706-574A-20	Sequence 20, App1
88	209	100.0	42	2	US-10-884-609-1	Sequence 1, App1
89	209	100.0	42	2	US-10-884-892-1	Sequence 1, App1
90	209	100.0	42	2	US-09-848-616-174	Sequence 174, App
91	209	100.0	42	2	US-10-933-559-1	Sequence 1, App1
92	209	100.0	42	2	US-10-815-404-1	Sequence 1, App1
93	209	100.0	42	3	US-10-816-380-1	Sequence 1, App1
94	209	100.0	42	3	US-10-363-082-1	Sequence 1, App1
95	209	100.0	42	5	PCT-US92-06700-2	Sequence 2, App1
96	209	100.0	42	5	PCT-US93-00328-1	Sequence 1, App1
97	209	100.0	43	1	US-08-235-400-1	Sequence 1, App1
98	209	100.0	43	1	US-08-437-067-1	Sequence 1, App1
99	209	100.0	43	1	US-08-302-808-6	Sequence 6, App1

100 209 100.0 43 1 US-08-079-511-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-744-767A-1
Sequence 1, Application US/07744767A
Patent No. 5434050
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Maneyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,767A
FILING DATE: 13-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.226-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-744-767A-1
Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGAV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGAV 40
RESULT 2
US-08-235-400-2
Sequence 2, Application US/08235400
Patent No. 5552426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Monn, James A.
APPLICANT: Zimmerman, Dennis M.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America

ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-2
Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGAV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGAV 40
RESULT 3
US-08-476-464A-2
Sequence 2, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 4
US-08-304-585-1

Sequence 1, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantlyn, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-1

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 5
US-08-302-808-3
Sequence 3, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349unhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-3

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 6
US-08-433-734-1
Sequence 1, Application US/08433734
Patent No. 5837473
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantlyn, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis

```

; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-734-1

Query Match          100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 7
US-08-609-090-8
; Sequence 8, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-8

Query Match          100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 8
US-07-737-371E-69
; Sequence 69, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-69

Query Match          100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 9
US-08-682-245A-2
; Sequence 2, Application US/08682245A
; Patent No. 5919631
```


GENERAL INFORMATION:
APPLICANT: GOVAL, SHEPALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHARABUDE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BAA PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-2

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 10
US-08-986-948-3
Sequence 3, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-3

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 11
US-08-461-216-1
Sequence 1, Application US/08461216
Patent No. 5958883
GENERAL INFORMATION:
APPLICANT: SNOW, A.D.
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-c
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,216
FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOPW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: {SYMBOL 98 \f "symbol"/A4(1-40);
; DESCRIPTION: FIGURES 23-29
;
US-08-461-216-1
;
Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 12
US-08-959-148-1
; Sequence 1, Application US/08959148
; Patent No. 6172277
; GENERAL INFORMATION:
; APPLICANT: Tate, Barbara A.
; APPLICANT: Majoche, Ronald
; APPLICANT: Newton, Julie L.
; TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
; FILE REFERENCE: 04930/022001
; CURRENT APPLICATION NUMBER: US/08/959,148
; FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-08-959-148-1
;
Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 13
US-09-242-724-22
; Sequence 22, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
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; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-242-724-22
;
Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 14
US-08-723-661B-1
; Sequence 1, Application US/08723661B
; Patent No. 6340783
; GENERAL INFORMATION:
; APPLICANT: Alan D Snow
; TITLE OF INVENTION: Animal Models of Human Amyloidoses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS (Windows 98)
; SOFTWARE: WordPerfect 5.2
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,661B
; FILING DATE: 31-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,216
; FILING DATE: 05-Jun-1995
; APPLICATION NUMBER: 07/969,734
; FILING DATE: 23-Oct-1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: 23-Sep-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTO.P00C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: /A4 (1-40); FIGURES 23-29
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
US-08-723-661B-1
;
Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
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RESULT 15
US-09-062-365-3
; Sequence 3, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stearn, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-3

Query Match          100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

RESULT 16
US-09-133-866-1
; Sequence 1, Application US/09133866
; Patent No. 6600017
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/09/133,866
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: 60/055,660
; EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-133-866-1

Query Match          100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

RESULT 17
US-09-988-842-3
; Sequence 3, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-3

Query Match          100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

RESULT 18
US-10-455-218-1
; Sequence 1, Application US/10455218
; Patent No. 6770448
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-218-1

Query Match          100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

RESULT 19
US-10-151-614-1
; Sequence 1, Application US/10151614
; Patent No. 6821504
; GENERAL INFORMATION:
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: TURNBULL, Daniel
; APPLICANT: SIGURDSSON, Einar
; APPLICANT: ZAIM WADGHIRI, Yousef
; TITLE OF INVENTION: DETECTION OF ALZHEIMER'S AMYLOID BY MAGNETIC RESONANCE
; FILE REFERENCE: WISNIEWSKI 2A
; CURRENT APPLICATION NUMBER: US/10/151,614
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,625
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-614-1

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 20

US-09-623-548A-956
Sequence 956, Application US/09623548A

PATENT NO. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 956
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-956

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 21

US-09-623-548A-978
Sequence 978, Application US/09623548A

PATENT NO. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110

CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 978
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-978

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 22

US-09-623-548A-989
Sequence 989, Application US/09623548A

PATENT NO. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 989
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-989

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 23

US-09-623-548A-1005

; Sequence 1005, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1005
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-1005

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40

RESULT 24
US-09-657-276-956
; Sequence 956, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 956
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide

US-09-657-276-956

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40

RESULT 25
US-09-657-276-978
; Sequence 978, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 978
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-978

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40

RESULT 26
US-09-657-276-989
; Sequence 989, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17

PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 989
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-989

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40

RESULT 27
US-09-657-276-1005
Sequence 1005, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaut, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1005
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1005

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40

RESULT 28
US-09-962-955D-36
Sequence 36, Application US/09962955D
Patent No. 6933280
GENERAL INFORMATION:
APPLICANT: CASTILLO, GERARDO

APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
FILE REFERENCE: PROTO. P0301
CURRENT APPLICATION NUMBER: US/09/962,955D
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/938,275
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/947,057
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: 60/027,981
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 36
LENGTH: 40
TYPE: PRT
ORGANISM: Mus musculus
US-09-962-955D-36

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 7,4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSV 40

RESULT 29
PCT-US92-06700-1
Sequence 1, Application PC/TUS9206700
GENERAL INFORMATION:
APPLICANT: Mantyh, Patrick W.
APPLICANT: Magglo, John E.
TITLE OF INVENTION: Labelled -Amyloid Peptide
TITLE OF INVENTION: and Alzheimer's Disease Detection
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Northwest Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: Northgate 386
OPERATING SYSTEM: DOS 4.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06700
FILING DATE: 19920810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600,226-WO-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Internal fragment of the -
NAME/KEY: amyloid peptide precursor
LOCATION: Represents isolated internal

LOCATION: sequence of 40 amino acid residues from
LOCATION: the -amyloid peptide precursor
PCT-US92-06700-1

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40

RESULT 30

US-08-302-808-4

Sequence 4, Application US/08302808

Patent No. 5750349

GENERAL INFORMATION:

APPLICANT: SUZUKI, No. 5750349uhiro

APPLICANT: ODAKA, Asano

APPLICANT: KITADA, Chieko

TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

DERIVATIVES AND USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRES:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02019

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,808

FILING DATE: 15-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00089

FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010332/1993

FILING DATE: 25-JAN-1993

APPLICATION NUMBER: 019035/1993

FILING DATE: 05-FEB-1993

APPLICATION NUMBER: 286985/1993

FILING DATE: 16-NOV-1993

APPLICATION NUMBER: 334773/1993

FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 44631

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-302-808-4

Query Match 100.0%; Score 209; DB 1; Length 41;

Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40

Search completed: September 28, 2006, 06:27:14
Job time: 29.1614 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:58:47 ; Search time 91.6592 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-2

Perfect score: 209
Sequence: 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIGIMVGVV 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	40	3	US-09-867-847-2
2	209	100.0	40	3	US-09-988-842-3
3	209	100.0	40	3	US-09-851-071-3
4	209	100.0	40	3	US-09-962-955C-36
5	209	100.0	40	3	US-09-792-079-12
6	209	100.0	40	4	US-10-007-779A-1
7	209	100.0	40	4	US-10-051-496-4
8	209	100.0	40	4	US-10-217-584-3
9	209	100.0	40	4	US-10-169-580-1
10	209	100.0	40	4	US-10-143-534-3
11	209	100.0	40	4	US-10-190-548A-4
12	209	100.0	40	4	US-10-051-663-3
13	209	100.0	40	4	US-10-151-614-1
14	209	100.0	40	4	US-10-159-279-12
15	209	100.0	40	4	US-10-455-218-1
16	209	100.0	40	4	US-10-366-125-27
17	209	100.0	40	4	US-10-337-261-1
18	209	100.0	40	4	US-10-683-815-1
19	209	100.0	40	4	US-10-810-919-1
20	209	100.0	40	5	US-10-864-107-1
21	209	100.0	40	5	US-10-485-310-18
22	209	100.0	40	5	US-10-481-387-1
23	209	100.0	40	5	US-10-481-954-5
24	209	100.0	40	5	US-10-698-259A-1
25	209	100.0	40	5	US-10-884-729-1
26	209	100.0	40	5	US-10-728-246-4
27	209	100.0	40	5	US-10-772-230-3

28	209	100.0	40	5	US-10-933-206-36	Sequence 36, Appl
29	209	100.0	40	5	US-10-825-958-2	Sequence 2, Appl
30	209	100.0	40	5	US-10-775-562-2	Sequence 2, Appl
31	209	100.0	40	5	US-10-296-168-1	Sequence 1, Appl
32	209	100.0	40	5	US-10-966-919B-2	Sequence 2, Appl
33	209	100.0	40	6	US-11-004-053-36	Sequence 36, Appl
34	209	100.0	40	6	US-11-007-643-36	Sequence 36, Appl
35	209	100.0	40	6	US-11-007-844-36	Sequence 36, Appl
36	209	100.0	40	6	US-11-007-669-36	Sequence 36, Appl
37	209	100.0	40	6	US-11-066-697-956	Sequence 956, App
38	209	100.0	40	6	US-11-066-697-978	Sequence 978, App
39	209	100.0	40	6	US-11-066-697-989	Sequence 989, App
40	209	100.0	40	6	US-11-066-697-1005	Sequence 1005, App
41	209	100.0	40	6	US-11-016-706-36	Sequence 36, Appl
42	209	100.0	40	6	US-11-207-954-2	Sequence 2, Appl
43	209	100.0	40	6	US-11-033-105A-18	Sequence 18, Appl
44	209	100.0	40	6	US-11-030-100-4	Sequence 4, Appl
45	209	100.0	40	6	US-11-194-889-15	Sequence 15, Appl
46	209	100.0	40	6	US-11-195-207-15	Sequence 15, Appl
47	209	100.0	40	6	US-10-051-496-3	Sequence 3, Appl
48	209	100.0	40	4	US-10-683-815-13	Sequence 13, Appl
49	209	100.0	40	4	US-10-190-548A-3	Sequence 18, Appl
50	209	100.0	40	6	US-11-194-889-18	Sequence 18, Appl
51	209	100.0	40	6	US-11-195-207-18	Sequence 18, Appl
52	209	100.0	40	2	US-08-922-930-2	Sequence 2, Appl
53	209	100.0	40	2	US-08-923-055-2	Sequence 2, Appl
54	209	100.0	40	2	US-09-867-847-1	Sequence 1, Appl
55	209	100.0	40	2	US-09-956-825-26	Sequence 26, Appl
56	209	100.0	40	2	US-09-731-860-1	Sequence 1, Appl
57	209	100.0	40	2	US-09-962-955C-37	Sequence 37, Appl
58	209	100.0	40	2	US-09-848-616-174	Sequence 174, App
59	209	100.0	40	2	US-09-865-294-65	Sequence 65, Appl
60	209	100.0	40	2	US-09-792-079-13	Sequence 13, Appl
61	209	100.0	40	2	US-09-825-842-1	Sequence 1, Appl
62	209	100.0	40	2	US-09-930-815A-293	Sequence 293, App
63	209	100.0	40	2	US-10-051-496-2	Sequence 2, Appl
64	209	100.0	40	2	US-10-082-804-7	Sequence 7, Appl
65	209	100.0	40	2	US-10-217-584-2	Sequence 2, Appl
66	209	100.0	40	2	US-10-169-580-2	Sequence 2, Appl
67	209	100.0	40	2	US-10-278-181-1	Sequence 1, Appl
68	209	100.0	40	2	US-10-143-534-2	Sequence 2, Appl
69	209	100.0	40	2	US-10-190-548A-1	Sequence 1, Appl
70	209	100.0	40	2	US-10-051-663-2	Sequence 2, Appl
71	209	100.0	40	2	US-10-159-279-13	Sequence 13, Appl
72	209	100.0	40	2	US-10-050-802-220	Sequence 220, App
73	209	100.0	40	2	US-10-050-898-220	Sequence 220, App
74	209	100.0	40	2	US-10-082-014-81	Sequence 81, Appl
75	209	100.0	40	2	US-10-372-076-82	Sequence 82, Appl
76	209	100.0	40	2	US-10-455-218-2	Sequence 2, Appl
77	209	100.0	40	2	US-10-231-898C-15	Sequence 15, Appl
78	209	100.0	40	2	US-10-231-898C-15	Sequence 15, Appl
79	209	100.0	40	2	US-10-231-063C-15	Sequence 15, Appl
80	209	100.0	40	2	US-10-366-125-28	Sequence 28, Appl
81	209	100.0	40	2	US-10-411-544-2	Sequence 2, Appl
82	209	100.0	40	2	US-10-231-813D-15	Sequence 15, Appl
83	209	100.0	40	2	US-10-231-114C-15	Sequence 15, Appl
84	209	100.0	40	2	US-10-337-261-2	Sequence 2, Appl
85	209	100.0	40	2	US-10-363-082-1	Sequence 1, Appl
86	209	100.0	40	2	US-10-433-885-6	Sequence 6, Appl
87	209	100.0	40	2	US-10-423-047-1	Sequence 1, Appl
88	209	100.0	40	2	US-10-617-876-7	Sequence 7, Appl
89	209	100.0	40	2	US-10-429-216-1	Sequence 1, Appl
90	209	100.0	40	2	US-10-656-624-5	Sequence 5, Appl
91	209	100.0	40	2	US-10-622-087-91	Sequence 91, Appl
92	209	100.0	40	2	US-10-683-815-11	Sequence 11, Appl
93	209	100.0	40	2	US-10-732-862A-95	Sequence 95, Appl
94	209	100.0	40	2	US-10-806-006-293	Sequence 293, App
95	209	100.0	40	2	US-10-416-262B-6	Sequence 6, Appl
96	209	100.0	40	2	US-10-677-974-82	Sequence 82, Appl
97	209	100.0	40	2	US-10-805-913-293	Sequence 293, App
98	209	100.0	40	2	US-10-816-022-1	Sequence 1, Appl
99	209	100.0	40	2	US-10-816-529-1	Sequence 1, Appl
100	209	100.0	40	2	US-10-815-353-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-867-847-2
; Sequence 2, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 1445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-2

Query Match 100.0%; Score 209; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 2
US-09-988-842-3
; Sequence 3, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-3

Query Match 100.0%; Score 209; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 3
US-09-851-071-3
; Sequence 3, Application US/09851071
; Patent No. US20020177550A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Anne Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/851,071
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human
US-09-851-071-3

Query Match 100.0%; Score 209; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 4
US-09-962-955C-36
; Sequence 36, Application US/09962955C
; Publication No. US20030013648A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo M. Castillo
; APPLICANT: Alan D. Snow
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: ProteoTech, Inc, 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Wordperfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,955C
; FILING DATE: 24-September-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/938,275
; FILING DATE: 22-August-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTEO.P03CI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR

ORIGINAL SOURCE:
ORGANISM: MOUSE
FEATURE:
OTHER INFORMATION: Also referred to in the specification as "AB 1-40"
US-09-962-955C-36

Query Match 100.0%; Score 209; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40

RESULT 5
US-09-792-079-12
Sequence 12, Application US/09792079
Publication No. US20030083277A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: Herish, Louis B.
APPLICANT: Mukherjee, Atish
TITLE OF INVENTION: Use Of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzheimer's Disease
FILE REFERENCE: 050229-0261
CURRENT APPLICATION NUMBER: US/09/792,079
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,826
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-09-792-079-12

Query Match 100.0%; Score 209; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40

RESULT 6
US-10-007-779A-1
Sequence 1, Application US/10007779A
Publication No. US20020168753A1
GENERAL INFORMATION:
APPLICANT: Cascilio, Gerardo and Snow, Alan
TITLE OF INVENTION: In Vitro Formation of Congophilic
Maltese-Cross Amyloid Plaques to Identify Anti-Plaque
Therapeutics for the Treatment of Alzheimer's and Prion Dis
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrick M. Dwyer
STREET: Proteotech, Inc., 1818 Westlake Ave N, Suite 114
CITY: Seattle
STATE: WA (Washington)
COUNTRY: USA
ZIP: 98109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: PC
OPERATING SYSTEM: Windows 98
SOFTWARE: WordPerfect 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,779A
FILING DATE: 28-Apr-2002
CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/267,795
FILING DATE: 12-March-1999
ATTORNEY/AGENT INFORMATION:
NAME: Dwyer, Patrick M.
REGISTRATION NUMBER: 32,411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 343-7074
TELEFAX: (206) 343-7085
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-007-779A-1

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGVV 40

RESULT 7
US-10-051-496-4
Sequence 4, Application US/10051496
Publication No. US20020182660A1
GENERAL INFORMATION:
APPLICANT: Kei-Lai L. Fong
TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
Abeta(1-41), Abeta(1-42) and Abeta(1-43)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kei-Lai L. Fong
STREET: 1004 West 8th Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US20020182660A1epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183,407
FILING DATE: 18-February-2000
ATTORNEY/AGENT INFORMATION:
NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein

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;
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1-40
; IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1-40
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;
; US-10-051-496-4
;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 8
; US-10-217-584-3
; Sequence 3, Application US/10217584
; Publication No. US2003007261A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Daniel
; APPLICANT: Mullian, Michael
; TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
; FILE REFERENCE: USF-1161XCI
; CURRENT APPLICATION NUMBER: US/10/217,584
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,656
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: A-beta 1-40 peptide
;
; US-10-217-584-3
;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 9
; US-10-169-580-1
; Sequence 1, Application US/10169580
; Publication No. US20030100477A1
; GENERAL INFORMATION:
; APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR SUPPRESSING B-AMYLOID PRODUCTION
; FILE REFERENCE: Q70898
; CURRENT APPLICATION NUMBER: US/10/169,580
; PRIOR FILING DATE: 2002-07-08
; CURRENT APPLICATION NUMBER: 2000-131037
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/J001/03555
;
; US-10-051-496-4
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; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
;
; US-10-169-580-1
;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 10
; US-10-143-534-3
; Sequence 3, Application US/10143534
; Publication No. US20030105152A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M00656/70078
; CURRENT APPLICATION NUMBER: US/10/143,534
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 10/051,663
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
;
; US-10-143-534-3
;
Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 11
; US-10-190-548A-4
; Sequence 4, Application US/10190548A
; Publication No. US20030109435A1
; GENERAL INFORMATION:
; APPLICANT: Griswold Preiner, Irene
; APPLICANT: Wright, Sarah
; APPLICANT: Yednock, Theodore
; APPLICANT: Rydel, Russell
; TITLE OF INVENTION: Methods of Inhibiting Amyloid Toxicity
; FILE REFERENCE: 08576.0030-00
; CURRENT APPLICATION NUMBER: US/10/190,548A
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
;
; US-10-190-548A-4
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Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 12
US-10-051-663-3
; Sequence 3, Application US/10051663
; Publication No. US20030114510A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M0656/7071
; CURRENT APPLICATION NUMBER: US/10/051,663
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-051-663-3
OTHER INFORMATION: Synthetic Peptide

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 13
US-10-151-614-1
; Sequence 1, Application US/10151614
; Publication No. US20030147811A1
; GENERAL INFORMATION:
; APPLICANT: WISNIEWSKI, Thomas
; APPLICANT: TURNBULL, Daniel
; APPLICANT: SIGURDSSON, Einar
; APPLICANT: ZAIM WADGHIRI, Yousef
; TITLE OF INVENTION: DETECTION OF ALZHEIMER'S AMYLOID BY MAGNETIC RESONANCE
; FILE REFERENCE: WISNIEWSKI 2A
; CURRENT APPLICATION NUMBER: US/10/151,614
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,625
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-614-1

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 14
US-10-159-279-12
; Sequence 12, Application US/10159279
; Publication No. US20030165481A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Hersh, Louis B.
; APPLICANT: Mukherjee, Atish
; TITLE OF INVENTION: Use Of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzhe

; FILE REFERENCE: 050229-0298
; CURRENT APPLICATION NUMBER: US/10/159,279
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/184,826
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/792,079
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-279-12

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 15
US-10-455-218-1
; Sequence 1, Application US/10455218
; Publication No. US20030204051A1
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; TITLE OF INVENTION: USFS THEREOF
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-218-1

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV 40

RESULT 16
US-10-366-125-27
; Sequence 27, Application US/10366125
; Publication No. US20030228259A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Hellerstein, Marc
/ TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
/ TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
/ TITLE OF INVENTION: EASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
/ TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
/ TITLE OF INVENTION: CATABOLIC PRODUCTS
/ FILE REFERENCE: 416272003500
/ CURRENT APPLICATION NUMBER: US/10/366,125
/ PRIOR FILING DATE: 2003-02-12
/ PRIOR APPLICATION NUMBER: US 60/356,008
/ PRIOR FILING DATE: 2002-02-12
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-366-125-27
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Query Match          100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
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RESULT 17
US-10-337-261-1
/ Sequence 1, Application US/10337261
/ Publication No. US20040028673A1
/ GENERAL INFORMATION:
/ APPLICANT: Netzer, William
/ APPLICANT: Greengard, Paul
/ APPLICANT: Xu, Huaxi
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTION AND TREATMENT OF AMYLOID-
/ TITLE OF INVENTION: PEPTIDE RELATED DISORDERS
/ FILE REFERENCE: 11181-014-999
/ CURRENT APPLICATION NUMBER: US/10/337,261
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: 60/345,009
/ PRIOR FILING DATE: 2002-01-04
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-337-261-1
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Query Match          100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
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```
RESULT 18
US-10-683-815-1
/ Sequence 1, Application US/10683815
/ Publication No. US20040146512A1
/ GENERAL INFORMATION:
/ APPLICANT: ROSENTHAL, Arnon
/ APPLICANT: LEVKOWITZ, Gili
/ TITLE OF INVENTION: METHODS OF TREATING ALZHEIMER'S DISEASE
/ TITLE OF INVENTION: USING ANTIBODIES DIRECTED AGAINST AMYLOID BETA PEPTIDE AND
/ TITLE OF INVENTION: COMPOSITIONS THEREOF
/ FILE REFERENCE: 514712001500
/ CURRENT APPLICATION NUMBER: US/10/683,815
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/ CURRENT FILING DATE: 2003-10-09
/ PRIOR APPLICATION NUMBER: US 60/417,232
/ PRIOR FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US 60/447,611
/ PRIOR FILING DATE: 2003-02-13
/ PRIOR APPLICATION NUMBER: US 60/464,754
/ PRIOR FILING DATE: 2003-04-22
/ PRIOR APPLICATION NUMBER: US 60/480,353
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-683-815-1
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Query Match          100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
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RESULT 19
US-10-810-919-1
/ Sequence 1, Application US/10810919
/ Publication No. US20040214774A1
/ GENERAL INFORMATION:
/ APPLICANT: Wisniewski, Thomas
/ APPLICANT: Sadowski, Marcin
/ APPLICANT: Sigurdsson, Einar M.
/ TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER AMYLOID
/ TITLE OF INVENTION: DEPOSITION
/ FILE REFERENCE: 57953/1211
/ CURRENT APPLICATION NUMBER: US/10/810,919
/ PRIOR FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER: 60/458,986
/ PRIOR FILING DATE: 2003-03-28
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide
US-10-810-919-1
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Query Match          100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
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RESULT 20
US-10-864-107-1
/ Sequence 1, Application US/10864107
/ Publication No. US20040224365A1
/ GENERAL INFORMATION:
/ APPLICANT: Glabe, Charles
/ APPLICANT: Garzon-Rodriguez, William
/ TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
/ TITLE OF INVENTION: USBS THEREOF
/ FILE REFERENCE: 50016/002002
/ CURRENT APPLICATION NUMBER: US/10/864,107
/ CURRENT FILING DATE: 2004-06-09
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PRIOR APPLICATION NUMBER: US/09/133,866
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/055,660
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-864-107-1

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 21
US-10-485-310-18
Sequence 18, Application US/10485310
Publication No. US20040234990A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: A Method For Screening A Gene Related To Alzheimer's Disease
FILE REFERENCE: P01-0277/PCT
CURRENT APPLICATION NUMBER: US/10/485,310
CURRENT FILING DATE: 2004-01-26
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 18
LENGTH: 40
TYPE: PRT
ORGANISM: Human
US-10-485-310-18

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 22
US-10-481-387-1
Sequence 1, Application US/10481387
Publication No. US20040248766A1
GENERAL INFORMATION:
APPLICANT: Leblanc, Andrea
TITLE OF INVENTION: Selective Inhibition of Intracellular Amyloid-Beta
FILE REFERENCE: 27848-501
CURRENT APPLICATION NUMBER: US/10/481,387
CURRENT FILING DATE: 2003-12-18
PRIOR APPLICATION NUMBER: 60/298,373
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/330,543
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: PCT/CA02/00916
PRIOR FILING DATE: 2002-06-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-481-387-1

Query Match 100.0%; Score 209; DB 5; Length 40;

Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 23
US-10-481-954-5
Sequence 5, Application US/10481954
Publication No. US20040253647A1
GENERAL INFORMATION:
APPLICANT: New York State Office of Mental Health
TITLE OF INVENTION: Cell-based High Throughput Screening Methods
FILE REFERENCE: 1079-4014PC
CURRENT APPLICATION NUMBER: US/10/481,954
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/300,959
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 5
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide recognized by JRF/Abtc/17 antibody.
US-10-481-954-5

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 24
US-10-698-259A-1
Sequence 1, Application US/10698259A
Publication No. US20040259211A1
GENERAL INFORMATION:
APPLICANT: NGUYEN, BETH P.
APPLICANT: CHOI, PATIA Y.
APPLICANT: SANDERS, VIRGINIA J.
APPLICANT: CASTILLO, GERARDO
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: RAPID INDUCTION OF ALZHEIMER'S AMYLOID PLAQUE FORMATION
FILE REFERENCE: PROTEO.P08CI
CURRENT APPLICATION NUMBER: US/10/698,259A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/007,779
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/267,795
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/423,185
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-698-259A-1

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 25

US-10-884-729-1
; Sequence 1, Application US/10884729
; Publication No. US2005009749A1
; GENERAL INFORMATION:
; APPLICANT: Sangmei AHN JO
; APPLICANT: Inho JO
; APPLICANT: Ho Jeong KWON
; APPLICANT: Chang Jin KIM
; APPLICANT: Jeong Eun PARK
; TITLE OF INVENTION: Protein inhibiting the aggregation of beta amyloid peptide
; FILE REFERENCE: 428,1042
; CURRENT APPLICATION NUMBER: US/10/884,729
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: 10-2003-0047199
; PRIOR FILING DATE: 2003-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-729-1

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 26

US-10-728-246-4
; Sequence 4, Application US/10728246
; Publication No. US20050026165A1
; GENERAL INFORMATION:
; APPLICANT: ORSER, Cindy
; APPLICANT: GROSSET, Anne
; APPLICANT: DAVIDSON, Eugene A.
; TITLE OF INVENTION: DETECTION OF CONFORMATIONALLY ALTERED PROTEINS AND PRIONS
; FILE REFERENCE: A28-011
; CURRENT APPLICATION NUMBER: US/10/728,246
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 10/161,061
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/295,456
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-728-246-4

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 27
US-10-772-230-3

; Sequence 3, Application US/10772230
; Publication No. US20050059084A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/10/772,230
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US/09/988,842
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-772-230-3

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Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 28

US-10-933-206-36
; Sequence 36, Application US/10933206
; Publication No. US20050059602A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTO.P03CID1
; CURRENT APPLICATION NUMBER: US/10/933,206
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; PRIOR APPLICATION NUMBER: 60/027,981
; PRIOR FILING DATE: 1996-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-933-206-36

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

RESULT 29
US-10-825-958-2


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; Sequence 2, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-2
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Query Match      100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
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RESULT 30
US-10-775-562-2
; Sequence 2, Application US/10775562
; Publication No. US20050095201A1
; GENERAL INFORMATION:
; APPLICANT: Poduslo, Joseph F.
; APPLICANT: Curran, Geoffrey L.
; APPLICANT: Mungenack, Thomas M.
; APPLICANT: McCormick, Daniel J.
; APPLICANT: Faug, Abdul H.
; TITLE OF INVENTION: Amino Acid Composition with Increased Blood Brain Barrier
; TITLE OF INVENTION: Permeability
; FILE REFERENCE: 630666.00028
; CURRENT APPLICATION NUMBER: US/10/775,562
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/515,460
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-562-2
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Query Match      100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
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Search completed: September 28, 2006, 07:09:26
Job time : 91.8259 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 ; Search time 15.6054 Seconds
(without alignments)
199.069 Million cell updates/sec

Title: US-09-731-899-2

Perfect score: 209
Sequence: 1 DAEFRHDSGYEVHOKLVFPAEDVGNKALIGLWGVV 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 285145 seqs, 77663843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lifting first 100 summaries

Database :

Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	40	1	US-09-731-899-2
2	209	100.0	40	6	US-10-966-645-17
3	209	100.0	42	6	US-10-890-071-42
4	209	100.0	42	6	US-10-544-093-1
5	209	100.0	42	6	US-10-546-547-3
6	209	100.0	42	6	US-10-966-645-36
7	209	100.0	42	7	US-11-104-300-2
8	209	100.0	42	7	US-11-297-316-1
9	209	100.0	42	7	US-11-287-157A-49
10	209	100.0	43	1	US-09-731-899-4
11	209	100.0	43	7	US-11-348-091-1
12	209	100.0	56	6	US-10-544-093-16
13	209	100.0	56	6	US-10-544-093-19
14	209	100.0	58	6	US-10-515-919A-30
15	209	100.0	58	6	US-10-544-093-12
16	209	100.0	58	6	US-10-544-093-14
17	209	100.0	58	6	US-10-544-093-27
18	209	100.0	59	1	US-09-731-899-1
19	209	100.0	60	6	US-10-544-093-10
20	209	100.0	64	6	US-10-544-093-13
21	209	100.0	79	6	US-10-544-093-15
22	209	100.0	99	6	US-10-544-093-22
23	209	100.0	99	6	US-10-544-093-24
24	209	100.0	142	6	US-10-544-093-17
25	209	100.0	142	6	US-10-544-093-21

26	209	100.0	142	6	US-10-544-093-23	Sequence 23, Appl
27	209	100.0	185	6	US-10-544-093-18	Sequence 18, Appl
28	209	100.0	203	6	US-10-544-093-26	Sequence 26, Appl
29	209	100.0	316	6	US-10-544-093-25	Sequence 25, Appl
30	209	100.0	695	6	US-10-515-919A-1	Sequence 1, Appl
31	209	100.0	695	6	US-10-511-269-7	Sequence 7, Appl
32	209	100.0	751	6	US-10-546-547-2	Sequence 2, Appl
33	209	100.0	770	6	US-10-511-269-9	Sequence 9, Appl
34	209	97.6	42	6	US-10-515-919A-3	Sequence 3, Appl
35	204	97.6	42	6	US-10-515-919A-13	Sequence 13, Appl
36	204	97.6	626	6	US-10-515-919A-13	Sequence 13, Appl
37	204	97.6	626	6	US-10-515-919A-18	Sequence 18, Appl
38	203	97.1	40	7	US-11-104-300-3	Sequence 3, Appl
39	203	97.1	42	1	US-09-731-899-3	Sequence 5, Appl
40	203	97.1	42	6	US-10-515-919A-5	Sequence 10, Appl
41	203	97.1	42	6	US-10-515-919A-10	Sequence 10, Appl
42	203	97.1	626	6	US-10-515-919A-15	Sequence 15, Appl
43	203	97.1	626	6	US-10-515-919A-20	Sequence 20, Appl
44	202	96.7	40	7	US-11-269-857-3	Sequence 3, Appl
45	202	96.7	42	6	US-10-515-919A-4	Sequence 4, Appl
46	202	96.7	42	6	US-10-515-919A-6	Sequence 6, Appl
47	202	96.7	42	6	US-10-515-919A-9	Sequence 9, Appl
48	202	96.7	42	6	US-10-515-919A-11	Sequence 11, Appl
49	202	96.7	42	7	US-11-269-857-5	Sequence 5, Appl
50	202	96.7	626	6	US-10-515-919A-14	Sequence 14, Appl
51	202	96.7	626	6	US-10-515-919A-16	Sequence 16, Appl
52	202	96.7	626	6	US-10-515-919A-19	Sequence 19, Appl
53	202	96.7	626	6	US-10-515-919A-21	Sequence 21, Appl
54	201	96.2	42	6	US-10-515-919A-2	Sequence 2, Appl
55	201	96.2	42	6	US-10-515-919A-7	Sequence 7, Appl
56	201	96.2	626	6	US-10-515-919A-12	Sequence 12, Appl
57	201	96.2	626	6	US-10-515-919A-17	Sequence 17, Appl
58	199	95.2	38	6	US-10-966-645-38	Sequence 38, Appl
59	199	95.2	40	6	US-10-966-645-38	Sequence 38, Appl
60	198	94.7	42	6	US-10-515-919A-22	Sequence 22, Appl
61	198	94.7	43	6	US-10-515-919A-23	Sequence 23, Appl
62	196	93.8	38	6	US-10-966-645-44	Sequence 44, Appl
63	194	92.8	40	1	US-09-731-899-5	Sequence 5, Appl
64	190	90.9	695	6	US-10-538-410-96	Sequence 96, Appl
65	190	90.9	770	7	US-11-104-300-1	Sequence 1, Appl
66	152	72.7	28	7	US-11-287-116-2	Sequence 2, Appl
67	147	70.3	32	1	US-09-731-899-6	Sequence 6, Appl
68	117	56.0	26	1	US-09-731-899-7	Sequence 7, Appl
69	116	55.5	21	6	US-10-966-645-42	Sequence 42, Appl
70	106	50.7	19	6	US-10-966-645-43	Sequence 43, Appl
71	103	49.3	19	6	US-10-966-645-45	Sequence 45, Appl
72	84	40.2	19	6	US-10-890-071-75	Sequence 75, Appl
73	66	31.6	13	6	US-10-890-071-72	Sequence 72, Appl
74	62	29.7	11	6	US-10-966-645-40	Sequence 40, Appl
75	61	29.2	10	6	US-10-890-071-13	Sequence 13, Appl
76	61	29.2	10	6	US-10-890-071-14	Sequence 14, Appl
77	59	28.2	10	6	US-10-890-071-12	Sequence 12, Appl
78	59	28.2	11	6	US-10-966-645-35	Sequence 35, Appl
79	58	27.8	10	6	US-10-890-071-15	Sequence 15, Appl
80	58	27.8	624	6	US-10-449-902-33879	Sequence 33879, A
81	57	27.3	10	6	US-10-890-071-9	Sequence 9, Appl
82	57	27.3	10646	6	US-10-449-902-51230	Sequence 51230, A
83	36	26.8	10	6	US-10-890-071-10	Sequence 10, Appl
84	36	26.8	10	6	US-10-890-071-11	Sequence 11, Appl
85	36	26.8	10	6	US-10-890-071-16	Sequence 16, Appl
86	36	26.8	10	6	US-10-890-071-17	Sequence 17, Appl
87	36	26.8	10	6	US-10-890-071-18	Sequence 18, Appl
88	36	26.8	618	6	US-10-449-902-47542	Sequence 47542, A
89	36	26.3	10	6	US-10-890-071-19	Sequence 19, Appl
90	36	26.3	10	6	US-10-890-071-21	Sequence 21, Appl
91	36	26.3	826	7	US-11-056-3558-87461	Sequence 87461, A
92	36	26.1	828	7	US-11-056-3558-87460	Sequence 87460, A
93	36	26.1	1063	7	US-11-056-3558-87459	Sequence 87459, A
94	36	25.8	10	6	US-10-890-071-20	Sequence 20, Appl
95	36	25.6	971	6	US-10-528-563-7	Sequence 7, Appl
96	36	25.4	10	6	US-10-890-071-22	Sequence 22, Appl
97	36	25.4	125	7	US-11-056-3558-25854	Sequence 25854, A
98	36	25.4	256	7	US-11-056-3558-25853	Sequence 25853, A

ALIGNMENTS

99 53 25.4 429 7 US-11-056-355B-53789 Sequence 53789, A
100 53 25.4 556 7 US-11-056-355B-53788 Sequence 53788, A

RESULT 1

US-09-731-899-2
; Sequence 2, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; TITLE OF INVENTION: FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
; FILE REFERENCE: 2055/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-2

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

Db

RESULT 2
US-10-966-645-37
; Sequence 37, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 37
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-37

Query Match 100.0%; Score 209; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

Db

RESULT 3
US-10-890-071-42
; Sequence 42, Application US/10890071

; Publication No. US20060121038A9
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-890-071-42

Query Match 100.0%; Score 209; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

Db

RESULT 4
US-10-544-093-1
; Sequence 1, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-544-093-1

Query Match 100.0%; Score 209; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVV 40

Db

RESULT 5
US-10-546-547-3
; Sequence 3, Application US/10546547
; Publication No. US20060188951A1
; GENERAL INFORMATION:
; APPLICANT: Mook, In Hee

```
; APPLICANT: Hui, Ji Yuen
; TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
; FILE REFERENCE: DE-1646
; CURRENT APPLICATION NUMBER: US/10/546,547
; PRIOR FILING DATE: 2005-08-23
; PRIOR APPLICATION NUMBER: PCT/KR2004/000371
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 1-42 amino acid of amyloid a4 precursor protein (APP)
US-10-546-547-3
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Query Match          100.0%; Score 209; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
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RESULT 6
US-10-966-645-36
; Sequence 36, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROUJ, ANDRE JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 36
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-36
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```
Query Match          100.0%; Score 209; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
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RESULT 7
US-11-104-300-2
; Sequence 2, Application US/11104300
; Publication No. US20060099211A1
; GENERAL INFORMATION:
; APPLICANT: Monthe, Carmen
; APPLICANT: Szabo, Paul
; APPLICANT: Weksler, Mark
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treating
; FILE REFERENCE: 1676.027051
; CURRENT APPLICATION NUMBER: US/11/104,300
```

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; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US 60/561,423
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-104-300-2
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```
Query Match          100.0%; Score 209; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
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```
RESULT 8
US-11-297-316-1
; Sequence 1, Application US/11297316
; Publication No. US20060141602A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; PRIOR FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-1
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```
Query Match          100.0%; Score 209; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
Db      1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVV 40
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```
RESULT 9
US-11-287-157A-49
; Sequence 49, Application US/11287157A
; Publication No. US20060154863A1
; GENERAL INFORMATION:
; APPLICANT: SKIBATCH, HANNA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
; FILE REFERENCE: 32051-701.201
; CURRENT APPLICATION NUMBER: US/11/287,157A
; PRIOR FILING DATE: 2005-11-25
; PRIOR APPLICATION NUMBER: 60/658,859
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/652,287
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/630,880
; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 49
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-287-157A-49
```

Query Match 100.0%; Score 209; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 10
US-09-731-899-4
Sequence 4, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
TITLE OF INVENTION: FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
FILE REFERENCE: 20555/1203433-US1
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-731-899-4

Query Match 100.0%; Score 209; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 11
US-11-348-091-1
Sequence 1, Application US/11348091
Publication No. US20060211679A1
GENERAL INFORMATION:
APPLICANT: Han, Qi
TITLE OF INVENTION: Substituted Lactams as Inhibitors of Abeta Protein Production
FILE REFERENCE: BMS-PH-7164.1(C)
CURRENT FILING DATE: 2006-02-06
PRIOR APPLICATION NUMBER: US 10/685,031
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 09/832,455
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/196,549
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-11-348-091-1

Query Match 100.0%; Score 209; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 12
US-10-544-093-16
Sequence 16, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial

FEATURE:
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (3)-(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (14)-(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16

Query Match 100.0%; Score 209; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 14 DAERHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 53

RESULT 13
US-10-544-093-19
Sequence 19, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial
FEATURE:
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (3)-(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (14)-(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16

```

; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (46)..(46)
; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-19
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```

Query Match          100.0%; Score 209; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
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RESULT 14
US-10-515-919A-30
; Sequence 30, Application US/10515919A
; Publication No. US20060160146A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
; FILE REFERENCE: 084952
; CURRENT APPLICATION NUMBER: US/10/515, 919A
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: PCT/JP03/06319
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: JP 2002-159472
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 30
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-515-919A-30
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Query Match          100.0%; Score 209; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 56
```

```

RESULT 15
US-10-544-093-12
; Sequence 12, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544, 093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444, 150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
; LENGTH: 58
; TYPE: PRT
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```

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12
```

```

Query Match          100.0%; Score 209; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
```

```

RESULT 16
US-10-544-093-14
; Sequence 14, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544, 093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444, 150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-14
```

```

Query Match          100.0%; Score 209; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFPADYVGSNKGAIIGLMVGGVV 40
```

```

RESULT 17
US-10-544-093-27
; Sequence 27, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
```

```

; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27
```

```

Query Match          100.0%; Score 209; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
```

RESULT 18

```

US-09-731-899-1
; Sequence 1, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 2055/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-1
```

```

Query Match          100.0%; Score 209; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
Db 5 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 44
```

RESULT 19

```

US-10-544-093-20
; Sequence 20, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
```

```

; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-20
```

```

Query Match          100.0%; Score 209; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
```

RESULT 20

```

US-10-544-093-13
; Sequence 13, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13
```

```

Query Match          100.0%; Score 209; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
```

```

; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13
```

```

Query Match          100.0%; Score 209; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
Db 1 DAEFRHDSGYEVHHQKLVFPFAEDVGSNKGAIIGLMVGSVV 40
```

```

RESULT 21
US-10-544-093-15
```



```
; Sequence 15, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-15
```

```
Query Match          100.0%; Score 209; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 2,3e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
```

```
RESULT 22
US-10-544-093-22
; Sequence 22, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FILE REFERENCE: 15270J-009820US
```

```
; LOCATION: (57)..(99)
; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-22
```

```
Query Match          100.0%; Score 209; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 2,9e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
```

```
RESULT 23
US-10-544-093-24
; Sequence 24, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FILE REFERENCE: 15270J-009820US
```

```
US-10-544-093-24
; LOCATION: (44)..(86)
; OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-24
```

```
Query Match          100.0%; Score 209; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 2,9e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVV 40
```

```
RESULT 24
US-10-544-093-17
; Sequence 17, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
```

;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 17
;; LENGTH: 142
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: A-beta-A-beta-A-beta-Padre fusion protein
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(43)
;; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (44)..(86)
;; OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (87)..(129)
;; OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (132)..(132)
;; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-17

Query Match 100.0%; Score 209; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.3e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 25
US-10-544-093-21

;; Sequence 21, Application US/10544093
;; Publication No. US20060188512A1
;; GENERAL INFORMATION:
;; APPLICANT: Vasquez, Ted
;; APPLICANT: Yednock, Nicki
;; APPLICANT: Bard, Frederique
;; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
;; FILE REFERENCE: 15270J-009820US
;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 21
;; LENGTH: 142
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Fusion protein
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (14)..(56)

;; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (57)..(99)
;; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (100)..(142)
;; OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-21

Query Match 100.0%; Score 209; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.3e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 14 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 53

RESULT 26
US-10-544-093-23

;; Sequence 23, Application US/10544093
;; Publication No. US20060188512A1
;; GENERAL INFORMATION:
;; APPLICANT: Yednock, Ted
;; APPLICANT: Vasquez, Nicki
;; APPLICANT: Bard, Frederique
;; APPLICANT: Seubert, Peter A.
;; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
;; FILE REFERENCE: 15270J-009820US
;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 23
;; LENGTH: 142
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Fusion protein
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(43)
;; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (44)..(86)
;; OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (87)..(129)
;; OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-23

Query Match 100.0%; Score 209; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 4.3e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

```
RESULT 27
US-10-544-093-18
; Sequence 18, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: NO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(56)
; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)..(99)
; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (100)..(142)
; OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (143)..(185)
; OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-18

Query Match          100.0%; Score 209; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db
14 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 53

RESULT 28
US-10-544-093-26
; Sequence 26, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
```

```
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: NO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (81)..(123)
; OTHER INFORMATION: Only a contiguous fragment of residues 81-123 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (161)..(203)
; OTHER INFORMATION: Only a contiguous fragment of residues 161-203 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-26

Query Match          100.0%; Score 209; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.4e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 29
US-10-544-093-25
; Sequence 25, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: NO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
```

```

;
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (109)..(151)
; OTHER INFORMATION: Only a contiguous fragment of residues 109-151 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (152)..(194)
; OTHER INFORMATION: Only a contiguous fragment of residues 152-194 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (195)..(237)
; OTHER INFORMATION: Only a contiguous fragment of residues 195-237 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (238)..(280)
; OTHER INFORMATION: Only a contiguous fragment of residues 238-280 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-25

```

```

Query Match          100.0%; Score 209; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGGVV 40
DB      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGGVV 40

```

```

RESULT 30
US-10-515-919A-1
; Sequence 1, Application US/10515919A
; Publication No. US20060160146A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
; FILE REFERENCE: 084952
; CURRENT APPLICATION NUMBER: US/10/515,919A
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: PCT/JP03/06319
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: JP 2002-159472
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-515-919A-1

```

```

Query Match          100.0%; Score 209; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGGVV 40
DB      597 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGGVV 636

```

```

Search completed: September 28, 2006, 07:10:56
Job time : 15.6054 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 112.251 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-3

Perfect score: 211
Sequence: 1 XAEFRHDSGYEVHQLVFF.....DVGSNKGAIIGLMWGVVIA 42

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_8:.*
2: geneseqp1980s:.*
3: geneseqp1990s:.*
4: geneseqp2000s:.*
5: geneseqp2001s:.*
6: geneseqp2002s:.*
7: geneseqp2003as:.*
8: geneseqp2003bs:.*
9: geneseqp2004s:.*
10: geneseqp2005s:.*
10: geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	42	2 AAR20330	AAR20330 Sequence
2	211	100.0	42	2 AAR60366	AAR60366 Beta-amy1
3	211	100.0	42	2 AAR95248	AAR95248 Beta/A4-a
4	211	100.0	42	2 AAR94591	AAR94591 Alzheimer
5	211	100.0	42	2 AAM12828	AAM12828 Beta A4 p
6	211	100.0	42	2 AAM64507	AAM64507 Neurotoxi
7	211	100.0	42	2 AAM42989	AAM42989 Full leng
8	211	100.0	42	2 AAM47230	AAM47230 Beta-amy1
9	211	100.0	42	2 AAY49691	AAY49691 Human bet
10	211	100.0	42	2 AAM99585	AAM99585 Mutant ag
11	211	100.0	42	2 AAM81474	AAM81474 Synthetic
12	211	100.0	42	2 AAY08607	AAY08607 Human bet
13	211	100.0	42	2 AAM29093	AAM29093 A-beta-bi
14	211	100.0	42	2 AAY25137	AAY25137 Human amy
15	211	100.0	42	2 AAY92726	AAY92726 Human lac
16	211	100.0	42	2 AAY33407	AAY33407 Human amy
17	211	100.0	42	3 AAY96956	AAY96956 Beta-amy1
18	211	100.0	42	4 AAB86134	AAB86134 Human Alz
19	211	100.0	42	4 AAB35589	AAB35589 Beta/A4-a
20	211	100.0	42	4 AAB49098	AAB49098 Human amy
21	211	100.0	42	4 AAB84427	AAB84427 Partial s
22	211	100.0	42	4 AAB48497	AAB48497 Human amy
23	211	100.0	42	4 AAB91779	AAB91779 Amyloid b

24	211	100.0	42	4 AAB91812	AAB91812 Amyloid b
25	211	100.0	42	4 AAB82622	AAB82622 Amyloid-b
26	211	100.0	42	4 AAB49395	AAB49395 Human amy
27	211	100.0	42	4 AAB48830	AAB48830 Human amy
28	211	100.0	42	4 AAE05484	AAE05484 Human pep
29	211	100.0	42	5 ABB81321	ABB81321 Amyloid p
30	211	100.0	42	5 AAU80961	AAU80961 Human amy
31	211	100.0	42	5 AAU98727	AAU98727 Human amy
32	211	100.0	42	5 ABG94281	ABG94281 Amyloid b
33	211	100.0	42	5 AAE21438	AAE21438 Human bet
34	211	100.0	42	5 ABB76029	ABB76029 Beta amy1
35	211	100.0	42	5 AAE25335	AAE25335 Modified
36	211	100.0	42	5 AAOL5848	AAOL5848 Beta-amy1
37	211	100.0	42	5 AAU76483	AAU76483 Amino aci
38	211	100.0	42	5 AAE26080	AAE26080 Beta amy1
39	211	100.0	42	5 AAG68314	AAG68314 Human bet
40	211	100.0	42	5 AAU96896	AAU96896 Human Amy
41	211	100.0	42	5 AAU93988	AAU93988 Human bet
42	211	100.0	42	5 AAE26300	AAE26300 Human bet
43	211	100.0	42	5 ABG80593	ABG80593 Human amy
44	211	100.0	42	5 AAM51864	AAM51864 Neuronal
45	211	100.0	42	5 AAU75433	AAU75433 Amyloid p
46	211	100.0	42	5 ABB83306	ABB83306 Amyloid-b
47	211	100.0	42	5 ABB77990	ABB77990 Beta-amy1
48	211	100.0	42	6 AAE35671	AAE35671 Human bet
49	211	100.0	42	6 AAOL6344	AAOL6344 A-beta pr
50	211	100.0	42	6 ABU08711	ABU08711 Amyloid b
51	211	100.0	42	6 ABU08506	ABU08506 Human amy
52	211	100.0	42	6 AAE33793	AAE33793 Beta-amy1
53	211	100.0	42	6 ABP99423	ABP99423 Beta-amy1
54	211	100.0	42	6 ABB82633	ABB82633 Abeta fib
55	211	100.0	42	6 ABP96144	ABP96144 Human Abe
56	211	100.0	42	6 ABG72233	ABG72233 Human bet
57	211	100.0	42	6 AAE35428	AAE35428 Abeta pro
58	211	100.0	42	6 AAE33218	AAE33218 Beta amy1
59	211	100.0	42	6 ABP97882	ABP97882 Amino aci
60	211	100.0	42	6 ABU63707	ABU63707 Rat amy1o
61	211	100.0	42	6 ADA89912	ADA89912 Abeta42 a
62	211	100.0	42	7 ADA37267	ADA37267 Human bet
63	211	100.0	42	7 ADB37652	ADB37652 Human bet
64	211	100.0	42	7 ADB85562	ADB85562 Beta-amy1
65	211	100.0	42	7 ADB75176	ADB75176 Amyloid b
66	211	100.0	42	7 AAE38649	AAE38649 Human amy
67	211	100.0	42	7 ADC66002	ADC66002 Human A(b
68	211	100.0	42	7 ADC35181	ADC35181 Beta-amy1
69	211	100.0	42	7 ADD20743	ADD20743 Human bet
70	211	100.0	42	7 ADB10848	ADB10848 Chimeric
71	211	100.0	42	7 ADF60932	ADF60932 Human bet
72	211	100.0	42	7 ADF56649	ADF56649 Human A b
73	211	100.0	42	7 ADM82703	ADM82703 Beta-amy1
74	211	100.0	42	7 ADM39753	ADM39753 B-cell pe
75	211	100.0	42	8 ADF53271	ADF53271 Amyloid A
76	211	100.0	42	8 ADG63948	ADG63948 Recombina
77	211	100.0	42	8 ADI40716	ADI40716 Human amy
78	211	100.0	42	8 ADS52267	ADS52267 Human amy
79	211	100.0	42	8 ADN00694	ADN00694 A42, SRQ
80	211	100.0	42	8 ADM97740	ADM97740 Native Am
81	211	100.0	42	8 ADN41875	ADN41875 Amino aci
82	211	100.0	42	8 ADOL61369	ADOL61369 Beta-amy1
83	211	100.0	42	8 ADP73482	ADP73482 Alzheimer
84	211	100.0	42	8 ADP64925	ADP64925 Beta-amy1
85	211	100.0	42	8 ADQ74960	ADQ74960 Human bet
86	211	100.0	42	8 ADQ26240	ADQ26240 Human amy
87	211	100.0	42	8 ADQ37252	ADQ37252 Vaccine a
88	211	100.0	42	8 ADRL6409	ADRL6409 Human Abe
89	211	100.0	42	8 ADRO4018	ADRO4018 Human amy
90	211	100.0	42	8 ADRI2775	ADRI2775 Human bet
91	211	100.0	42	8 ADRA33293	ADRA33293 Abeta42 B
92	211	100.0	42	8 ADRA30645	ADRA30645 GPPB cata
93	211	100.0	42	8 ADR90380	ADR90380 Beta-amy1
94	211	100.0	42	8 ADT77110	ADT77110 Human amy
95	211	100.0	42	8 ADU04665	ADU04665 Beta-amy1
96	211	100.0	42	8 ADU47120	ADU47120 Human bet

AAB91812	Amyloid b
AAB82622	Amyloid-b
AAB49395	Human amy
AAB48830	Human amy
AAE05484	Human pep
ABB81321	Amyloid p
AAU80961	Human amy
AAU98727	Human amy
ABG94281	Amyloid b
AAE21438	Human bet
ABB76029	Beta amy1
AAE25335	Modified
AAOL5848	Beta-amy1
AAU76483	Amino aci
AAE26080	Beta amy1
AAG68314	Human bet
AAU96896	Human Amy
AAU93988	Human bet
AAE26300	Human bet
ABG80593	Human amy
AAM51864	Neuronal
AAU75433	Amyloid p
ABB83306	Amyloid-b
ABB77990	Beta-amy1
AAE35671	Human bet
AAOL6344	A-beta pr
ABU08711	Amyloid b
ABU08506	Human amy
AAE33793	Beta-amy1
ABP99423	Beta-amy1
ABB82633	Abeta fib
ABP96144	Human Abe
ABG72233	Human bet
AAE35428	Abeta pro
AAE33218	Beta amy1
ABP97882	Amino aci
ABU63707	Rat amy1o
ADA89912	Abeta42 a
ADA37267	Human bet
ADB37652	Human bet
ADB85562	Beta-amy1
ADB75176	Amyloid b
AAE38649	Human amy
ADC66002	Human A(b
ADC35181	Beta-amy1
ADD20743	Human bet
ADB10848	Chimeric
ADF60932	Human bet
ADF56649	Human A b
ADM82703	Beta-amy1
ADM39753	B-cell pe
ADF53271	Amyloid A
ADG63948	Recombina
ADI40716	Human amy
ADS52267	Human amy
ADN00694	A42, SRQ
ADM97740	Native Am
ADN41875	Amino aci
ADOL61369	Beta-amy1
ADP73482	Alzheimer
ADP64925	Beta-amy1
ADQ74960	Human bet
ADQ26240	Human amy
ADQ37252	Vaccine a
ADRL6409	Human Abe
ADRO4018	Human amy
ADRI2775	Human bet
ADRA33293	Abeta42 B
ADRA30645	GPPB cata
ADR90380	Beta-amy1
ADT77110	Human amy
ADU04665	Beta-amy1
ADU47120	Human bet

97	211	100.0	42	8	ADU24433	Novel	glu
98	211	100.0	42	8	ADU46707	Amyloid b	
99	211	100.0	42	8	ADW00020	Beta-amy1	
100	211	100.0	42	9	ADW95946	Human amy	

ALIGNMENTS

RESULT 1

AAR20330
ID AAR20330 standard; peptide; 42 AA.

XX AAR20330;

XX 25-MAR-2003 (revised)

DT 14-APR-1992 (first entry)

XX Sequence of A99 (beta-amyloid core domain).

XX Transgenic mice; Alzheimer's disease; diagnosis; beta-amyloid precursor;

KM plaque core protein.

XX Homo sapiens.

XX WO9119810-A.

XX 26-DEC-1991.

XX 15-JUN-1990; 90US-00538857.

XX 15-JUN-1990; 90US-00538857.

PR 17-JUN-1991; 91US-00716725.

XX (CALD) CALIFORNIA BIOTECHNOLOGY INC.

XX Cordell B;

XX WPI; 1992-024426/03.

XX Transgenic mice as models for studying Alzheimer's disease proteins -

PT contg. cells with promoter and beta-amyloid precursor protein

XX deoxyribonucleic acid, useful for testing anti-Alzheimer's drugs.

XX Disclosure; Fig 3; 98pp; English.

XX The inventors specifically claim transgenic mice contg. DNA encoding A42

CC (beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid carboxy

CC tail) (AAR20329), A695 (beta-amyloid precursor protein), A751 (precursor

CC plus inhibitor) or A41 (protease inhibitor) (AAR20328). Human fibroblast

CC cDNA clone lambda dAFCP16814 was deposited at ATCC on July 1, 1987 and has

CC accession No. 40347. The promoter is pref. the NSB promoter with the A751

CC or the A695 sequence. (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 42 AA;

XX Query Match 100.0%; Score 211; DB 2; Length 42;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-23;

XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 AEFRRDSGYEVHOKLVFAEDVGSNKGATIGLMVGAVIA 42

DB 2 AEFRRDSGYEVHOKLVFAEDVGSNKGATIGLMVGAVIA 42

XX 25-MAR-2003 (revised)

DT 15-MAR-1995 (first entry)

XX Beta-amyloid (1-42).

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;

KW anti-beta-amyloid antibody; diagnosis.

XX Homo sapiens.

XX WO9417197-A1.

XX 04-AUG-1994.

XX 24-JAN-1994; 94WO-JP000089.

XX 25-JAN-1993; 93JP-00010132.

PR 05-FEB-1993; 93JP-00019035.

PR 16-NOV-1993; 93JP-00286985.

XX 28-DEC-1993; 93JP-00334773.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Suzuki N, Odaka A, Kitada C;

XX WPI; 1994-264110/32.

XX Antibodies recognising specific parts of beta-amyloid - can be used for

PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's

XX disease.

XX Disclosure; Page 83; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid

CC protein are claimed. Specifically, the antibodies (which are pref.

CC monoclinal) recognise residues 1-16 and/or 1-28 from the N-terminal

CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from

CC the C-terminal portion. The antibodies are useful for assaying beta-

CC amyloid and its derivatives for diagnosis of Alzheimer's disease.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 42 AA;

XX Query Match 100.0%; Score 211; DB 2; Length 42;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-23;

XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 AEFRRDSGYEVHOKLVFAEDVGSNKGATIGLMVGAVIA 42

DB 2 AEFRRDSGYEVHOKLVFAEDVGSNKGATIGLMVGAVIA 42

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-MAR-2003 (revised)

XX 22-NOV-1994; 94US-00347144.
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 1996-268332/27.
XX
XX Use of agents which bind beta-amyloid peptide - for diagnosis, prevention
PT and treatment of vascular damage caused by amyloid deposits, partic. in
PT hemorrhaging and Alzheimer's disease.
XX
XX Example 1; Fig 1; 52pp; English.
XX
XX To investigate the effects of beta-amyloid peptide (BAP) on tissue
CC plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide
CC contained 42 amino acids and corresp. to the full length BAP (AAR95248).
CC The other 2 peptides (AAR95249 and 50) contained the 28 N-terminal
CC residues of the BAP found in Alzheimer's disease and hereditary cerebral
CC hemorrhage with amyloidosis-Dutch type (HCHMA-D), respectively. In an
CC assay to determine the effect of the peptides on t-PA activation, each
CC peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation
CC (k_{app}) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and
CC 7.8 for null and fibrinogen controls. The results demonstrate that the
CC BAP are able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHMA-D and cerebral amyloid
CC angiotrophy related cerebral haemorrhage
XX
XX Sequence 42 AA;
SQ

Query Match 100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 4
AAR94591
ID AAR94591 standard; peptide; 42 AA.
XX
XX AAR94591;
AC
XX
XX 25-MAR-2003 (revised)
DT 21-AUG-1996 (first entry)
DT
XX
XX
DE Alzheimer amyloid beta-protein active site sequence.
XX
XX Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;
KW serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;
KM complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.
XX
XX Synthetic.
OS
XX
XX US5506097-A.
PN
XX
XX 09-APR-1996.
PD
XX
XX 10-JAN-1994; 94US-00179574.
PF
XX
XX 24-AUG-1990; 90US-00572671.
PR 13-JAN-1992; 92US-00819361.
PR 13-JAN-1993; 93WO-US000325.
XX
XX (HARD) HARVARD COLLEGE.
PA
XX Kayyali U, Potter H;
PI
XX WPI; 1996-200270/20.
DR

XX Inhibiting enzymatic activity of Alzheimer amyloid beta-protein - using p
PT -amido:phenyl:methanesulphonyl fluoride or ebelactone A, for treatment,
PT study and diagnosis of Alzheimer's disease, etc.
XX
XX Disclosure; Fig 1; 17pp; English.
XX
XX This is the sequence of a fragment of the beta-amyloid protein associated
CC with Alzheimer's disease. The protein contains esterase (cholinesterase
CC and lipase) activities based on active site similarities with serine
CC proteases (see AAR94592-96). The esterase activity of the beta-amyloid
CC protein is inhibited by the cpds. of the invention i.e. ebelactone A or
CC para-amidinophenylmethanesulphonyl fluoride. Inhibition of these
CC activities prevent complex formation between the beta-amyloid protein and
CC alpha(1)-antichymotrypsin, thus can be used to treat, study or diagnose
CC Alzheimer's or Down's diseases or normal ageing. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
XX Sequence 42 AA;
SQ

Query Match 100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 5
AAW12828
ID AAW12828 standard; peptide; 42 AA.
XX
XX AAW12828;
AC
XX
XX 08-DEC-1997 (first entry)
DT
XX
XX Beta A4 peptide.
DE
XX
XX Beta A4 peptide; Alzheimer's disease; peptide aggregation; brain;
KW therapy; inhibitor.
KW
XX
XX Homo sapiens.
OS
XX
XX WO9707403-A1.
PN
XX
XX 27-FEB-1997.
PD
XX
XX 23-JUL-1996; 96WO-US012034.
PF
XX
XX 16-AUG-1995; 95US-00515606.
PR
XX
XX (HMRI) HOECHST MARION ROUSSEL INC.
PA
XX Goyal S, Paul J, Riedel NG, Sahasrabudhe SR;
PI
XX WPI; 1997-165447/15.
DR
XX
XX Determn. of the degree of betaA4 peptide aggregation using binding agent
PT - used to screen cpds. for possible use in Alzheimer's disease treatment.
PT
XX
XX Disclosure; Page 10; 18pp; English.
XX

This sequence represents the beta A4 peptide. The degree of aggregation
CC of this peptide is determined using the method of the invention. The beta
CC A4 peptide is present in the brain of Alzheimer's disease patients, but
CC not in the brain of non-Alzheimer's disease individuals. The peptide
CC clumps or aggregates in the brain of Alzheimer's disease patients, where
CC it may be responsible for the destruction of normal brain cells. Once the
CC clumps or aggregates form, the formulation is almost irreversible. The
CC method of the invention comprises reacting this sequence with a binding
CC reagent capable of binding to it only in its non-aggregated state, to
CC form an amount of a beta A4 peptide-bound reagent and an amount of

CC protein free reagent. The amount of the beta A4 peptide, binding reagent
 CC complex is then measured. Compounds which inhibit aggregation of beta A4
 CC peptide are potentially useful for treatment of Alzheimer's disease
 XX
 SQ Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 DB 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 6
 AAM64507 standard; peptide; 42 AA.
 XX
 AC AAM64507;

DT 20-OCT-1998 (first entry)

DE Neurotoxic beta-amyloid peptide decoy peptide #20.

KM Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
 KM aggregate; Alzheimers disease; decoy; treatment.

OS Synthetic.

XX WO9830229-A1.

PD 16-JUL-1998.

PF 09-JAN-1998; 98WO-US000653.

PR 10-JAN-1997; 97US-0035847P.

PR 29-OCT-1997; 97US-00960188.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Ingram VM, Blanchard BJ;

DR WPI; 1998-398795/34.

PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor, useful
 PT for, e.g. treating Alzheimer's disease.

XX Example 8; Page 46; 68pp; English.

CC AAM64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid
 CC peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates
 CC that increase calcium influx into neuronal cells. Such peptides can be
 CC used in the treatment of diseases associated with neurotoxic aggregates
 CC of beta-AP specifically Alzheimer's disease. The peptides are
 CC administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and
 CC orally, or from slow-release implants

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 DB 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 7
 AAM42989 standard; peptide; 42 AA.
 ID AAM42989

XX AAM42989;

AC 01-MAY-1998 (first entry)

XX Full length beta-amyloid peptide (BAP).

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
 XX cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KM amyloid precursor protein; APP; secretase; BAP aggregation;
 KM abnormal proteolytic cleavage.

XX Homo sapiens.

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-00464248.

XX 01-MAY-1992; 92US-00877675.

XX 20-SEP-1993; 93US-00123659.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1998-076482/07.

PT Amyloid precursor protein fusion polypeptides - comprising APP fragment
 PT and marker, useful for research and drug screening.

XX Disclosure; Col 7; 84pp; English.

CC The present sequence represents a beta-amyloid peptide (BAP). Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
 CC 770. These isoforms are derived by alternative splicing. APP-APP 751 is a
 CC deletion construct of APP-751, which has a deletion of 276 amino acids to
 CC within 15 amino acids of the BAP domain. APP can be used as a substrate
 CC for studying abnormal proteolytic cleavage which results in the release
 CC of BAP, and also to screen for drugs that will inhibit such cleavage

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 DB 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 8

AAM47230 standard; peptide; 42 AA.

XX AAM47230;

XX 22-MAY-1998 (first entry)

XX Beta-amyloid peptide residues 1-42.

XX Screening assay: beta-amyloid peptide; treatment; amyloidosis disease;
 KM Alzheimer's disease.

OS Homo sapiens.
 XX
 PN US5721106-A.
 XX
 PD 24-FEB-1998.
 XX
 PF 12-SEP-1994; 94US-00304585.
 XX
 PR 13-AUG-1991; 91US-00744767.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Man'yh PM, Maggio JE;
 XX
 DR WPI; 1998-168404/15.
 XX
 PT New in vitro screening assay for Alzheimer's disease drugs - comprises
 PT assessing binding of labelled beta-amyloid peptide to silk sample.
 XX
 PS Claim 8; Col 29-30; 36pp; English.
 XX
 CC The present sequence was used in the development of a novel in vitro
 CC screening assay for agents capable of affecting the deposition of beta-
 CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk
 CC sample with labelled BAP, optionally in the presence of a test agent,
 CC detecting the amount of label bound to the silk and assessing the effect
 CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
 CC to silk are potentially useful for treating amyloidosis diseases,
 CC especially Alzheimer's disease
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSQVIA 42
 DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSQVIA 42
 XX
 RESULT 9
 AAY49691
 ID AAY49691 standard; peptide; 42 AA.
 XX
 AC AAY49691;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human beta amyloid precursor protein peptide.
 XX
 KM Human; beta amyloid precursor protein; APP; beta secretase inhibition;
 KM alpha secretase; neurological disorder; Alzheimer's disease;
 KM Down's syndrome; mutation.
 XX
 OS Homo sapiens.
 OS
 PN WO9951752-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-JP001701.
 XX
 PR 31-MAR-1998; 98JP-00101821.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ozawa K, Ikeda S, Tabira T;
 XX
 DR WPI; 1999-620208/53.
 XX
 PT A cell line which produces beta amyloid precursor protein, used in the

PT investigation of neurological disorders such as Alzheimer's disease.
 XX
 PS Disclosure; Page 41; 70pp; Japanese.
 XX
 CC The present invention describes a cell line which produces beta amyloid
 CC precursor protein (APP) and expresses alpha secretase activity but
 CC expresses beta secretase activity only under an external stimulus. Also
 CC described is a cloning method for DNA encoding beta secretase,
 CC comprising: (1) inserting a DNA library into the cell line, expressing
 CC the inserted DNA, and selecting cells expressing beta secretase then
 CC isolating the beta secretase DNA from them; or (2) isolating nucleic acid
 CC from the cell line with or without external stimulation and performing
 CC subtractive cloning to identify DNA expressed only under stimulation.
 CC Products from the present invention may be used in the investigation of
 CC neurological disorders such as Alzheimer's disease and Down's syndrome and
 CC in particular the association of mutations of the beta APP with them. The
 CC present sequence represents a human beta APP peptide
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSQVIA 42
 DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSQVIA 42
 XX
 RESULT 10
 AAM99585
 ID AAM99585 standard; peptide; 42 AA.
 XX
 AC AAM99585;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE Mutant aggregating amyloid-beta peptide.
 XX
 KM Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KM diagnosis; Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO9908695-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 13-AUG-1998; 98WO-US016809.
 XX
 PR 14-AUG-1997; 97US-0055660P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Glabe C, Garzon-Rodriguez W;
 XX
 DR WPI; 1999-190112/16.
 XX
 PT New fluorescent labeled amyloid A-beta peptides.
 XX
 PS Example 1; Page 21; 50pp; English.
 XX
 CC This sequence corresponds to a mutant aggregating amyloid-beta peptide
 CC which can be covalently labelled with a fluorescent group. The detection
 CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
 CC or detect a predisposition to Alzheimer's disease. The screening assays
 CC can be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid-beta peptide are also useful for exploring other aspects of
 CC amyloid structure
 XX
 SQ Sequence 42 AA;
 XX

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42
 |||
 DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42

RESULT 11
 AAW81474

ID AAW81474 standard; peptide; 42 AA.

XX AAW81474;

AC 28-JAN-1999 (first entry)

XX Synthetic amyloid beta (Abeta) peptide 9 (residues 1-42).

DE Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;

KM research; neurotoxicity; free-radical; glutamine synthetase.

XX Synthetic.

OS US5840838-A.

PN 24-NOV-1998.

PD 29-FEB-1996; 96US-00609090.

XX 29-FEB-1996; 96US-00609090.

XX (KENT) UNIV KENTUCKY RES FOUND.

PI Aksekov M, Carney JM, Hensley K, Butterfield DA;

XX WPI; 1999-034120/03.

PT Process for treating synthetic amyloid beta peptides - by organic solvent

PT treatment, useful for studying neurotoxicity.

XX Claim 5; Col 11-12; 14pp; English.

CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)

CC peptides. The invention provides a process for treating a synthetic Abeta

CC peptide that comprises dissolving the peptide in a deoxygenated solvent

CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl

CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and

CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution

CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by "evaporative

CC deposition" in 5-10 minutes. Synthetic amyloid beta peptides are useful

CC as research tools for studying neurotoxicity resulting from Abeta peptide

CC -enhanced free-radical production. The treatment increases the activity

CC of the synthetic Abeta peptides in tests to determine free-radical

CC generating capacity and glutamine synthetase inactivation

XX Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42
 |||
 DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42

RESULT 12

AAAY08607

ID AAY08607 standard; proetin; 42 AA.

XX AAY08607;

XX 05-AUG-1999 (first entry)
 DT Human beta-amyloid precursor core protein A42.
 XX
 DE

KW APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
 KW Alzheimer's disease; model; therapeutic compound; brain; mechanism;
 KW nerve tissue specific promoter; synthesis; inhibitor; deposition;
 KW plaque formation; treatment; A42.

XX Homo sapiens.

OS US5912410-A.

PN 15-JUN-1999.

PD 13-APR-1995; 95US-00422333.

PF 15-JUN-1990; 90US-00538857.

PR 17-JUN-1991; 91US-00716725.

PR 21-OCT-1994; 94US-00327381.

XX (SCIO-) SCIOS INC.

PI Cordell B;

XX WPI; 1999-357231/30.

PT Transgenic mice useful for studying compounds potentially useful in the

PT treatment of Alzheimer's disease.

XX Disclosure; Fig 3; 72pp; English.

CC This invention describes novel transgenic mice expressing proteins

CC related to the pathology of Alzheimer's disease and which provide models

CC for studying potentially therapeutic compounds. The transgenic mice

CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)

CC and a nerve tissue specific promoter operably linked to the beta-APP

CC allowing its expression to form beta-amyloid protein deposits in the

CC animal's brain. The transgenic mouse is useful for elucidating the

CC molecular mechanisms involved in the synthesis of and, more importantly,

CC inhibiting the synthesis and deposition of beta-amyloid proteins (most

CC importantly in the brain where plaque formation is associated with

CC Alzheimer's disease) by inhibiting production and/or increasing cleavage

CC after production. The transgenic animals provide useful models for

CC studying the in vivo relationships of the proteins to each other and to

CC other compounds being tested for their usefulness in treating Alzheimer's

CC disease

XX Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42
 |||
 DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVVIA 42

RESULT 13

AAW29093

ID AAW29093 standard; peptide; 42 AA.

XX AAW29093;

AC 20-JUL-1999 (first entry)

XX A-beta-binding peptide 1-42.

DE Cyclosporin; A-beta peptide; conjugate; neurological disease; Alzheimer;

KW multiple sclerosis; amyotrophic lateral sclerosis; ALS;

KW non-immunosuppressive; amyloid plaque formation.

XX Homo sapiens.
 OS
 XX
 PN WO9910374-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 25-AUG-1998; 98WO-US017544.
 XX
 PR 26-AUG-1997; 97US-0057751P.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Rich DH, Solomon ME;
 XX
 DR WPI; 1999-276928/23.
 XX
 PT New A-b-binding peptide conjugates and Csa analogs - useful in treatment
 PT of neurological diseases e.g. Alzheimer's disease, Multiple Sclerosis
 PT etc.
 XX
 PS Claim 5; Page 98; 129pp; English.
 XX
 CC New conjugates are disclosed which are of formula A-Z, in which: A is (1)
 CC a cyclosporin A analogue described in AAW29087 or (2) an FK506 binding
 CC peptide inhibitor; and Z is a polypeptide comprising 5 or more contiguous
 CC residues of A-beta peptide. The compounds are novel chemical inducers of
 CC dimerization which are non-immunosuppressive and which are inhibitors of
 CC A-beta peptide aggregation and deposition in amyloid plaques. The adverse
 CC consequences of amyloid plaque formation can be prevented or ameliorated
 CC by sequestering the A-beta peptide in monomeric form with a conjugate
 CC which links the A-beta to cyclophilin or FKBP, therefore providing a
 CC mechanism to minimize the amount of free A-beta available for fibril
 CC formation and deposition. The compounds can be used for the treatment of
 CC Alzheimer's disease, multiple sclerosis and amyotrophic lateral sclerosis
 CC
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGWVIA 42
 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGWVIA 42
 DB
 RESULT 14
 AAY25137
 ID AAY25137 standard; peptide; 42 AA.
 XX
 AC AAY25137;
 XX
 DT 26-AUG-1999 (first entry).
 XX
 DE Human amyloid beta-A4 peptide 5.
 XX
 KW Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KW therapeutic drug; brain; Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS
 PN USS919631-A.
 XX
 PD 06-JUL-1999.
 XX
 PF 17-JUL-1996; 96US-00682245.
 XX
 PR 17-JUL-1996; 96US-00682245.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Sahaarabudhe SR, Paul JW, Goyal S, Riedel NG;

XX WPI; 1999-403957/34.
 XX
 DR Determination of degree of aggregation of a peptide, useful for
 PT identifying therapeutic drugs for treating Alzheimer's disease.
 PT
 XX
 PS Claim 1; Col 7-8; 8pp; English.
 XX
 CC This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated (I) with
 CC Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
 CC (I); (b) measuring the amount of (II) bound to (I) to obtain a value (1);
 CC (c) repeating steps (a) and (b) with a second sample at a different time
 CC to obtain a second value (ii); and (d) determining the difference between
 CC (1) and (ii) which is inversely related to the degree of aggregation of
 CC (I). This method may be applied to a screen for compounds that inhibit
 CC aggregation of (I). These inhibitors may be used as therapeutic drugs to
 CC inhibit the formation of these aggregates in the brains of patients
 CC suffering from Alzheimer's disease
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGWVIA 42
 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGWVIA 42
 DB
 RESULT 15
 AAW92726
 ID AAW92726 standard; peptide; 42 AA.
 XX
 AC AAW92726;
 XX
 DT 20-MAR-2003 (revised)
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #72.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 OS
 PN USS876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 29-JUL-1991; 91US-00737371.
 XX
 PR 27-JUL-1990; 90US-00559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
 XX
 PS Disclosure; Col 41-42; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)

XX
 XX Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42
 |||||
 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 16
 AAY33407
 ID AAY33407 standard; peptide; 42 AA.

XX AAY33407;
 AC
 XX 03-DEC-1999 (first entry)
 DT
 XX
 DE Human amyloidogenic A-beta peptide 1.

KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
 KM fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
 KM Down's Syndrome.

XX Homo sapiens.

XX MO9941279-A2.

XX 19-AUG-1999.

XX 12-FEB-1999; 99WO-US003231.

XX 13-FEB-1998; 98US-0074658P.

XX (ARCH-) ARCH DEV CORP.

XX Lynn DG, Meredith SC, Burkoch TS;

XX WPI; 1999-561326/47.

XX Inhibiting amyloid plaque formation in humans suffering from amyloidosis,
 PT Alzheimer's disease or Down's Syndrome.

XX Claim 21; Page 140; 141pp; English.

XX This invention describes a novel method for inhibiting amyloid
 CC fibrillogenesis which comprises contacting tissue with a composition
 CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
 CC at an end terminal or a side chain, by conjugation to polyethylene
 CC glycol, by conjugation to a second compound and a pharmaceutically
 CC acceptable buffer, solvent or diluent. The methods are used to inhibit
 CC amyloid plaque formation in humans suffering from amyloidosis,
 CC Alzheimer's disease or Down's Syndrome. This sequence represents a
 CC fragment of the beta-amyloid peptide described in the method of the
 CC invention

XX Sequence 42 AA;

Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42
 |||||
 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 17
 AAY96956
 ID AAY96956 standard; peptide; 42 AA.

XX AAY96956;

XX 31-OCT-2000 (first entry)
 DT
 XX
 DE Beta-amyloid 1-42 peptide.

KW pUBER3; polypeptide; tag; rubredoxin; antigen; vaccine; carrier;
 KM immunogenic; flag tag; beta-amyloid; fusion.

XX Homo sapiens.

XX WO200039310-A1.

XX 06-JUL-2000.

XX 29-DEC-1999; 99WO-US031176.

XX 29-DEC-1998; 98US-00114034.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Przybyla A, Menon N;

XX WPI; 2000-452403/39.

XX Nucleic acids encoding fusion peptides comprising rubredoxin, useful as
 PT vaccines.

XX Example 2; Page 63; 67pp; English.

XX Fusion proteins comprising rubredoxin and fused antigens and/or happens
 CC may be used as vaccines to initiate immune responses. In this case, the
 CC rubredoxin acts as a carrier. The fusion protein is capable of binding
 CC iron (Fe-2+) when properly folded, giving it a red color that makes it
 CC easy to identify following or during purification. The C-terminal fused
 CC protein may be insoluble or known to form inclusion bodies in a host
 CC cell. The rubredoxin serves as the carrier molecule to yield immunogenic
 CC fusion products. As rubredoxin is itself only negligibly antigenic, there
 CC is no need to include a cleavage site in the fusion product to allow
 CC cleavage of the N-terminal and C-terminal constituents

XX Sequence 42 AA;

Query Match 100.0%; Score 211; DB 3; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42
 |||||
 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42

DB 2 AEFRRDSGYEVHOKLVFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 18
 AAB86134
 ID AAB86134 standard; protein; 42 AA.

XX AAB86134;

XX 31-JUL-2001 (first entry)

XX Human Alzheimer-beta-peptide (1-42).

XX Beta-peptide; subunit-containing molecular associate; gene therapy;
 KW neurodegenerative disorder; amyloidogenic disorder; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; type II diabetes mellitus;
 KW transmissible spongiform encephalopathy; muscular dystrophy;
 KW virus-like protein shell.

OS	Homo sapiens.
XX	
PN	WO200132694-A2.
XX	
PD	10-MAY-2001.
XX	
PF	03-NOV-2000; 2000WO-EP010877.
XX	
PR	03-NOV-1999; 99DE-01052955.
XX	
PA	(ACCT-) ACCT PROENOMICS AG.
XX	
PI	Boehm G, Schmidt U;
XX	
DR	WPI, 2001-316418/33.
XX	
PT	Characterizing molecular associates of subunits, useful e.g. for
XX	diagnosis of neurodegenerative diseases, by fluorescence-activated cell
PT	sorting of associates containing labeled subunits.
XX	
PS	Disclosure; Page 45; 45pp; German.
XX	
CC	This invention describes a novel method for characterizing subunit (SU)-
XX	containing molecular associates (A) by: (i) labeling non-associated SU
CC	with a fluorescent dye (I); (ii) contacting labeled SU, with each other
XX	or with unlabelled SU or with (A), so that labeled (A) are formed by
CC	attachment of labeled SU; (iii) characterizing the labeled (A) by
XX	fluorescence-activated cell sorting (FACS); and (iv) optionally
CC	separating (A) by known methods. The method is used to characterize (and
XX	optionally separate) (A): (i) associated with a wide range of
CC	neurodegenerative or other amyloidogenic disorders, e.g. Alzheimer's,
XX	Huntington's or Parkinson's diseases, transmissible spongiform
CC	encephalopathies, type II diabetes mellitus and muscular dystrophy, for
XX	diagnosis and prediction of such diseases; or (ii) produced during
CC	recombinant protein production (inclusion bodies). It may also be used to
XX	detect homologous subunits and for measuring kinetics of
CC	aggregate/associate formation. A particular application is determining
XX	the packaging efficiency of virus-like protein shells for therapeutic
CC	proteins and nucleic acid, for use as gene therapy vectors. Separated (A)
XX	are useful experimentally, e.g. in cell cultures or animal models. The
CC	method has high specificity and sensitivity for detection/quantification
XX	of disease-related associates, and can provide an unequivocal diagnosis,
CC	at an early stage to allow treatment to start before symptoms are
XX	evident. Fluorescence-activated cell sorting (FACS) is a standardizable
CC	and generally applicable method, suitable for automation and high
XX	throughput screening. This sequence represents the human Alzheimer's
CC	disease associated beta-peptide (1-42) which is used to illustrate the
XX	method of the invention
XX	
SO	Sequence 42 AA;
XX	
Query Match	100.0%; Score 211; DB 4; Length 42;
Best Local Similarity	100.0%; Pred. No. 1.66-23;
Matches	41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	2 AEFRRDSGYEVHQRKLVFFAEDVGSNKAATIGLWGVVIA 42
XX	
DB	2 AEFRRDSGYEVHQRKLVFFAEDVGSNKAATIGLWGVVIA 42
XX	
RESULT 19	
AAAB35589	
ID	AAAB35589 standard; peptide; 42 AA.
XX	
AAAB35589;	
XX	
AC	
XX	
DT	15-FEB-2001 (first entry)
XX	
DE	Beta/A4-amyloid peptide.
XX	
XX	Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW	acute cardiovascular disease; therapy.
XX	

```

OS      Unidentified.
XX      XX
XX      PN      US6136548-A.
XX      PD      24-OCT-2000.
XX      PF      02-SEP-1999;      99US-00388890.
XX      PR      22-NOV-1994;      94US-003477144.
XX      PR      22-NOV-1995;      95WO-US015007.
XX      PR      26-JUL-1996;      96US-00686959.
XX      PA      (RUF ) UNIV RUTGERS STATE NEW JERSEY.
XX      PI      Anderson S;
XX      DR      WPI; 2001-030939/04.
XX      PT      Identifying mutant tissue-type plasminogen activator (t-PA) for improving
XX      PT      thrombolytic therapy or treating vascular hemorrhaging, by determining
XX      PS      whether t-PA binds to fibrin but not to a beta amyloid peptide.
XX      CC      Disclosure; Col 10; 23pp; English.
XX      CC      The present invention describes a method for identifying mutant
XX      CC      derivatives of tissue-type plasminogen activator, which involves
XX      CC      determining whether or not they bind to beta-amyloid peptides and fibrin.
XX      CC      Mutants will only bind to the latter. These mutants are useful in
XX      CC      improved thrombolytic therapies, in the treatment of Alzheimer's disease
XX      CC      and in the treatment of acute cardiovascular disease, which may be caused
XX      CC      by myocardial infarction, stroke, ischaemia and pulmonary embolism
XX      SQ      Sequence 42 AA;

Query Match      100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No.1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      2 AEFRRDSGYEVHOKLVFEADVGSNGKAIIGLVGVVIA 42
        |||||||
        2 AEFRRDSGYEVHOKLVFEADVGSNGKAIIGLVGVVIA 42
DB      2 AEFRRDSGYEVHOKLVFEADVGSNGKAIIGLVGVVIA 42

RESULT 20
AAB49098
ID      AAB49098 standard; peptide; 42 AA.
XX      AC      AAB49098;
XX      DT      27-MAR-2001 (first entry)
XX      DE      Human amyloid beta peptide A-beta 42, SRQ ID NO:1.
XX      KW      Amyloid disease; amyloid fibril deposition; amyloid plaque; immunogenic;
XX      KW      antibody; vaccine; Alzheimer's disease; type 2 diabetes;
XX      KW      reactive system amyloidosis; systemic senile amyloidosis;
XX      KW      familial amyloid cardiomyopathy; transmissible spongiform encephalopathy;
XX      KW      Creutzfeldt-Jakob disease; kuru;
XX      KW      haemodialysis-associated beta-2-microglobulin deposition;
XX      KW      amyloid beta peptide; A-beta 42.
XX      OS      Homo sapiens.
XX      PN      WO200072876-A2.
XX      PD      07-DEC-2000.
XX      PF      01-JUN-2000; 2000WO-US015239.
XX      PR      01-JUN-1999;      99US-0137010P.
XX      PA      (NEUR-) NEURALAB LTD.
XX      XX

```

PI Schenk DB;
 XX
 DR MPI; 2001-070921/08.
 XX
 PT Pharmaceutical composition comprising immunogen against amyloid component
 XX such as fibril peptide or protein, or antibody against amyloid component
 PT useful for treating amyloid diseases or amyloidoses.
 XX
 PS Disclosure; Page 24; 140pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril deposits
 CC (amyloid plaques) in a patient. The pharmaceutical composition comprises
 CC an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining the
 CC prognosis of a patient undergoing treatment for an amyloid disorder which
 CC involves measuring a patient serum amount of immunoreactivity against a
 CC selected amyloid component. A patient serum immunoreactivity of at least
 CC four times a base line serum immunoreactivity control level indicates a
 CC prognosis of improved status with respect to the disorder. The
 CC pharmaceutical compositions of the invention are useful for treating a
 CC wide variety of disorders characterised by amyloid fibril deposition in a
 CC patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSSA); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeldt-Jakob disease, Kuru) characterised by
 CC prion protein deposits; and beta-2-microglobulin deposits which form as a
 CC result of long term haemodialysis treatment. The present sequence
 CC represents human amyloid beta peptide A-beta 42
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVTA 42
 ID AAB84427
 XX AAB84427 standard; peptide; 42 AA.
 AC AAB84427;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 XX
 KM Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KM vaccine.
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 1 /note= "L-Asp, D-Asp or L-iso-Asp"
 XX
 PN WO200142306-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 08-DEC-2000; 2000WO-US033203.
 XX
 PR 08-DEC-1999; 99US-0169687P.
 PR

XX
 PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain B;
 XX
 DR MPI; 2001-381648/40.
 XX
 PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 XX
 PS Claim 3; Page 42; 47pp; English.
 XX
 CC The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 211; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVTA 42
 ID AAB84897
 XX AAB84897 standard; protein; 42 AA.
 AC AAB84897;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Human amyloid protein.
 XX
 KM Neurotropic; neuroprotective; antifibrillogenic; amyloidosis inhibitor;
 KM cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KM Alzheimer's disease; human; amyloid protein.
 OS Homo sapiens.
 OS
 XX
 PN WO2000068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PF 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Gervais F, Gupta A;
 XX
 DR MPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for

PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
XX its isomer or peptidomimetic.
XX
PS Disclosure; Fig 1; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein (the present sequence)
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
RESULT 23
AAB91779
ID AAB91779 standard; peptide; 42 AA.
XX
AC AAB91779;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:955.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 506; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
RESULT 24
AAB91812
ID AAB91812 standard; peptide; 42 AA.
XX
AC AAB91812;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:988.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000MO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 517-518; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention

XX Sequence 42 AA;
SQ
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRHDSGYEVHHQKLVFPAEDVGSNKGAITGLMVGGVIA 42
Db 2 AEFRRHDSGYEVHHQKLVFPAEDVGSNKGAITGLMVGGVIA 42
RESULT 25
AAB82622 standard; peptide; 42 AA.
XX AAB82622;
XX 02-OCT-2001 (first entry)
XX Amyloid-beta peptide.
XX Amyloid-beta peptide; human; vaccine; Alzheimer's disease; amyloidosis;
XX Amyloid-related disease; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 10..16 /note= "cell surface adherence"
XX Region 13..16 /note= "GAG binding site/microglia activation"
XX Region 16..21 /note= "beta-sheet"
XX Region 40..42 /note= "C-terminal"
XX WO200139796-A2.
XX PD 07-JUN-2001.
XX 29-NOV-2000; 2000WO-CA001413.
XX 29-NOV-1999; 99US-0168594P.
XX 28-NOV-2000; 2000US-00724842.
XX (NEUR-) NEUROCHEM INC.
XX Chalfour R, Hebert L, Kong X, Gervais F,
XX WPI; 2001-441458/47.
XX Preventing/treating amyloid-related disease, especially Alzheimer's
XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
XX PT which elicits production of antibodies to prevent fibrillogenesis and
XX associated cellular toxicity.
XX PS Disclosure; Fig 1; 31pp; English.
XX The present sequence is that of amyloid-beta peptide, a 40-42 amino acid
XX peptide that is produced through cleavage of the beta-amyloid precursor
XX protein. The invention relates to a stereochemically based 'non-self'
XX antigen vaccine for the prevention and/or treatment of Alzheimer's
XX disease and other amyloid related diseases in humans (claimed). The
XX vaccine preferably comprises an all-D peptide that interacts with at
XX least 1 region of an amyloid protein, e.g. the beta sheet region and GAG
XX binding site region, and their immunogenic fragments, protein conjugates,
XX immunogenic derivative peptides and immunogenic peptidomimetics. Examples
XX include all-D peptides corresponding to residues 1-42, 1-40, 1-35, 1-28,
XX 1-7, 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
XX derivative peptides given in AAB82623-64. The vaccine elicits a
XX preferential TH-2 or TH-1 response, preventing fibrillogenesis and
XX associated cellular toxicity. The amyloid related diseases may be

CC localised amyloidosis, e.g. diabetes type II, neurodegenerative diseases,
CC e.g. scrapie, bovine spongiform encephalitis, Creutzfeldt-Jakob disease,
CC cerebral amyloid angiopathy, and prion protein related disorders, or
CC systemic amyloidosis associated with chronic infection (e.g.
CC tuberculosis) or chronic inflammation (e.g. rheumatoid arthritis),
CC familial Mediterranean fever (FMF) and systemic amyloidosis found in long
CC term haemodialysis patients. The novel vaccines do not present the
CC drawbacks of 'self' proteins and do not need to be aggregated to induce
CC an immune response
CC SQ Sequence 42 AA;
CC Query Match 100.0%; Score 211; DB 4; Length 42;
CC Best Local Similarity 100.0%; Pred. No. 1.6e-23;
CC Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRHDSGYEVHHQKLVFPAEDVGSNKGAITGLMVGGVIA 42
Db 2 AEFRRHDSGYEVHHQKLVFPAEDVGSNKGAITGLMVGGVIA 42
RESULT 26
AAB49395 standard; peptide; 42 AA.
XX AAB49395;
XX 06-MAR-2001 (first entry)
XX Human amyloid peptide protein fragment SEQ ID NO: 10.
XX Human, immunogenic peptide; immune response; monophosphoryl lipid A;
XX antigen; infection; cancer; amyloid deposition.
XX Homo sapiens.
XX WO200069456-A2.
XX PN 23-NOV-2000.
XX PD 12-MAY-2000; 2000WO-US013156.
XX 13-MAY-1999; 99US-0133633P.
XX (AMCY) AMERICAN CYANAMID CO.
XX Hagen M;
XX WPI; 2001-024946/03.
XX Antigenic composition having an antigen (e.g. viral protein) and an
XX adjuvant, useful for enhancing humoral and cellular immune response in a
XX host or as a prophylaxis against virus, bacterium, parasite, cancer cell
XX or allergen.
XX PS Disclosure; Page 39; 129pp; English.
XX The present invention provides an antigenic composition comprising an
XX antigen with a 3-O-deacylated monophosphoryl lipid A or monophosphoryl
XX lipid A adjuvant. The presence of the adjuvant causes an increased immune
XX response. The antigen may be from a pathogenic bacterium, fungus, virus
XX or parasite, a cancer cell, an allergen or from amyloid peptide protein.
XX The composition can be used in the prevention and treatment of infection,
XX cancer and diseases caused by amyloid deposition. It is particularly
XX useful against HIV, Neisseria gonorrhoeae and respiratory syncytial virus
XX SQ Sequence 42 AA;
XX Query Match 100.0%; Score 211; DB 4; Length 42;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-23;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRHDSGYEVHHQKLVFPAEDVGSNKGAITGLMVGGVIA 42

Db 2 AEFRRHDSGYEVHHQKLVFFPAEDVGSNKGAIIIGLMVGCVIA 42
|||||
RESULT 27
AAB48830
ID AAB48830 standard; peptide; 42 AA.
XX
AC AAB48830;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human amyloid-beta peptide, A-beta 42.
XX
KM Amyloid-beta peptide; A-beta 42; human; amyloid precursor protein;
KM APP cleavage product; immunogenic composition; solubilisation;
KM Alzheimer's disease; vaccine; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200072870-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US015302.
XX
PR 01-JUN-1999; 99US-0137047P.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Hirtzer P, Patel N;
XX
PI WPI; 2001-061445/07.
XX
PT New compositions comprising an aqueous solution of a solubilised amyloid
PT beta 42 peptide useful for invoking antibody response against amyloid
PT beta peptide, and for preventing or treating Alzheimer's disease.
XX
PS Claim 6; Page 9; 49pp; English.
XX
CC The invention relates to a novel composition comprising an aqueous
CC solution of at least 0.0mg/ml of amyloid-beta (A-beta) peptide, where
CC the aqueous solution is maintained at a pH sufficient to solubilise the A
CC -beta peptide. In particular, the A-beta peptide in the composition is A-
CC beta 42 (AAB48830). The invention also relates to methods of producing
CC the composition of the invention, and the use of the A-beta peptide
CC composition to induce an immunogenic response in a mammal for the #
CC treatment or prevention of Alzheimer's disease. The sterile composition
CC of A-beta is useful for the manufacture of a vaccine for invoking an
CC antibody response against an A-beta peptide, and for preventing or
CC treating Alzheimer's disease. The present sequence represents the A-beta
CC 42 peptide, which is particularly preferred for use in the composition of
CC the invention
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHHQKLVFFPAEDVGSNKGAIIIGLMVGCVIA 42
Db 2 AEFRRHDSGYEVHHQKLVFFPAEDVGSNKGAIIIGLMVGCVIA 42
|||||
RESULT 28
AAB05484
ID AAB05484 standard; peptide; 42 AA.
XX
AC AAB05484;
XX
DT 24-SEP-2001 (first entry)
XX

DE Human peptide antigen comprising beta amyloid (Abeta) 42.
XX
KM Human; heat shock protein; hsp; A beta 42; beta amyloid; hypotensive;
KM neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
KM age-related cognitive function loss; senile dementia; Wilson's disease;
KM Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;
KM cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
KM Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
KM Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
KM myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
KM Gilles de la Tourette's syndrome; noctopic; chronic seizure disorder;
KM brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
KM AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological;
KM autonomic function disorder; Friedreich's ataxia; schizophrenia; therapy;
KM vasotropic; neuroprotective; anti-HIV; human immunodeficiency virus;
KM anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
OS Homo sapiens.
XX
PN WO200152890-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001825.
XX
PR 21-JAN-2000; 2000US-00489216.
XX
PA (UYCO-) UNIV CONNECTICUT HEALTH CENT.
XX
PI Srivastava PK;
XX
PI WPI; 2001-451897/48.
XX
PT Heat shock protein and antigenic molecule complexes, useful for the
PT prevention and treatment of neurodegenerative disorders e.g. senile
PT dementia, Alzheimer's disease and epilepsy.
XX
PS Disclosure; Page 14; 65pp; English.
XX
CC The present invention relates to pharmaceutical compositions comprising
CC complexes of heat shock proteins (hsps) in association with antigenic
CC molecules for use in treatment and prevention of neurodegenerative
CC disorders and diseases. The complexes of hsp and antigenic peptides are
CC used as vaccines for the treatment or prevention of neurodegenerative
CC disorders e.g. Alzheimer's disease, age-related loss of cognitive
CC function, senile dementia, Parkinson's disease, amyotrophic lateral
CC sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear
CC palsy, Guam disease, Lewy body dementia, prion diseases, spongiform
CC encephalopathies, Creutzfeldt-Jakob disease, polyglutamine diseases,
CC Huntington's disease, myotonic dystrophy, Friedreich's ataxia, ataxia,
CC Gilles de la Tourette's syndrome, seizure disorders, epilepsy, chronic
CC seizure disorder, stroke, brain trauma, spinal cord trauma, acquired
CC immunodeficiency syndrome (AIDS) dementia, alcoholism, autism, retinal
CC ischaemia, glaucoma, autonomic function disorder, hypertension,
CC neuropsychiatric disorder, schizophrenia or schizoaffective disorder and
CC for eliciting an immune response. The present sequence is human peptide
CC antigen comprising beta amyloid (Abeta) 42
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHHQKLVFFPAEDVGSNKGAIIIGLMVGCVIA 42
Db 2 AEFRRHDSGYEVHHQKLVFFPAEDVGSNKGAIIIGLMVGCVIA 42
|||||
RESULT 29
AAB81321
ID AAB81321 standard; peptide; 42 AA.
XX

AC ABB81321;
XX
XX 21-AUG-2002 (first entry)
XX
XX Amyloid precursor protein (APP) A-beta domain peptide 1-42.
DE
XX Amyloid precursor protein; APP; A-beta domain; tumour growth; metastasis;
KM gene therapy; immunostimulation; anticancer; vaccine; cytostatic; cancer.
XX
XX Homo sapiens.
OS
XX WO200234878-A2.
PN
XX 02-MAY-2002.
PD
XX 25-OCT-2001; 2001WO-11000986.
PF
XX 26-OCT-2000; 2000IL-00139308.
PR
XX (YEDA) YEDA RES & DEV CO LTD.
PA (MARI/) MARIKOVSKY M.
XX
XX Marikovsky M, Groner Y, Harris-Cerruti C;
PI WPI; 2002-479715/51.
XX
XX Pharmaceutical composition for the treatment or prevention of tumor
PT growth or metastases, and for immunostimulation, comprises a non-
PT glycosylated peptide of the amyloid precursor protein.
XX
XX Disclosure; Page 6; 38pp; English.
XX
XX The present invention describes a pharmaceutical composition (I) for the
CC treatment or prevention of tumour growth or metastases, or for
CC immunostimulation, comprising a non-glycosylated peptide (II) of the
CC amyloid precursor protein (APP), as an active ingredient, with a
CC pharmaceutically acceptable diluent or carrier. Also described: (1)
CC treating an immunocompromised individual, by administering an
CC immunostimulatory pharmaceutical composition comprising APP; (2) treating
CC (a) a subject, by administering a vector or cells comprising a
CC polynucleotide construct encoding (II) or APP; (3) treating a subject, by
CC administering an anticancer pharmaceutical comprising APP; and (4) use of
CC APP for the manufacture of a medicament for treating or preventing tumour
CC growth or metastasis, or for immunostimulation. (I) have cytostatic
CC activity and can be used in gene therapy and vaccine production. (I) is
CC useful for treating a subject with cancer, and for treating an
CC immunocompromised individual. (I) is also useful in the manufacture of a
CC medicament for treating or preventing human growth or metastasis, and
CC for immunostimulation. The present sequence represents an amino acid
CC sequence given in the exemplification of the present invention
XX
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIITGLMVGSVIA 42
DB 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIITGLMVGSVIA 42
RESULT 30
AAU80961
ID AAU80961 standard; protein; 42 AA.
XX
XX AAU80961;
AC
XX 09-APR-2002 (first entry)
DT
XX Human amyloid beta protein precursor.
DE
XX Vaccine; molecular scaffold; pilus; pilin; HBcAg; antigen;
KM

KM hepatitis B virus capsid protein; JUN; FOS; HIV gp140;
KM measles virus N protein; bee venom phospholipase; Th type 2 T-helper;
KM Th2; Sindbis virus E2 protein; amyloid beta; influenza M2 antigen;
KM human immunodeficiency virus infection; viral hepatitis; measles;
KM chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy; cancer;
KM chronic disease; arthritis; colitis; diabetes; multiple sclerosis.
XX
XX Homo sapiens.
OS
XX WO200185208-A2.
PN
XX 15-NOV-2001.
PD
XX 02-MAY-2001; 2001WO-1B000741.
PF
XX 05-MAY-2000; 2000US-0202341P.
PR
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (SEBB/) SEBBEL P.
PA (DUNA/) DUNANT N.
PA (BACH/) BACHMANN M.
PA (TIS/) TISSOT A.
PA (LECH/) LECHNER F.
XX
XX Sebbel P, Dunant N, Bachmann M, Tissot A, Lechner F;
PI WPI; 2002-055561/07.
XX
XX New composition, useful for vaccine production, comprises antigen or
PT antigenic determinant and non-natural molecular scaffold comprising
PT organizer and core particle such as bacterial pilus or pilin protein.
XX
XX Disclosure; Page 281; 287pp; English.
XX
XX The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold (molecular scaffold) which comprises a core particle
CC such as a bacterial pilus or pilin protein, a recombinant form of the
CC protein, a virus-like particle or a hepatitis B virus capsid protein
CC (HBcAg), and an organizer; and (b) an antigen or antigenic determinant,
CC where the molecular scaffold and antigenic determinant interact to form
CC an ordered and repetitive antigen array. Suitable antigenic determinants
CC include JUN, FOS, HIV gp140, measles virus N protein, bee venom
CC phospholipase, Sindbis virus E2 protein, amyloid beta derived peptides and
CC influenza M2 antigen. The composition (or vaccine) is useful for
CC immunisation, by administration to a subject, where the administration
CC produces an immune response, such as humoral, cellular or protective
CC immune response, preferably a Th type 2 T-helper (Th2) response that is
CC specific for the antigenic determinant. The administration induces
CC antibodies specific for the antigenic determinant of a subtype
CC corresponding to the Th2 subtype in the subject. The subject does not
CC generate a Th2 subtype that is specific for pilus or pilin polypeptide or
CC antigenic determinant. The composition is useful for the production of
CC vaccines for prevention of infectious diseases such as human
CC immunodeficiency virus, viral hepatitis, measles, chicken pox, pneumonia,
CC tuberculosis, syphilis, malaria, and for treating allergy, cancer, and
CC chronic diseases induced or accelerated by a Th1 type immune response,
CC such as arthritis, colitis, diabetes and multiple sclerosis. The
CC composition is useful to generate defined self-specific antibodies and
CC specific immune responses of the Th2 type and allows the creation of
CC highly efficient vaccines against infectious diseases, and for treating
CC allergy, cancer, and chronic diseases induced or accelerated by a Th1
CC type immune response. The present sequence is a peptide or protein
CC incorporated into the compositions of the invention
XX
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 211; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIITGLMVGSVIA 42
DB 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIITGLMVGSVIA 42

Search completed: September 28, 2006, 06:10:42
Job time : 113.251 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 17.3274 Seconds
(without alignments) 233.221 Million cell updates/sec

Title: US-09-731-899-3
Perfect score: 211
Sequence: 1 XAEFRHDSGEVHHQKLVF.....DVGSNKGATIGLMVGVIA 42

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	211	100.0	42	2	PM0512
2	211	100.0	57	2	AE0045
3	211	100.0	57	2	AE0045
4	211	100.0	57	2	AE0045
5	211	100.0	57	2	AE0045
6	211	100.0	57	2	AE0045
7	211	100.0	57	2	AE0045
8	211	100.0	82	2	P00438
9	211	100.0	695	1	A49795
10	211	100.0	770	1	ORHUA4
11	192	91.0	695	2	A27485
12	192	91.0	695	2	S00550
13	192	91.0	747	2	UH0773
14	127	60.2	33	2	S23094
15	63	29.9	755	2	A13228
16	62	29.4	755	1	OQAG4T
17	61	28.9	755	1	DAAGWT
18	57	27.0	503	2	S73843
19	56.5	26.8	378	2	S61992
20	55.5	26.3	678	2	G71526
21	55	26.1	291	2	F95015
22	55	26.1	317	2	H97888
23	55	26.1	488	2	S27652
24	54.5	25.8	678	2	C81683
25	54.5	25.8	832	2	H84848
26	54	25.6	763	2	A13443
27	53.5	25.4	708	2	T24727
28	53	25.1	327	2	S11435
29	53	25.1	390	2	C75103

30	53	25.1	422	2	D72302	hypothetical prote
31	53	25.1	601	2	T02581	modulin-like prote
32	52.5	24.9	314	2	F86805	cation transporter
33	52.5	24.9	678	2	C86495	hypothetical prote
34	52.5	24.9	678	2	H72128	3-methyl-2-oxobuta
35	52.5	24.6	272	2	F70979	hypothetical prote
36	52	24.6	339	2	A81351	signal transductio
37	52	24.6	417	2	F70132	conserved hypotnet
38	52	24.6	527	2	T18232	conserved hypotnet
39	52	24.6	611	2	S19434	probable transport
40	52	24.6	738	2	C95936	conserved hypotnet
41	51.5	24.4	1364	2	T51920	probable xanthine
42	51	24.2	103	2	D75449	BUG protein - Dei
43	51	24.2	257	2	AC1024	probable dimethyl
44	51	24.2	494	2	C70940	probable cobp prot
45	51	24.2	769	1	TC1121	leukocyte adhesion
46	51	24.2	3063	2	TS0166	genome polyprotein
47	50.5	23.9	165	2	H90519	ABC transporter at
48	50.5	23.9	245	2	AH1098	a probable phospho
49	50.5	23.9	245	2	AG1461	probable phospho-b
50	50.5	23.9	292	2	H87260	asparaginase fam1
51	50.5	23.9	621	2	AF3016	Na+/H+ antiporter
52	50.5	23.9	642	2	B98268	probable sodium/hy
53	50.5	23.9	833	2	T01547	probable phosphoi
54	50.5	23.9	1014	2	T17275	legume protein 7
55	50.5	23.9	1345	2	S55669	hypothetical glyci
56	50	23.7	234	2	G95989	hypothetical glyci
57	50	23.7	284	2	S04723	genome polyprotein
58	50	23.7	285	1	B64105	naphthoate synthas
59	50	23.7	285	2	A69856	polyugar dehydrin
60	50	23.7	390	2	H71083	probable Na+/H+-ex
61	50	23.7	441	2	T31482	hypothetical prote
62	50	23.7	487	2	T49424	hypothetical prote
63	50	23.7	946	1	TC5667	multidrug resistan
64	50	23.7	971	2	D70128	conserved hypotnet
65	50	23.7	1286	2	T02187	probable ABC trans
66	50	23.7	1292	2	T48007	P-glycoprotein hom
67	49.5	23.5	297	2	G69525	formylmethanofuran
68	49.5	23.5	311	2	G86324	hypothetical prote
69	49.5	23.5	1068	2	T48756	mitochondrial nico
70	49.5	23.5	1162	2	S07421	E2 glycoprotein pr
71	49	23.2	246	2	S29716	triase-phosphate 1
72	49	23.2	316	2	D97865	hypothetical prote
73	49	23.2	322	2	E71647	hypothetical prote
74	49	23.2	403	2	T36019	phosphoglycerate k
75	49	23.2	469	2	C90446	permease, multidru
76	49	23.2	489	2	F82085	glutamate synthase
77	49	23.2	527	2	A43938	Pseudomonas cytoch
78	49	23.2	533	2	E84858	phosphoprotein pho
79	49	23.2	568	1	OSPSA	Pseudomonas cytoch
80	49	23.2	577	2	A84681	nodulin-like prote
81	49	23.2	649	2	S58054	bdc protein - fru
82	49	23.2	674	2	S39476	kinase-like trans
83	49	23.2	704	2	A34287	storage protein 2
84	49	23.2	891	2	G96636	hypothetical prote
85	49	23.2	1150	2	AB0064	probable membrane
86	49	23.2	1555	2	JT0959	hypothetical prote
87	48.5	23.0	144	2	AC2572	hypothetical prote
88	48.5	23.0	378	2	T49164	zinc transporter-1
89	48.5	23.0	390	2	B95954	probable membrane-
90	48.5	23.0	393	2	S59499	cellulase egli - B
91	48.5	23.0	459	2	I64224	aromatic amino aci
92	48.5	23.0	497	2	G81588	serine hydroxymeth
93	48.5	23.0	510	2	S55124	probable membrane
94	48.5	23.0	519	2	B86555	serine hydroxymeth
95	48.5	23.0	519	2	H72067	glycine hydroxymet
96	48.5	23.0	547	2	AD2250	acetylacetic synth
97	48.5	23.0	614	2	B71551	probable s/c prote
98	48	22.7	77	2	C97027	foaa-like protein,
99	48	22.7	269	2	C97027	naphthoate synthas
100	48	22.7	311	2	AH1628	L-lactate dehydrat

ALIGNMENTS

RESULT 1

beta-amyloid protein - guinea pig (fragment)

C/Species: Cavia porcellus (guinea pig)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: PM0512

R/Shimomigishi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment

A/Reference number: PM0512; MUID:93290653; PMID:7685598

A/Accession: PM0512

A/Molecule type: protein

A/Residues: 1-42 <SH1>

A/Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 211; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: A60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: A60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56125

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 7 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 3

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: F60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: F60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 7 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 4

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: D60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: D60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56124

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 7 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 5

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C/Species: Ovis sp. (sheep)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: B60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: B60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56130

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.9e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
 Db 7 AEFPHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 6

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C/Species: Cavia porcellus (guinea pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: G60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: G60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2,9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 7 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 47

RESULT 7

B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>

A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 211; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2,9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 7 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 47

RESULT 8

PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, U.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>

A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 211; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4,3e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 18 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 58

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podilansky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A:Reference number: A49795; MUID:91273111; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>

A:Cross-references: UNIPARC:UPI00002A2AF2; GB:M58727; NID:g342062; PIDN:AAA6829.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 211; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 4,4e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 598 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 10

QRH0N4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)

C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I59652; A44
4668; A28583; A29302; A60805; J10038; S06122; A60355; A59011; A38384; S29076; S38252; S3

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA

A:Cross-references: UNIPARC:UPI00002A2AF2; EMBL:X13466
A:Residues: 1-288; 'V', 365-770 <LEM1>
A:Note: alternative splice form APP(695)

A:Cross-references: UNIPARC:UPI000016A551; EMBL:X13466
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194

A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: UNIPARC:UPI000016A551; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID

A:Note: alternative splice form APP(695)
R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakts, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote

A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>

A:Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:g341202; PIDN:AA313
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>

A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of ;

A/Reference number: A35486; MUID:90321244; PMID:2196878
 A/Accession: A35486
 A/Molecule type: DNA
 A/Residues: 672-710 <PRE1>
 A/Cross-references: UNIPARC:UPI0000148176
 A/Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R/Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A/Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A/Reference number: I39451; MUID:90236318; PMID:2110105
 A/Accession: I39451
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A/Molecule type: DNA
 A/Residues: 1-770 <YOS1>
 A/Cross-references: UNIPARC:UPI000002DB1C; GB:M31112; NID:g178613; PIDN:AA59502.1; PID:
 A/Accession: I39451
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A/Molecule type: DNA
 A/Residues: 1-530, 'OMLMPVIPAFAWEAKYGR' <YOS2>
 A/Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AA59501.1; PID:
 R/Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A/Reference number: A59020; MUID:91340168; PMID:1908403
 A/Status: annotation; extratum
 A/Content: revised physical map for reference I39451
 R/Levy, E.; Carmo, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1121-1126, 1990
 A/Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A/Reference number: I39453; MUID:90260663; PMID:2111584
 A/Accession: I39453
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 656-737 <LEV>
 A/Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:
 A/Note: a mutation with 693-Gln is presented
 R/Murteil, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A/Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A/Reference number: I59562; MUID:9202553; PMID:1925564
 A/Accession: I59562
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 689-716, 'F', 718-737 <MUR>
 A/Cross-references: UNIPARC:UPI000011F7BA; GB:S57665; NID:g236720; PIDN:AA19991.1; PID:
 R/Kamito, K.; Orr, H.T.; Payami, H.; Wiseman, E.M.; Alonzo, M.E.; Puls, S.M.; Anderson,
 araki, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A/Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A/Reference number: A44017; MUID:93035397; PMID:1415269
 A/Accession: A44017
 A/Molecule type: DNA
 A/Residues: 687-692, 'G', 694-718 <KAM1>
 A/Cross-references: UNIPARC:UPI000011F7BA; GB:S45135; NID:g237377; PIDN:AA23645.1; PID:
 A/Experimental source: familial Alzheimer disease family SB
 A/Note: sequence extracted from NCBI backbone (NCBI:P:115376)
 A/Accession: B44017
 A/Molecule type: DNA
 A/Residues: 687-718 <KAM2>
 A/Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g237379; PIDN:AA23646.1; PID:
 A/Experimental source: familial Alzheimer disease family LT
 A/Note: sequence extracted from NCBI backbone (NCBI:P:115376)
 A/Note: this sequence has a silent mutation
 R/Kang, J.; Lemstra, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A/Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
 A/Reference number: A03134; MUID:87144572; PMID:2881207
 A/Accession: A03134
 A/Molecule type: mRNA
 A/Residues: 1-288, 'V', 365-770 <KAN>
 A/Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:
 A/Note: alternative splice form APP(695)
 R/Robak, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A/Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular ar
 A/Reference number: A29030; MUID:87231971; PMID:3035574
 A/Accession: A29030
 A/Molecule type: mRNA
 A/Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A/Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:
 R/Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 880-884, 1987
 A/Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the
 A/Reference number: A47585; MUID:87120329; PMID:2949367
 A/Accession: A47585
 A/Molecule type: mRNA
 A/Residues: 674-703 <TAN1>
 A/Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:
 R/Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemstra, H.G.; Kang, J.; Mueller,
 EMBO J. 7, 949-957, 1988
 A/Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A/Reference number: S02638; MUID:88236437; PMID:2900137
 A/Accession: S02638
 A/Molecule type: mRNA
 A/Residues: 672-678 <DYR>
 A/Cross-references: UNIPARC:UPI000003A5B0
 R/Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve,
 Nature 331, 528-530, 1988
 A/Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associate
 A/Reference number: S00707; MUID:88122640; PMID:2853290
 A/Accession: S00707
 A/Molecule type: mRNA
 A/Residues: 286-344, 'I', 365-366 <TAN2>
 A/Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g288177; PIDN:CAA30042.1; PID:
 A/Experimental source: promyelocytic leukemia cell line HL60
 R/Ponte, P.; Gonzalez-Demhilt, P.; Schilling, J.; Miller, J.; Hau, D.; Greenberg, B.; Dav
 Nature 331, 525-527, 1988
 A/Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitt
 A/Reference number: S00925; MUID:88122639; PMID:2853289
 A/Accession: S00925
 A/Molecule type: mRNA
 A/Residues: 1-344, 'I', 365-770 <PO2>
 A/Cross-references: UNIPARC:UPI000002A2F2; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30042.1; PID:
 R/Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 520-522, 1988
 A/Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory
 A/Reference number: A38949; MUID:88122641; PMID:2853291
 A/Accession: A38949
 A/Molecule type: mRNA
 A/Residues: 287-367 <KIT>
 A/Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:
 A/Experimental source: glioblastoma cell line
 A/Note: alternative splice form APP(751)
 R/Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton,
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A/Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three pr
 A/Reference number: A30320
 A/Accession: A30320
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 284-288, 'V', 365-770 <VIT1>
 A/Cross-references: UNIPARC:UPI0000174094
 A/Accession: B30320
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA


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A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
A;Cross-references: UNIPARC:UPI0000174094
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA

Query Match          100.0%; Score 211; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
2 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db
673 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 713

RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: protelinsulin nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YMM>
A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Bergh, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BA01456.1; PID:
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match          91.0%; Score 192; DB 2; Length 695;
Best Local Similarity 92.7%; Pred. No. 1.5e-17;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy
2 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db
598 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat

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N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hildich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2F9; EMBL:X07648; NID:g55616; PIDN
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Heese, L.; Behr, D.; Maerker, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;65-648/Domain: transmembrane #status predicted <TMM>

Query Match          91.0%; Score 192; DB 2; Length 695;
Best Local Similarity 92.7%; Pred. No. 1.5e-17;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy
2 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db
598 AEFRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AA024853.1; PID:
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match          91.0%; Score 192; DB 2; Length 747;
Best Local Similarity 87.8%; Pred. No. 1.6e-17;
Matches 36; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

Qy 2 AEFRRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 Db 650 SEYRHDTAYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 690

RESULT 14

S23094
 beta-amyloid protein precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C/Accession: S23094
 R/Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A/Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A/Reference number: S23094; MUID:92316198; PMID:1618239
 A/Accession: S23094
 A/Molecule type: protein
 A/Residues: 1-33 <KOJ>
 A/Cross-references: UNIPARC:UPI00001777FB
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 60.2%; Score 127; DB 2; Length 33;
 Best Local Similarity 88.9%; Pred. No. 2.6e-10;
 Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 AEFRRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 28
 Db 7 AEFGRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 33

RESULT 15

A13228
 tryptophan 2-monooxygenase tmel [imported] - Agrobacterium tumefaciens (strain C58, Dupc
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
 C/Accession: A13228
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, P.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
 Science 294, 2317-2333, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, B.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: A13228
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-755 <KUR>
 A/Cross-references: UNIPROT:Q8U6A3; UNIPARC:UPI00000274E; GB:AB008690; PIDN:AAL46247.1;
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Gene: tmel
 A/Genome: plasmid
 C/Superfamily: tryptophan 2-monooxygenase

Query Match 29.9%; Score 63; DB 2; Length 755;
 Best Local Similarity 44.4%; Pred. No. 2.7;
 Matches 16; Conservative 5; Mismatches 9; Indels 6; Gaps 1;
 Qy 7 DSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 Db 223 DSG-----RIGFPEDVPRKXAVIGAGISGLVVA 252

RESULT 16

QOAG4T
 tryptophan 2-monooxygenase (EC 1.13.12.3) - Agrobacterium tumefaciens plasmid pTiAch5,
 C/Species: Agrobacterium tumefaciens
 C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 05-Oct-2004
 C/Accession: A04497; S28687; A20966
 R/Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, M.; V
 EMBO J. 3, 835-846, 1984

A/Title: The complete nucleotide sequence of the T-DNA of the Agrobacterium tumefaciens

A/Reference number: A91001; MUID:84207942; PMID:6327292

A/Accession: A04497

A/Molecule type: DNA

A/Residues: 1-755 <GIB>

A/Cross-references: UNIPROT:P04029; UNIPARC:UPI00001372AD

A/Genetics: G1

R/Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.

Plant Mol. Biol. 2, 335-350, 1983

A/Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo

A/Reference number: S28683

A/Accession: S28687

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-362; 'H', 364-596, 'S', 598-717, 'IO', 720, 'A', 722-755 <BAR>

A/Cross-references: UNIPARC:UPI0000081590; EMBL:X00493; NID:939062; PIDN:CAA25167.1; PID

A/Experimental source: strain octopline

A/Genetics: G2

R/Klee, H.; Montoya, A.; Horodyski, F.; Lichtenstein, C.; Garfinkel, D.; Fuller, S.; Plo

Proc. Natl. Acad. Sci. U.S.A. 81, 1728-1732, 1984

A/Title: Nucleotide sequence of the tms genes of the pTiA6NC octopline T1 plasmid: two ge

A/Reference number: A20966; MUID:84170374; PMID:6584906

A/Accession: A20966

A/Molecule type: DNA

A/Residues: 1-717, 'IO', 720, 'A', 722-755 <KLE>

A/Cross-references: UNIPARC:UPI0000170D07; GB:X02554; NID:9154747; PIDN:AAA92550.1; PID:5

A/Experimental source: strain octopline

A/Genetics: G3

C/Genetics: <G1>

A/Genome: plasmid

A/Note: plasmid pTiAch5

C/Genetics: <G2>

A/Genome: plasmid

A/Note: plasmid pTi15955

C/Genetics: <G3>

A/Gene: tmel

A/Genome: plasmid

A/Note: plasmid pTiA6NC

C/Function: tryptophan metabolism; auxin biosynthesis

A/Note: catalyzes the first step in the biosynthesis of auxins from tryptophan

C/Superfamily: tryptophan 2-monooxygenase

C/Keywords: monooxygenase; oxidoreductase

Query Match 29.4%; Score 62; DB 1; Length 755;
 Best Local Similarity 41.7%; Pred. No. 3.7;
 Matches 15; Conservative 1; Mismatches 9; Indels 6; Gaps 1;
 Qy 7 DSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 Db 223 DSG-----RIGFPEDVPRKXAVIGAGISGLVVA 252

RESULT 17

DAAGMT
 tryptophan 2-monooxygenase (EC 1.13.12.3) TA - Agrobacterium tumefaciens plasmid pTiTm4
 C/Species: Agrobacterium tumefaciens
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
 C/Accession: S15002; S15450
 R/Bonnard, G.; Vincent, F.; Otten, L.
 Plant Mol. Biol. 16, 733-738, 1991
 A/Title: Sequence of Agrobacterium tumefaciens biotype III auxin genes.
 A/Reference number: S15001; MUID:91329707; PMID:1868204
 A/Accession: S15002
 A/Molecule type: DNA
 A/Residues: 1-755 <BO2>
 A/Cross-references: UNIPARC:UPI00001372B1; EMBL:X56185; NID:939133; PIDN:CAA39646.1; PID
 A/Experimental source: strain Tm4; strain octopline
 C/Genetics:
 A/Gene: taam
 A/Genome: plasmid pTiTm4
 C/Function:
 A/Pathway: tryptophan metabolism; auxin biosynthesis

A>Note: catalyzes the first step in the biosynthesis of auxins from tryptophan
A:Superfamily: tryptophan 2-monooxygenase
C:Keywords: monooxygenase; oxidoreductase

Query Match 28.9%; Score 61; DB 1; Length 755;
Best Local Similarity 41.7%; Pred. No. 5;
Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

Qy 7 DSGEVHOKLVFPAEDVGSNKGAIIIGLWGVVIA 42
Db 223 DSG-----RIGFPEEDVPRKVAIVGAGISGLVVA 252

RESULT 18

S73843
general amino acid permease GAP1 homolog F10_orf503 - Mycoplasma pneumoniae (strain ATCC
N/Aternate names: hypothetical protein F10_orf503
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S73843
R:Hillemeier, R.; Hillebert, H.; Plagens, H.; Pitkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996

A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A/Reference number: S73327; MUID:97105885; PMID:8948633
A/Accession: S73843

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-503 <HMM>
A/Cross-references: UNIPROT:P75462; UNIPARC:UPI00001394B1; EMBL:AE000051; GB:U00089; NID
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: gap1
A:Genetic code: SGC3

Query Match 27.0%; Score 57; DB 2; Length 503;
Best Local Similarity 61.1%; Pred. No. 11;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 24 VGSNKGAIIIGLWGVVIA 41
Db 131 VKDNMGALIGLVGPFVL 148

RESULT 19

S61992
SLG1 protein - yeast (Saccharomyces cerevisiae)

N/Aternate names: protein O2545; protein UNP378; protein YOR008c

C:Species: Saccharomyces cerevisiae

C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S61992; S66873; S72141
R:Stierly, F.; Uhlen, M.

A/Reference number: S61981

A/Accession: S61992

A:Molecule type: DNA

A:Residues: 1-378 <STE>
A/Cross-references: UNIPROT:P54867; UNIPARC:UPI0000135A12; EMBL:U43491; NID:g1150992; PT
R:Pettersson, B.; Stierly, F.; Uhlen, M.

A/Reference number: S66682

A/Accession: S66873

A:Molecule type: DNA

A:Residues: 1-378 <PPT>
A/Cross-references: UNIPARC:UPI0000135A12; EMBL:Z74916; NID:g1420101; PID:e252318; PID:g
R:Stierly, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.

Yeast 12, 1091-1095, 1996

A>Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacchar
A/Reference number: S72130; MUID:97051599; PMID:8896276

A/Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-378 <STM>
A/Cross-references: UNIPARC:UPI0000135A12; EMBL:U43491; NID:g1150992; PIDN:AAQ49488.1; P
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

C:Genetics:
A:Gene: SCD:SLG1
A/Cross-references: SGD:S0005534; MIPS:YOR008c
A/Map position: 15R
C:Keywords: transmembrane protein
F:270-286/Domain: transmembrane #status predicted <TM>

Query Match 26.8%; Score 56.5; DB 2; Length 378;
Best Local Similarity 42.4%; Pred. No. 9.3;
Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

Qy 8 SGYEVHOKLVFPAEDVGSNKGAIIIGLWGVV 40
Db 251 SGSKTHKK-----ANVGAIVGVGVGV 274

RESULT 20

G71526
3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain pdhA/
N/Aternate names: oxoisovalerate dehydrogenase

C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C/Accession: G71526

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998

A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A/Reference number: A71570; MUID:99000809; PMID:9784136

A/Accession: G71526

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-678 <ARN>
A/Cross-references: UNIPROT:O84344; UNIPARC:UPI00000D7604; GB:AE001307; GB:AE001273; NID
A/Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: pdhA/B

C:Keywords: oxidoreductase

Query Match 26.3%; Score 55.5; DB 2; Length 678;
Best Local Similarity 37.5%; Pred. No. 24;
Matches 12; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Qy 3 EFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGL 34
Db 364 EMQRDPG-----VVFGEDVAGNKGKGVGV 388

RESULT 21
F95015
glycosyl transferase, family 2 SP0136 [imported] - Streptococcus pneumoniae (strain TIGR
C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: F95015
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, I.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:11357209; PMID:11163916

A/Accession: F95015

A>Status: preliminary

A:Molecule type: DNA
A/Residues: 1-291 <KUR>
A/Cross-references: UNIPROT:Q97T23; UNIPARC:UPI00000512F6; GB:AE005672; PIDN:AAK74319.1;

A/Experimental source: strain TIGR4

C:Genetics:
A:Gene: SP0136

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 26.1%; Score 55; DB 2; Length 291;

C;Genetics:
A;Gene: BME11535
A;Map position: 1
C;Superfamily: Na(+)/H(+) antiporter 1/protease IV-related
C;Keywords: hydrolase

Query Match 25.6%; Score 54; DB 2; Length 763;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 16; Conservative 5; Mismatches 17; Indels 2; Gaps 2;

QY 4 FRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGVI 42
DB 552 YRRIIDLAERHOKKVFVEVDVAASGGYIAL-AGDEIIA 590

RESULT 27

T24727
hypothetical protein T09A5.12 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24727

R;Lighting, J. submitted to the EMBL Data Library, August 1994

A;Reference number: Z19928

A;Accession: T24727

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-708 <WIL>

A;Cross-references: UNIPROT:P45972; UNIPARC:UPI000013BBE3; EMBL:Z36753; PIDN:CAA85341.1;

A;Experimental source: clone T09A5

C;Genetics:

A;Gene: CESP.T09A5.12

A;Map position: 2

A;Insertions: 22/3; 49/3; 100/3; 130/2; 167/2; 269/2; 316/3; 461/3; 487/1; 540/1; 562/3; 55

C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09A5.12

Query Match 25.4%; Score 53.5; DB 2; Length 708;
Best Local Similarity 38.2%; Pred. No. 46;

Matches 13; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

QY 6 HDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGVI 39
DB 444 HHSGEIDHTRMV-----LESNELASIGALVDV 472

RESULT 28

S11435
genome polypeptide - potato virus Y (fragment)

N;Contains: coat protein; Nib protein

C;Species: potato virus Y, PVY

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C;Accession: S11435; S11549; UCL526

R;Zhou, X.R.; Fang, R.X.; Wang, C.Q.; Mang, K.Q.

Nucleic Acids Res. 18, 5554, 1990

A;Title: cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).

A;Reference number: S11435; MUID:91016851; PMID:2216735

A;Accession: S11435

A;Molecule type: mRNA

A;Residues: 1-327 <ZH01>

A;Cross-references: UNIPROT:P21294; UNIPARC:UPI000017871F; EMBL:X54058

R;Zhou, X.R. submitted to the EMBL Data Library, July 1990

A;Reference number: S11549

A;Accession: S11549

A;Molecule type: mRNA

A;Residues: 1-90, 'E', '92-327 <ZH02>

A;Cross-references: UNIPARC:UPI0000131E66; EMBL:X54058; NID:961219; PIDN:CAA37993.1; PID

Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991

A;Title: Comparison of biological properties, serological characteristics and amino acid

A;Reference number: JCI526

A;Accession: JCI526

A;Molecule type: genomic RNA

A;Residues: 61-68, 'E', '71-73, 'E', '76-111, 'S', '113-201, 'E', '203-327 <OHS>
A;Cross-references: UNIPARC:UPI0000178720
C;Genetics:
A;Start codon: GCA
C;Superfamily: tobacco etch virus genome polypeptide
C;Keywords: coat protein; polypeptide
F;61-327/Product: coat protein #status predicted <COP>

Query Match 25.1%; Score 53; DB 2; Length 327;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 4; Indels 10; Gaps 3;

QY 3 EFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGVI 28
DB 49 EFERDS-YEVHQQ-----ANDTIDAVGDNK 72

RESULT 29

C75103
na+/h+ antiporter (napa-4) PAB0809 - *Pyrococcus abyssi* (strain Orsay)

C;Species: *Pyrococcus abyssi*

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: C75103

R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999

A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Accession: C75103

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-390 <KAW>

A;Cross-references: UNIPROT:Q9UZD1; UNIPARC:UPI0000034520; GB:AJ248286; GB:AL096836; NID

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: napa-4; PAB0809

C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napa1

Query Match 25.1%; Score 53; DB 2; Length 390;
Best Local Similarity 46.2%; Pred. No. 28;

Matches 12; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 17 LVFPAEDVGSNKGAIIIGLMVGVI 42
DB 225 LAFLAEDIGLNO--ILGAVLAGLIS 248

RESULT 30

D72302
hypothetical protein TM1021 - *Thermotoga maritima* (strain MSB8)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: D72302

R;Neilson, K.E.; Claydon, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M. Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: D72302

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-422 <ARN>

A;Cross-references: UNIPROT:O50548; UNIPARC:UPI000003833; GB:AE001764; GB:AE000512; NID

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1021

C;Superfamily: chloramphenicol resistance homolog ywfa

Query Match 25.1%; Score 53; DB 2; Length 422;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 12; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

QY 4 FRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGVI 39

Db ||:| ||| :|: ||:|:|:|:
 241 FRREGISVETATVFPVFGIGN---IVGIIIGL 272

Search completed: September 28, 2006, 06:24:31
Job time : 19.3274 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:51 / Search time 136.735 Seconds
(without alignments)
284.130 Million cell updates/sec

Title: US-09-731-899-3

Perfect score: 211
Sequence: 1 XAEFRHDSGYEHHOKLVF.....DVGSKGALIGLVGVVIA 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	42	2	056J16 GRAGR
2	211	100.0	42	2	056J17 TURTR
3	211	100.0	42	2	07M088_CAVPO
4	211	100.0	57	1	A4_URSWA
5	211	100.0	58	1	A4_CANFA
6	211	100.0	58	1	A4_RABIT
7	211	100.0	58	1	A4_SHEEP
8	211	100.0	59	1	A4_BOVIN
9	211	100.0	113	2	08JH58_CHESE
10	211	100.0	534	2	093296_CHICK
11	211	100.0	569	2	09PVL1_CHICK
12	211	100.0	695	2	02XQAO_PIG
13	211	100.0	695	2	056J13 CANFA
14	211	100.0	695	2	05R477_PONPY
15	211	100.0	695	2	06RH29_CANFA
16	211	100.0	695	2	09DG08_CHICK
17	211	100.0	714	2	056J14 CANFA
18	211	100.0	749	1	A4_SAIISC
19	211	100.0	751	1	056J12 STECO
20	211	100.0	751	2	06GSGO_HUMAN
21	211	100.0	751	2	04R488_CANFA
22	211	100.0	751	2	056J15 CANFA
23	211	100.0	751	2	06RH28_CANFA
24	211	100.0	751	2	02XQ99_PIG
25	211	100.0	751	2	09DGJ7_CHICK
26	211	100.0	770	1	A4_CAVPO
27	211	100.0	770	1	A4_HUMAN
28	211	100.0	770	1	A4_MACFA
29	211	100.0	770	1	A4_PANTR
30	211	100.0	770	1	A4_PIG
31	211	100.0	770	2	056J16 CANFA

32	211	100.0	770	2	06RH30_CANFA	06rh30 canis faml
33	206	97.6	52	2	08W259_HUMAN	08w259 homo sapien
34	201	95.3	64	2	03M025_ANTST	03m025 antechinus
35	192	91.0	79	2	035463_CRIGR	035463 cricetus
36	192	91.0	218	2	08BPV5_MOUSE	08bpv5 mus musculu
37	192	91.0	384	2	08BPC7_MOUSE	08bpc7 mus musculu
38	192	91.0	633	2	098SG0_XENLA	098sg0 xenopus lae
39	192	91.0	635	2	06GR18_MOUSE	06gr18 mus musculu
40	192	91.0	733	2	06PE05_RAT	06pe05 rattus norv
41	192	91.0	747	2	091963_PIP1	091963 xenopus . ap
42	192	91.0	749	2	06NR11_XENLA	06nr11 xenopus lae
43	192	91.0	750	2	06DU16_XENLA	06du16 xenopus tro
44	192	91.0	752	2	03TWF3_MOUSE	03twf3 mus musculu
45	192	91.0	752	2	03TX19_MOUSE	03tx19 mus musculu
46	192	91.0	770	1	A4_MOUSE	PI2023 m amyloid b
47	192	91.0	770	1	A4_RAT	P08592 r amyloid b
48	192	91.0	770	2	053ZT3_MOUSE	053zt3 mus musculu
49	192	91.0	770	2	0547B7_RAT	0547b7 rattus norv
50	189	89.6	635	2	07ZX00_XENLA	07zx00 xenopus lae
51	189	89.6	635	2	098SF9_XENLA	098sf9 xenopus lae
52	186	88.2	639	2	057394_NARJA	057394 narke japon
53	173	82.0	754	2	04RY33_TETNG	04ry33 tetradon n
54	173	82.0	780	1	A4_TETFL	073683 tetradon f
55	170	80.6	33	2	09UC33_HUMAN	09uc33 homo sapien
56	170	80.6	737	1	A4_FUGRU	093229 fugu rubrip
57	170	80.6	759	2	04S0J4_TETNG	04s0j4 tetradon n
58	155.5	73.7	357	2	08U108_BRARE	08u108 brachydanio
59	155.5	73.7	472	2	08U108_BRARE	08u108 brachydanio
60	155.5	73.7	612	2	0919E7_BRARE	0919e7 brachydanio
61	155.5	73.7	618	2	07ZZT1_BRARE	07zzt1 brachydanio
62	155.5	73.7	728	2	06NU21_BRARE	06nu21 brachydanio
63	155.5	73.7	738	2	090W28_BRARE	090w28 brachydanio
64	151	71.6	239	2	08U1Y7_BRARE	08u1y7 brachydanio
65	151	71.6	362	2	05XIY5_BRARE	05xiy5 brachydanio
66	151	71.6	644	2	08URP9_BRARE	08urp9 brachydanio
67	121	57.3	49	2	097917_BOVIN	097917 bos taurus
68	121	57.3	49	2	02XQ98_PIG	02xq98 sus scrofa
69	64	30.3	328	2	09RPS4_ENTFA	09rps4 enterococcu
70	63	29.9	321	2	08RG41_FUSNN	08rg41 fusobacteri
71	63	29.9	755	2	09R472_9RHIZ	09r472 agrobacteri
72	63	29.9	755	2	09R694_9RHIZ	09r694 agrobacteri
73	63	29.9	755	2	09R717_9RHIZ	09r717 agrobacteri
74	63	29.9	755	2	08UGA3_AGR75	08uga3 agrobacteri
75	62.5	29.6	545	2	07NGT4_GLOVI	07ngt4 gloebacter
76	62	29.4	755	1	TR2M_AGR74	Pa3372 agrobacteri
77	62	29.4	755	1	TR2W_AGR74	Pa3373 agrobacteri
78	62	29.4	755	2	044388_9RHIZ	044388 agrobacteri
79	61	28.7	755	1	TR2N_AGR71	Pe5017 agrobacteri
80	60.5	28.7	252	2	06LJ99_PHOPR	06lj99 photobacter
81	60	28.4	351	2	08HMW7_SQUAC	08hmw7 squallus aca
82	60	28.4	419	2	041M97_SOLUS	041m97 solibacter
83	60	28.4	755	2	09WMA1_9RHIZ	09wma1 agrobacteri
84	59	28.4	3336	2	081KE1_PLAF7	081ke1 plasmodiul
85	59	28.0	332	2	05K514_9VIRU	05k514 bacterioph
86	58	27.5	288	2	044IH4_CHEL1	044ih4 chromohalo
87	58	27.5	320	2	07PAH7_FUSNV	07pah7 fusobacteri
88	58	27.5	368	2	08G2C8_BRUSU	08g2c8 brucella su
89	58	27.5	481	2	041IH0_GIBBE	041ih0 gibberella
90	58	27.5	624	2	06Z4F2_ORYSA	06z4f2 oryza sativ
91	58	27.5	763	2	02YMB3_BRUA2	02ymb3 brucella ab
92	57.5	27.3	333	2	04UB56_THENP	04ub56 theileria a
93	57.5	27.3	405	2	04NSD6_THEPA	04nsd6 theileria p
94	57.5	27.3	895	2	09AMB6_LYCES	09amb6 lycoperisio
95	57	27.0	105	2	022662_RRARI	022662 arabidopsis
96	57	27.0	214	2	04SS77_CHLUI	04ss77 chlorobium
97	57	27.0	324	2	05WIS6_LEGEL	05wis6 legionella
98	57	27.0	334	2	05X504_LEGPA	05x504 legionella
99	57	27.0	342	2	05ZV81_LEGPH	05zv81 legionella
100	57	27.0	331	2	040FX5_9RHOB	040fx5 jamaeschia

ALIGNMENTS

RESULT 1
 Q56J36 GRAGR PRELIMINARY; PRT; 42 AA.
 AC Q56J36; 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Amyloid beta protein (Fragment).
 OS Grampus griseus (Risso's dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Grampus.
 NCBI_TaxID=83653;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarsa M.,
 RT "The molecular machinery of Alzheimer's disease in the dolphin.",
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2,8e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 2
 Q56J37 TURTR PRELIMINARY; PRT; 42 AA.
 AC Q56J37; 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Amyloid beta protein (Fragment).
 OS Turstrops truncatus (Atlantic bottlenose dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Turstrops.
 NCBI_TaxID=9739;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarsa M.,
 RT "The molecular machinery of Alzheimer's disease in the dolphin.",
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2,8e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

FT NON TER 42 42
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
 Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2,8e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 3
 Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
 AC Q7M088; 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Beta-amyloid protein (Fragment).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hysticognathhi; Caviidae; Cavia.
 NCBI_TaxID=10141;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=9329053; PubMed=7685598;
 RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
 RA Kamiya H., Ohno M.,
 RT "Receptor-mediated specific biological activity of a beta-amyloid
 RT protein fragment for NK-1 substance p receptors.",
 RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
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Query Match 100.0%; Score 211; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2,8e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 4
 A4 UR5MA STANDARD; PRT; 57 AA.
 ID A4 UR5MA; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 AC Q29149;
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 GN Ursus maritimus (Polar bear) (Thalarcos maritimus).
 OS Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

CC	Mammalia, Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC	Ursus.
OX	NCBI TaxID=29073;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RC	TISSUE=Brain;
RX	MEDLINE=E9M01079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT	"Conservation of the sequence of the Alzheimer's disease amyloid
RT	peptide in dog, polar bear and five other mammals by cross-species
RT	polymerase chain reaction analysis.";
RL	Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC	-I- FUNCTION: Functional neuronal receptor which couples to
CC	intracellular signaling pathway through the GTP-binding protein
CC	G(iO) (By similarity).
CC	-I- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC	protein.
CC	-I- SIMILARITY: Belongs to the APP family.
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerive License
CC	
DR	EMBL; X56128; CAA39593.1; -; mRNA.
DR	PIR; B60045; B60045.
DR	HSSP; P08592; 1NMJ.
DR	InterPro; IPR008155; A4_APP.
DR	InterPro; IPR001255; Beta-APP.
DR	PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR	Pfam; PF03494; Beta-APP; 1.
DR	PRINTS; PR00204; BETRAYOID.
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.
KW	Amyloid; Membrane; Transmembrane.
FT	CHAIN <1> >57
FT	/FTid=PRO_000026244.
FT	Soluble APP-beta (By similarity).
FT	/FTid=PRO_0000000191.
FT	CTF-alpha (By similarity).
FT	/FTid=PRO_0000000192.
FT	Beta-amyloid protein 42 (By similarity).
FT	/FTid=PRO_0000000193.
FT	Beta-amyloid protein 40 (By similarity).
FT	/FTid=PRO_0000000194.
FT	Gamma-CTF(59) (By similarity).
FT	/FTid=PRO_0000000195.
FT	Gamma-CTF(57) (By similarity).
FT	/FTid=PRO_0000000196.
FT	Extracellular (Potential).
SEQ	SEQUENCE 57 AA; 6172 MW; 84209D80EBA82DFA CRC64;
QY	Query Match 100.0%; Score 211; DB 1; Length 57;
Db	Best Local Similarity 100.0%; Pred. No. 3; De-20;
	Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	2 AEFRHDSGEVHHOKLVEFAEDVGSKKATITGLMWGVVIA 42
	7 AEFRHDSGEVHHOKLVEFAEDVGSKKATITGLMWGVVIA 47
RESULT 5	
ID	A4_CANPA STANDARD; PRT; 58 AA.
AC	Q26280;
DT	01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT	01-NOV-1997, sequence version 1.
DT	07-MAR-2006, entry version 37.
DE	Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE	protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE	Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE	APP40); Gamma-CTF(59) (gamma-secretase C-terminal fragment 59); Gamma-

DE CTF(577) (Gamma-secretase C-terminal fragment 577) (Fragment).

OS Name-APP;

OS Canis familiaris (dog).

OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

OC Canis.

OX NCBI_TaxID=9615;

PN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Kidney; PubMed=1656157, DOI=10.1016/0169-328X(91)90088-F;

RA MEDLINE=92011079; PubMed=1656157, DOI=10.1016/0169-328X(91)90088-F;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -! FUNCTION: Functional neuronal receptor which couples to

CC intracellular signaling pathway through the GTP-binding protein

CC G1O (By similarity).

CC -! SUBCELLULAR LOCATION: Membrane; single-pass type I membrane

CC protein.

CC -! SIMILARITY: Belongs to the APP family.

CC -----

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CC -----

CC EMBL; X56125; CAA39590.1; -; mRNA.

DR HSSP; P08592; INMU.

DR Ensembl; ENSCAFG0000008557; Canis familiaris.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR PANTHER; PTHR10083.SF6; Beta-APP, 1.

DR Pfam; PF03494; Beta-APP, 1.

DR PRINTS; PR00204; BETAAMYLOID.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Amyloid; Membrane; Transmembrane.

KW CHAIN

FT <1 >58

FT Amyloid beta A4 protein.

FT /Frid=PRO_0000226241.

FT Soluble APP-beta (By similarity).

FT /Frid=PRO_0000000070.

FT CTF-alpha (By similarity).

FT /Frid=PRO_0000000071.

FT Beta-amyloid protein 42 (By similarity).

FT /Frid=PRO_0000000072.

FT Beta-amyloid protein 40 (By similarity).

FT /Frid=PRO_0000000073.

FT Gamma-CTF(59) (By similarity).

FT /Frid=PRO_0000000074.

FT Gamma-CTF(57) (By similarity).

FT /Frid=PRO_0000000075.

FT Extracellular (Potential).

FT Potential.

FT CHAIN

FT 49 >58

FT Gamma-CTF(57) (By similarity).

FT /Frid=PRO_0000000075.

FT Extracellular (Potential).

FT Potential.

FT TOPO_DOM

FT <1 34

FT TRANSMEM

FT 35 58

FT NON_TER

FT 1 1

FT NON_TER

FT 58 58

FT SEQUENCE

FT 58 AA; 6285 MW; 8465D480A212DFA CRC64;

Query Match 100.0%; Score 211; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 3.9e-20;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 AEFPHDSGYEVHOKLVFAEDVGSNGKATIGLVGVVIA 42

8 AEFPHDSGYEVHOKLVFAEDVGSNGKATIGLVGVVIA 48

RESULT 6

A4_RABIT

ID A4_RABIT STANDARD; PRT; 58 AA.

Q28748;

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1997, sequence version 1.

DT 07-MAR-2006, entry version 37.

DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) [contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Oryzctylagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryzctylagus.
 OC NCBI_TaxID=9986;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC
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 CC
 CC EMBL: X56129; CAA39594.1; -; mRNA.
 CC HSSP: P08592; INMU.
 DR InterPro: IPR008155; A4_APP.
 DR PANTHER: PTHR10083; SF6; Beta-APP, 1.
 DR Pfam: PF03494; Beta-APP, 1.
 DR PRINTS: PR00204; BETAAMYLOID.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4_INTRA; PARTIAL.
 KM Amyloid; Membrane; Transmembrane.
 FT CHAIN <1
 FT FT >58
 FT FT /FTId=PRO_0000226242.
 FT FT Soluble APP-beta (By similarity).
 FT FT /FTId=PRO_0000000153.
 FT FT CTF-alpha (By similarity).
 FT FT /FTId=PRO_0000000154.
 FT FT Beta-amyloid protein 42 (By similarity).
 FT FT /FTId=PRO_0000000155.
 FT FT Beta-amyloid protein 40 (By similarity).
 FT FT /FTId=PRO_0000000156.
 FT FT Gamma-CTF(59) (By similarity).
 FT FT /FTId=PRO_0000000157.
 FT FT Gamma-CTF(57) (By similarity).
 FT FT /FTId=PRO_0000000158.
 FT FT Extracellular (Potential).
 FT FT Potential.
 FT FT Cytoplasmic (Potential).
 FT NON_TER 1
 FT NON_TER 58
 FT NON_TER 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 211; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3, 9e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 A4_SHEEP
 ID_A4_SHEEP STANDARD; PRT; 58 AA.

AC Q28757;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) [contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC
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 CC
 CC EMBL: X56130; CAA39595.1; -; mRNA.
 CC HSSP: P08592; INMU.
 DR InterPro: IPR008155; A4_APP.
 DR PANTHER: PTHR10083; SF6; Beta-APP, 1.
 DR Pfam: PF03494; Beta-APP, 1.
 DR PRINTS: PR00204; BETAAMYLOID.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4_INTRA; PARTIAL.
 KM Amyloid; Membrane; Transmembrane.
 FT CHAIN <1
 FT FT >58
 FT FT /FTId=PRO_0000226243.
 FT FT Soluble APP-beta (By similarity).
 FT FT /FTId=PRO_0000000185.
 FT FT CTF-alpha (By similarity).
 FT FT /FTId=PRO_0000000186.
 FT FT Beta-amyloid protein 42 (By similarity).
 FT FT /FTId=PRO_0000000187.
 FT FT Beta-amyloid protein 40 (By similarity).
 FT FT /FTId=PRO_0000000188.
 FT FT Gamma-CTF(59) (By similarity).
 FT FT /FTId=PRO_0000000189.
 FT FT Gamma-CTF(57) (By similarity).
 FT FT /FTId=PRO_0000000190.
 FT FT Extracellular (Potential).
 FT FT Potential.
 FT FT Cytoplasmic (Potential).
 FT NON_TER 1
 FT NON_TER 58
 FT NON_TER 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 211; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3, 9e-20;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 A4_SHEEP
 ID_A4_SHEEP STANDARD; PRT; 58 AA.

RESULT 8
A4 BOVIN STANDARD: PRT: 59 AA.
AC 026053:
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name:APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL: X56124; CAA39589.1; -; mRNA.
DR EMBL: X56126; CAA39591.1; -; mRNA.
DR HSSP: P08592; INMJ.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAMYLLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1 6
FT FT SOLUBLE APP-beta (By similarity).
FT FT /FTID=PRO_0000000064.
FT CHAIN 7 >59
FT FT CTF-alpha (By similarity).
FT CHAIN 7 48
FT FT Beta-amyloid protein 42 (By similarity).
FT FT /FTID=PRO_0000000066.
FT CHAIN 7 46
FT FT Beta-amyloid protein 40 (By similarity).
FT FT /FTID=PRO_0000000067.
FT CHAIN 47 >59
FT FT Gamma-CTF(59) (By similarity).
FT CHAIN 49 >59
FT FT Gamma-CTF(57) (By similarity).
FT FT /FTID=PRO_0000000069.
FT TOPO_DOM 35 58
FT TOPO_DOM 59 >59
FT FT Extracellular (Potential).
FT FT Potential.
FT NON_TER 1 1
FT NON_TER 59 59
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;
Query Match 100.0%; Score 211; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 42

Db 8 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 48
|||||
RESULT 9
Q8JH58 CHESE PRELIMINARY; PRT: 113 AA.
ID Q8JH58; CHESE PRELIMINARY; PRT: 113 AA.
AC Q8JH58;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Amyloid beta protein (Fragment).
DE Chelydra serpentina serpentina (common snapping turtle).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11892478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
CC -----
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CC -----
DR EMBL: AF541917; AAN04908.1; -; mRNA.
DR HSSP: Q16019; ILYT.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMYLLOID.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1 1
FT SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
Query Match 100.0%; Score 211; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.7e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 42

Db 16 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 56
|||||
RESULT 10
Q93296 CHICK PRELIMINARY; PRT: 534 AA.
ID Q93296; CHICK PRELIMINARY; PRT: 534 AA.
AC Q93296;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
CC -----

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EMBL; AF042098; AAC25052.1; -; mRNA.
 HSSP; Q16019; 11YT.
 SMR; O93296; 224-333.
 Ensemble; ENSGALG0000015770; Gallus gallus.
 GO; GO:0016021; C:integral to membrane; IEA.
 GO; GO:0005488; F:binding; IEA.
 InterPro; IPR008155; A4_APP.
 InterPro; IPR008154; A4_EXTRA.
 InterPro; IPR001255; Beta-APP.
 PANTHER; PTHR10083.SF6; Beta-APP; 5.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta-APP; 1.
 PRINTS; PR00203; AMYLOIDA4.
 PRINTS; PR00204; BETAAMYLOID.
 PROSITE; PS00319; A4_EXTRA; 1.
 PROSITE; PS00320; A4_INTRA; 1.
 NON_TER 1_1

SEQUENCE 534 AA; 60597 MW; FB53ECC2B66D4C92 CRC64;
 Query Match 100.0%; Score 211; DB 2; Length 534;
 Best local Similarity 100.0%; Pred. No. 3.9e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 42
 437 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 477

RESULT 11
 ID Q9PVL1_CHICK PRELIMINARY; PRT; 569 AA.
 AC Q9PVL1;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE Amyloid protein (Fragment).
 GN Name=APP;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCB1_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 tells us about its function."
 RL Neurochem. Int. 0:0-0(2000).
 CC -----
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 CC -----
 EMBL; AF030341; AAF12698.1; -; mRNA.
 HSSP; Q16019; 11YT.
 SMR; Q9PVL1; 1-64; 260-369.
 Ensemble; ENSGALG0000015770; Gallus gallus.
 GO; GO:0016021; C:integral to membrane; IEA.
 GO; GO:0005488; F:binding; IEA.
 InterPro; IPR008155; A4_APP.
 InterPro; IPR008154; A4_EXTRA.
 InterPro; IPR001255; Beta-APP.
 PANTHER; PTHR10083.SF6; Beta-APP; 5.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta-APP; 1.
 PRINTS; PR00203; AMYLOIDA4.
 PRINTS; PR00204; BETAAMYLOID.
 PROSITE; PS00319; A4_EXTRA; 1.
 PROSITE; PS00320; A4_INTRA; 1.
 NON_TER 1_1

SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
 Query Match 100.0%; Score 211; DB 2; Length 569;
 Best local Similarity 100.0%; Pred. No. 4.1e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 42
 473 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 513

RESULT 12
 ID Q2XQA0_PIG PRELIMINARY; PRT; 695 AA.
 AC Q2XQA0;
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Amyloid protein variant 1.
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 CC Sus.
 CC NCB1_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Oerum M.A., Larsen K., Bendixen C.;
 RT "Porcine amyloid precursor protein, APP: Cloning and characterization
 of cDNAs."
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 EMBL; DQ267684; AB82033.1; -; mRNA.
 SEQUENCE 695 AA; 78615 MW; 825A7E4AC10E8F0B CRC64;

Query Match 100.0%; Score 211; DB 2; Length 695;
 Best local Similarity 100.0%; Pred. No. 5.1e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 42
 598 AEFRRDSGYEVHOKLVFPFADVGSNKGAIIGLMVGVVIA 638

RESULT 13
 ID Q56UK3_CANFA PRELIMINARY; PRT; 695 AA.
 AC Q56UK3;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Beta-amyloid protein 695.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 CC Canis.
 CC NCB1_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
 RT "Relationship between canine dementia and Alzheimer's disease."
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 EMBL; AY926582; AAX81911.1; -; mRNA.
 SMR; Q56UK3; 28-123; 124-189; 385-494.
 GO; GO:0016021; C:integral to membrane; IEA.
 GO; GO:0005488; F:binding; IEA.

DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome C_R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETRANMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 100.0%; Score 211; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 42
DB 598 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 14
OY 05R477_PONPY PRELIMINARY; PRT; 695 AA.
AC 05R477_PONPY
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein DKFZp459D212.
GN Name=DKFZp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pongo.
OX NCB1_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex.
RG The German cDNA Consortium;
RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Foko G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CR861380; CAH93439.1; -; mRNA.
DR SMR; 05R477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome C_R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETRANMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 78627 MW; 0B55D93BA213E49 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 42
DB 598 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 15
OY 06RH29_CANFA PRELIMINARY; PRT; 695 AA.
AC 06RH29_CANFA
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Beta amyloid protein isoform APP695.
GN Name=Beta APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCB1_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY488707; AAR97727.1; -; mRNA.
DR HSSP; Q16019; 1BA4.
DR SMR; 06RH29; 28-123, 124-189, 385-494.
DR Ensemble; ENSCAFG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETRANMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 42
DB 598 AEFRRDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 16
OY 09DG38_CHICK PRELIMINARY; PRT; 695 AA.
AC 09DG38_CHICK
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:16039787; DOI:10.1016/j.neuroscience.2005.05.020;
RA Carrodegua J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,

A4_SAI5C
 ID A4_SAI5C STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1997, sequence version 1.
 DT 07-MAR-2006, entry version 60.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE Amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
 OC Cebinae; Saimiri.
 ON NCBI_TaxID=9521;
 RX NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
 RT amyloid angiopathy".
 RL Neurobiol. Aging 16:805-808 (1995).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(iO) and JIP (By
 CC similarity). Inhibits G(iO) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, PPRL1, APPB1, IBI, KNS2
 CC (via its IPR domains) (By similarity), APPB2 (via BASS) and DDB1.
 CC In vitro, it binds MAP7 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized into the endosomal and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY secretase motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 CC -----
 CC EMBL, S81024, M614347.1, -, mRNA.
 CC PDB, 1RW6; X-ray; A=346-551.
 CC SMR, Q95241; 28-123, 124-189, 287-342.
 CC InterPro: IPR008155; A4 APP.
 CC InterPro: IPR008154; A4 extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER, PTHR10083:SF6; Beta-APP; 5.
 CC Pfam, PF02177; A4 EXTRA; 1.
 CC Pfam, PF03494; Beta-APP; 1.
 CC Pfam, PF00014; Kunitz BPTI; 1.
 CC PRINTS, PR00203; AMYLOIDA.
 CC PRINTS, PR00759; BASICPTASE.
 CC PRINTS, PR00204; BETAAMYLOID.
 CC ProDom, PD000222; Prot_inh_Kunz-m; 1.
 CC SMART, SM00131; KU; 1.
 CC SMART, SM00006; A4 EXTRA; 1.
 CC PROSITE, PS00319; A4 EXTRA; 1.
 CC PROSITE, PS00320; A4 INTTRA; 1.
 CC PROSITE, PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE, PS50279; BPTI_KUNITZ_2; 1.
 CC 3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion;

DB 654 AEFRRDSCGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 694

```

RESULT 21
Q64R48_MACFA PRELIMINARY; PRT; 751 AA.
AC Q64R48;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Brain cDNA, clone: Q61A-13524, similar to human amyloid beta (A4)
DE protein (protease nexin-11, Alzheimer disease) (APP), transcript
DE variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15944441; DOI=10.1093/molbev/msi187;
RA Osada N., Hirta M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL Mol. Biol. Evol. 22:1976-1982(2005).
[2]
RN NUCLEOTIDE SEQUENCE.
RP International consortium for macaque cDNA sequencing and analysis;
RG "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL: AB169826; BA001907.1; mRNA.
DR SMR: Q64R48; 28-123, 124-189, 287-342, 441-550.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR012282; Cytochrome c R.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPT1; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYL0ID.
DR PRODom: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE: PS50279; BPT1_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 751 AA; 84817 MW; 83C1CD96AD355158 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 AEFRRDSCGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 42

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DB 654 AEFRRDSCGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 694

```

RESULT 22
Q56UK5_CANFA PRELIMINARY; PRT; 751 AA.
AC Q56UK5;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: AY926580; AAX81909.1; mRNA.
DR SMR: Q56UK5; 28-123, 124-189, 287-342, 441-550.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR012282; Cytochrome c R.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPT1; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYL0ID.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE: PS50279; BPT1_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84520 MW; C1CD20377DFP8550 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 AEFRRDSCGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 42
DB 654 AEFRRDSCGYEVHOKLVFFAEDVGSNKGAIIIGLWGVVIA 694

RESULT 23
Q6RH28_CANFA PRELIMINARY; PRT; 751 AA.
AC Q6RH28;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Beta amyloid protein isoform APP751.
CN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

```

CC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakaya M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY498708; AAR9728.1; -; mRNA.
DR HSSP; Q16019; 1AAP.
DR SMR; O6RH28; 28-123, 124-189, 287-342, 441-550.
DR Ensemble; ENSGAFG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4-EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4-EXTRA; 1.
DR PROSITE; PS00320; A4-INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 654 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 694

RESULT 24
Q2XQ99_PIG PRELIMINARY; PRT; 751 AA.
AC Q2XQ99-
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 1.
DE Amyloid protein variant 2.
GN Name=APP;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Butleria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oertum M.A., Larsen K., Bendixen C.; APP: Cloning and characterization
of CDNA's.
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; DQ267685; ABB82034.1; -; mRNA.

SQ SEQUENCE 751 AA; 84799 MW; 37868743880C369F CRC64;

Query Match 100.0%; Score 211; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 654 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 694

RESULT 25
Q9DGJ7_CHICK PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7-
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 22.
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed; 16039787; DOI=10.1016/j.neuroscience.2005.05.020;
RA Carrodegues J.A., Rodolosse A., Garza M.V., Sanz-Clemente A.,
RA Perez-Pe R., Lacoeta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RA Sorribas V., Sastre M.;
RT "The chick embryo appears as a natural model for research in beta-
amyloid precursor protein processing.";
RL Neuroscience 134:1285-1300(2005).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF289219; AAC00594.1; -; mRNA.
DR HSSP; Q16019; 1IYT.
DR SMR; Q9DGJ7; 28-123, 124-189, 287-342, 441-550.
DR Ensemble; ENSGALG00000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4-EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4-EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4-EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4-EXTRA; 1.
DR PROSITE; PS00320; A4-INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84706 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 211; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 654 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 694

RESULT 26
 A4_CAVPO STANDARD; PRT; 770 AA.
 AC 060495; 060496; integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 56.
 DE Amyloid-beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homologue) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31).
 GN Name=APP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-8781(96)00232-1;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RN INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Mao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RN PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;
 RA Beck M., Bruckner M.K., Holzer M., Kaap S., Fannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein";
 RL Neuroscienc 95:243-254(2000).
 RN [4]
 RN GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;
 RA Plamix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative C-
 RT terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G1O and JIP (By
 CC similarity). Inhibits G1O alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-mediated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins E and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Apicant elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) and Dab1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC APOE3 appears to be the preferred amyloid binding isoform, while
 CC the APOE4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC applicans;
 CC Name=APP770;
 CC IsoId=O60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=O60495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicstrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).

CC -1- PPM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).
 CC -1- PPM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the apolipans (By similarity).
 CC -1- PPM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.
 CC -1- PPM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 DR EMBL: X97631; CA66230.1; -; mRNA.
 DR EMBL: X99198; CA67589.1; -; mRNA.
 DR HSSP: P08592; INMJ.
 DR SMR: O60495; 28-123, 124-189, 287-342, 460-569.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Prot_inh_Kunz-m.
 DR PANTHER: PTHR10083:SF6; Beta-APP; 6.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPPASE.
 DR PRINTS: PR00204; BETAMAMLOID.
 DR PRODOM: PD000222; Prot_inh_Kunz-m; 1.
 DR SMART: SMO0006; A4_EXTRA; 1.
 DR SMART: SMO0131; KUI; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 DR Alternative splicing: Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
 KW Metal-binding; Notch signaling pathway; Phosphorylation;
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KW Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 Soluble APP-alpha (By similarity).
 FT CHAIN 18 671 Soluble APP-beta (By similarity).
 FT CHAIN 672 770 CTF-alpha (By similarity).
 FT CHAIN 672 770 /FTId=PRO_0000000079.

Query Match 100.0%; Score 211; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFPHDSGYEVHOKLVFAEDVSGNSKAIIGLMVGAVIA 42
 Db 673 AEFPHDSGYEVHOKLVFAEDVSGNSKAIIGLMVGAVIA 713

RESULT 27
 A4_HUMAN STANDARD. PRT: 770 AA.
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9BT38; Q9UC49; Q9UCB6; Q9UCB8; Q9UCD1; Q9U058;
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1991, sequence version 3.
 DT 07-MAR-2006, entry version 111.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein) (cerebral vascular amyloid peptide) (CVAp) (Protease
 DE nexin-II) (Pv-II) (APP) (PreA4) [contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59)
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CRF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CRF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN Name=APP; Synonyms=A4, AD1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207; DOI=10.1038/325733a0;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RL cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;
 RA Ponte P., Gonzalez-Dewilte P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is
 RL encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;
 RA Yoshikai S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERATUM.
 RX MEDLINE=1908403; DOI=10.1016/0378-1119(91)90093-Q;
 RA Yoshikai S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;
 RA Hattori M., Tanahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for

RT sequencing of a 300 kb region of human APP locus." ;
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA DOI=10.1046/j.1460-9568.2003.02731.x;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639." ;
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LYS-501.
RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
RA Nguyen C.P., Gilderleeve H., Cassidy C.M., Johnson E.J.,
RA Swenson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).
RC TISSUE=Eye, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomihata S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 1-10.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide." ;
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RP ERRATUM, AND SEQUENCE REVISION.
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [13]
RP NUCLEOTIDE SEQUENCE OF 1-75.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene." ;
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [14]
RP PROTEIN SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts." ;
RL J. Biol. Chem. 262:8508-8514(1987).
RN [15]
RP PROTEIN SEQUENCE OF 18-40.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;

RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides." ;
RL Nat. Biotechnol. 21:566-569(2003).
RN [16]
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein." ;
RL Science 245:651-653(1989).
RN [17]
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Winiawski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides." ;
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [18]
RP NUCLEOTIDE SEQUENCE OF 286-366.
RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Nave R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease." ;
RL Nature 331:528-530(1988).
RN [19]
RP NUCLEOTIDE SEQUENCE OF 287-367.
RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
RT inhibitory activity." ;
RL Nature 331:530-532(1988).
RN [20]
RP NUCLEOTIDE SEQUENCE OF 507-770.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex." ;
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [21]
RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
RA Behr D., Heese L., Masters C.L., Multhaup G.;
Query Match 100.0%; Score 211; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5,6e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRDSGYEVHHOKLVFPAEDVGSNKGATITGLWGVVIA 42
DB 673 AEFRRDSGYEVHHOKLVFPAEDVGSNKGATITGLWGVVIA 713
RESULT 28
ID A4_MACPA STANDARD; PRT; 770 AA.
AC P53601; Q60HH7; Q95KN7;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 22-FEB-2003, sequence version 3.
DT 07-FEB-2006, entry version 55.
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE soluble APP-beta (S-APP-beta)]; C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DR secretase C-terminal fragment 50) ; C31) .
 GN Name=APP; ORFNames=OCC-15949;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey) .
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 CC Cercopithecoidea; Cercopithecinae; Macaca.
 CC NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS APP695 AND APP770) .
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlasky M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.";
 RU Am. J. Pathol. 138:1423-1435 (1991) .
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3) .
 RC TISSUE=Brain cortex;
 RA Kusuda J., Osada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;
 RT "Isolation and characterization of cDNA for macaque neurological disease genes.";
 RU Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G10 and JIP (By similarity). Inhibits G10 alpha Arpase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metalated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPT domain possess protease inhibitor activity (By similarity) .
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity) .
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity) .
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APPA family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FFRLL, APPBP1, IBL, KMS2 (via its TPR domain) (By similarity), APPB2 (via BASS), and DDB1. In vitro, it binds MAP7 via the MT-binding domain (By similarity). Associates with microtubules in the presence of APP and in a kinase-dependent manner (By similarity) .
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity) .
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing. Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;

CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC Name=3;
 CC IsoId=P53601-3; Sequence=VSP_013360, VSP_013361;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity) .
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acid either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity) .
 CC -1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity) .
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity) .
 CC -1- PTM: N- and O-glycosylated (By similarity) .
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity) .
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity) .
 CC Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity) .
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: M58726; AAA36828.1; -; mRNA.
 CC EMBL: M58727; AAA36829.1; -; mRNA.
 CC EMBL: AB125150; BAD51938.1; -; mRNA.
 CC HSPD: P08592; 1NMJ.
 CC SMR: P53601; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER: PTHR10083; SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF02194; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz_BPT1; 1.
 CC PRINTS: PR00203; AMYLOID4.
 CC PRINTS: PR00759; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunz-m; 1.
 CC SMART: SM00111; KU; 1.
 CC SMART: SM00111; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPT1_KUNITZ; 1.
 CC PROSITE: PS0279; BPT1_KUNITZ_2; 1.
 CC Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;

KM	Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
KM	Metal-binding; Notch signaling pathway; Phosphorylation;
KM	Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
KM	Transmembrane; Zinc.
FT	CHAIN 1 17
FT	CHAIN 18 770
FT	CHAIN 18 687
FT	CHAIN 18 671
FT	CHAIN 672 770
FT	CHAIN 672 713
FT	CHAIN 672 711
FT	CHAIN 688 770
FT	CHAIN 688 713
FT	PEPTIDE 688 711
FT	PEPTIDE 688 712
FT	CHAIN 714 770
FT	CHAIN 721 770
FT	CHAIN 740 770
FT	TOPO DOM 18 699
FT	TRANSEM 700 723
FT	TOPO DOM 724 770
FT	DOMAIN 291 341
FT	REGION 96 110
FT	REGION 181 188
FT	REGION 391 423
FT	REGION 491 522
FT	REGION 523 540
FT	REGION 732 751
FT	MOTIF 724 734
Query Match	Score 211; DB 1; Length 770;
Best Local Similarity	100.0%; Pred. No. 5.6e-19;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	2 AEPFHDSGYEYHOKLVFPAEDVGSNKGAIIGLMVGWVIA 42
Db	673 AEPFHDSGYEYHOKLVFPAEDVGSNKGAIIGLMVGWVIA 713
RESULT 29	
A4_PANTR	STANDARD; PRT; 770 AA.
AC	Q5TS80;
DT	15-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT	07-FEB-2006, entry version 16.
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE	soluble protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE	Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE	APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE	Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE	(Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE	secretase C-terminal fragment 50); C31].
GN	Name-APP;
OS	Pan troglodytes (Chimpanzee).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC	NCBI_Taxid=9598;

RN	[1]
NP	NCLECTIDE SEQUENCE [mRNA].
RP	PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
RA	Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
RA	Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.,
RT	"Accelerated evolution of nervous system genes in the origin of Homo
RT	sapiens.",
RL	Cell 119:1027-1040(2004).
CC	-1- FUNCTION: Functions as a cell surface receptor and performs
CC	physiological functions on the surface of neurons relevant to
CC	neurite growth, neuronal adhesion and axogenesis. Involved in
CC	cell mobility and transcription regulation through protein-protein
CC	interactions (By similarity). Can promote transcription activation
CC	through binding to APBB1/Tip60 and inhibit Notch signaling through
CC	interaction with Numb (By similarity). Couples to apoptosis-
CC	inducing pathways such as those mediated by G10 and JIP (By
CC	similarity). Inhibits G10 alpha ARPAse activity (By similarity).
CC	Acts as a kinesin I membrane receptor, mediating the axonal
CC	transport of beta-secretase and presenilin 1 (By similarity). May
CC	be involved in copper homeostasis/oxidative stress through copper
CC	ion reduction. In vitro, copper-metalated APP induces neuronal
CC	death directly or is potentiated through Cu(2+)-mediated low-
CC	density lipoprotein oxidation (By similarity). Can regulate
CC	neurite outgrowth through binding to components of the
CC	extracellular matrix such as heparin and collagen I and IV (By
CC	similarity). The splice isoforms that contain the BPTI domain
CC	possess protease inhibitor activity (By similarity).
CC	-1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC	with metal-reducing activity. Bind transient metals such as
CC	copper, zinc and iron (By similarity).
CC	-1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC	peptides, including C31, are potent enhancers of neuronal
CC	apoptosis (By similarity).
CC	-1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC	cytoplasmic proteins, including APPB family members, the ABA
CC	family, MAP81P1, and SHC1, Numb and Dab1 (By similarity). Binding
CC	to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC	interacts with GPCR-like protein BPP, FPR1, APPB1, IBI, KNS2
CC	(via its TPR domains) (By similarity), APPB2 (via BASS) and DDB1.
CC	In vitro, it binds MAPT via the MT-binding domains (By
CC	similarity). Associates with microtubules in the presence of ATP
CC	and in a kinesin-dependent manner (By similarity).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC	protein that rapidly becomes internalized via clathrin-coated
CC	pits. During maturation, the immature APP (N-glycosylated in the
CC	endoplasmic reticulum) moves to the Golgi complex where complete
CC	maturation occurs (O-glycosylated and sulfated). After alpha-
CC	secretase cleavage, soluble APP is released into the extracellular
CC	space and the C-terminal is internalized to endosomes and
CC	lysosomes. Some APP accumulates in secretory transport vesicles
CC	leaving the late Golgi compartment and returns to the cell
CC	surface. Gamma-CTF(55) peptide is located to both the cytoplasm
CC	and nuclei of neurons (By similarity).
CC	-1- DOMAIN: The basolateral sorting signal (BASS) is required for
CC	sorting of membrane proteins to the basolateral surface of
CC	epithelial cells (By similarity).
CC	-1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC	phosphorylated proteins is required for the specific binding of
CC	the PID domain. However additional amino acids either N- or C-
CC	terminal to the NPXY motif are often required for complete
CC	interaction. The PID domain-containing proteins which bind APP
CC	are independent of phosphorylation on the terminal tyrosine
CC	residue. The NPXY site is also involved in clathrin-mediated
CC	endocytosis (By similarity).
CC	-1- PTM: Proteolytically processed under normal cellular conditions.
CC	Cleavage by alpha-secretase or alternatively by beta-secretase
CC	leads to generation and extracellular release of soluble APP
CC	peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC	retention of corresponding membrane-anchored C-terminal fragments,
CC	C83 and C99. Subsequent processing of C83 by gamma-secretase
CC	yields P3 peptides. This is the major secretory pathway and is
CC	nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated

CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PPM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PPM: N- and O-glycosylated (By similarity).
 CC -1- PPM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL: AY665248; AAV74286.1; -, mRNA.
 CC SMR: OS1880; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR01255; Beta-APP.
 CC InterPro: IPR01282; Cytochrome C R.
 CC InterPro: IPR002223; Prot inh Kunz-m.
 CC PANTHER: PTHR10083:SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRINTS: PR00759; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot inh Kunz-m; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00289; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC KAMyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
 CC Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding;
 CC Notch signaling pathway; Phosphorylation; Protease inhibitor;
 CC Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 CC SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT FT /FTid=PRO_0000000127.
 FT CHAIN 18 687 Soluble APP-alpha (Potential).
 FT FT /FTid=PRO_0000000128.
 FT CHAIN 18 671 Soluble APP-beta (Potential).
 FT FT /FTid=PRO_0000000129.
 FT CHAIN 672 770 C99 (Potential).
 FT FT /FTid=PRO_0000000130.
 FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
 FT FT /FTid=PRO_0000000131.
 FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
 FT FT /FTid=PRO_0000000132.
 FT CHAIN 688 770 C83 (Potential).
 FT FT /FTid=PRO_0000000133.
 FT CHAIN 688 713 P3(42) (Potential).
 FT FT /FTid=PRO_0000000134.
 FT CHAIN 688 711 P3(40) (Potential).
 FT FT /FTid=PRO_0000000135.
 FT CHAIN 712 770 Gamma-CTF(59) (Potential).
 FT FT /FTid=PRO_0000000136.
 FT CHAIN 714 770 Gamma-CTF(57) (Potential).
 FT FT /FTid=PRO_0000000137.

FT CHAIN 721 770 Gamma-CTF(50) (Potential).
 FT FT /FTid=PRO_0000000138.
 FT CHAIN 740 770 C31 (Potential).
 FT FT /FTid=PRO_0000000139.
 FT TOPO_DOM 18 699 Extracellular (Potential).
 FT TRANSMEM 700 723 Potential.
 FT TOPO_DOM 724 770 Cytoplasmic (Potential).
 FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
 FT REGION 96 110 Heparin-binding (By similarity).
 FT REGION 181 188 Zinc-binding (By similarity).
 FT REGION 391 423 Heparin-binding (By similarity).
 FT REGION 491 522 Heparin-binding (By similarity).
 FT REGION 523 540 Collagen-binding (By similarity).
 FT REGION 732 751 Interaction with G(o)-alpha (By similarity).
 FT MOTIF 724 734 Basolateral sorting signal (By similarity).
 FT MOTIF 759 762 NPXY motif; contains endocytosis signal.
 FT COMPBIAS 230 260 Asp/Glu-rich (acidic).
 FT COMPBIAS 274 280 Poly-Thr.
 FT METAL 137 137 Copper (By similarity).
 FT METAL 147 147 Copper (By similarity).
 FT METAL 149 149 Copper (By similarity).
 FT METAL 151 151 Copper (By similarity).
 FT METAL 677 677 Copper or zinc (By similarity).
 FT METAL 681 681 Copper or zinc (By similarity).
 FT METAL 684 684 Copper or zinc (By similarity).
 FT METAL 685 685 Copper or zinc (By similarity).
 FT SITE 144 144 Required for Cu(2+) reduction (By similarity).
 FT SITE 301 302 Reactive bond (By similarity).
 FT SITE 671 672 Cleavage (by beta-secretase) (By similarity).
 FT SITE 672 673 Cleavage (by caspase-6) (By similarity).
 FT SITE 687 688 Cleavage (by alpha-secretase) (By similarity).
 FT FT

Query Match 100.0%; Score 211; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5,6e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVYA 42
 Db 673 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVYA 713

RESULT 30
 ID A4_PIG STANDARD; PRT; 770 AA.
 AC P75307; Q29023; O9TU10;
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 50.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homolo5) (Containing: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31).
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9923;
 RN [1]
 RN NUCLEOTIDE SEQUENCE (mRNA).
 RP Kimura A., Takahashi T.,
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) OF 1-136.

CC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library." (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 667-723.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and GIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPB1, IBL, KMS2
 CC (via its TPR domains) (By similarity), APPB2 (via BASS) and DBL1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CRF(53) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP

CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields p3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-156, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL: AB022550; BAA4580.1; -, mRNA.
 CC EMBL: Z84022; CAB06313.1; -, mRNA.
 CC EMBL: X56127; CAA39592.1; -, mRNA.
 CC HSSP: P08592; INMJ.
 CC SMR: P79307; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_EXTRA.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Prot_inh_Kunzt-m.
 CC PANTHER: PTHR10083:SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz_BPT1; 1.
 CC PRINTS: PR00203; AMYLOID4.
 CC PRINTS: PR00709; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunzt-m; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPT1_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPT1_KUNITZ_2; 1.
 CC Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
 CC Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding;
 CC Niche signaling pathway; Phosphorylation; Protease inhibitor;
 CC Serine protease inhibitor; Signal; Transmembrane; Zinc.
 CC SIGNAL 1 17
 CC CHAIN 18 770
 CC /FTid=PRO_0000000140.
 CC /FTid=PRO_0000000140.
 CC Soluble APP-alpha (Potential).
 CC /FTid=PRO_0000000141.
 CC Soluble APP-beta (Potential).
 CC /FTid=PRO_0000000142.
 CC C99 (By similarity).
 CC /FTid=PRO_0000000143.
 CC Beta-amyloid protein 42 (By similarity).
 CC /FTid=PRO_0000000144.
 CC Beta-amyloid protein 40 (By similarity).
 CC /FTid=PRO_0000000145.
 CC CHAIN 672 713
 CC CHAIN 672 711

FT	CHAIN	688	770	C83 (By similarity).
FT	PEPTIDE	688	713	/FtId=PRO_0000000146.
FT	PEPTIDE	688	711	P3(42) (By similarity).
FT	PEPTIDE	688	711	/FtId=PRO_0000000147.
FT	CHAIN	712	770	P3(40) (By similarity).
FT	CHAIN	714	770	/FtId=PRO_0000000148.
FT	CHAIN	721	770	Gamma-CTF(59).
FT	CHAIN	740	770	/FtId=PRO_0000000149.
FT	CHAIN	740	770	Gamma-CTF(57).
FT	CHAIN	740	770	/FtId=PRO_0000000150.
FT	CHAIN	740	770	Gamma-CTF(50) (By similarity).
FT	CHAIN	740	770	/FtId=PRO_0000000151.
FT	CHAIN	740	770	C31 (By similarity).
FT	CHAIN	740	770	/FtId=PRO_0000000152.
FT	CHAIN	740	770	Extracellular (Potential).
FT	CHAIN	740	770	Potential.
FT	CHAIN	740	770	Cytoplasmic (Potential).
FT	CHAIN	740	770	BPT/Kunitz inhibitor.
FT	CHAIN	740	770	Heparin-binding (By similarity).
FT	CHAIN	740	770	Copper-binding (By similarity).
FT	CHAIN	740	770	Zinc-binding (By similarity).
FT	CHAIN	740	770	Heparin-binding (By similarity).
FT	CHAIN	740	770	Collagen-binding (By similarity).
FT	CHAIN	740	770	Interaction with G(c)-alpha (By similarity).
FT	CHAIN	740	770	Basolateral sorting signal.
FT	CHAIN	740	770	NPXY motif; contains endocytosis signal.
FT	CHAIN	740	770	Asp/Glu-rich (acidic).

Query Match 100.0%; Score 211; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AEFRRDSGYEVHOKLVFAEDVGSNKGAIGLWVGIVIA 42
 Db 673 AEFRRDSGYEVHOKLVFAEDVGSNKGAIGLWVGIVIA 713

Search completed: September 28, 2006, 06:22:55
 Job time : 138.735 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:23:21 ; Search time 29.5695 Seconds
(without alignments)
124.327 Million cell updates/sec

Title: US-09-731-899-3

Perfect score: 211

Sequence: 1 XAEFRHDSGYEVHQKLVF.....DVGSNKALIGMGVIA 42

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/Ptodata/2/1aa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/Ptodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/Ptodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/Ptodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/Ptodata/2/1aa/PCITS_COMB.pep:*
6: /EMC_Celerra_SIDS3/Ptodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/Ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	42	1	US-07-744-767A-2
2	211	100.0	42	1	US-08-179-574-1
3	211	100.0	42	1	US-08-347-144-1
4	211	100.0	42	1	US-08-462-859A-19
5	211	100.0	42	1	US-08-123-659A-19
6	211	100.0	42	1	US-08-464-247A-19
7	211	100.0	42	1	US-08-464-248A-19
8	211	100.0	42	1	US-08-476-464A-1
9	211	100.0	42	1	US-08-304-585-2
10	211	100.0	42	1	US-08-302-808-5
11	211	100.0	42	1	US-08-268-348A-1
12	211	100.0	42	1	US-08-433-734-2
13	211	100.0	42	1	US-08-609-090-9
14	211	100.0	42	1	US-07-737-371E-72
15	211	100.0	42	1	US-08-422-333-4
16	211	100.0	42	1	US-08-682-245A-4
17	211	100.0	42	1	US-08-986-948-5
18	211	100.0	42	2	US-08-717-551A-2
19	211	100.0	42	2	US-09-388-890-1
20	211	100.0	42	2	US-09-005-215-20
21	211	100.0	42	2	US-09-242-724-23
22	211	100.0	42	2	US-08-922-930-2
23	211	100.0	42	2	US-09-660-954-1
24	211	100.0	42	2	US-08-523-055-2
25	211	100.0	42	2	US-08-922-889-2
26	211	100.0	42	2	US-09-731-460-1

27	211	100.0	42	2	US-09-133-866-2	Sequence 2, App11
28	211	100.0	42	2	US-09-723-384-1	Sequence 1, App11
29	211	100.0	42	2	US-09-724-961-42	Sequence 42, App1
30	211	100.0	42	2	US-09-724-552-1	Sequence 1, App1
31	211	100.0	42	2	US-09-580-018-42	Sequence 42, App1
32	211	100.0	42	2	US-10-455-218-2	Sequence 2, App1
33	211	100.0	42	2	US-09-723-927-1	Sequence 1, App1
34	211	100.0	42	2	US-09-724-488-1	Sequence 1, App1
35	211	100.0	42	2	US-09-724-477-1	Sequence 1, App1
36	211	100.0	42	2	US-09-723-762-1	Sequence 1, App1
37	211	100.0	42	2	US-09-201-430-1	Sequence 1, App1
38	211	100.0	42	2	US-09-724-551-42	Sequence 42, App1
39	211	100.0	42	2	US-10-815-353-1	Sequence 1, App1
40	211	100.0	42	2	US-10-278-181-1	Sequence 1, App1
41	211	100.0	42	2	US-10-816-529-1	Sequence 1, App1
42	211	100.0	42	2	US-09-623-548A-955	Sequence 955, App
43	211	100.0	42	2	US-09-623-548A-988	Sequence 988, App
44	211	100.0	42	2	US-10-815-391-1	Sequence 1, App1
45	211	100.0	42	2	US-10-816-022-1	Sequence 1, App1
46	211	100.0	42	2	US-09-724-953-34	Sequence 34, App1
47	211	100.0	42	2	US-09-657-276-955	Sequence 955, App
48	211	100.0	42	2	US-09-657-276-988	Sequence 988, App
49	211	100.0	42	2	US-09-724-567-34	Sequence 34, App1
50	211	100.0	42	2	US-09-724-940-42	Sequence 42, App1
51	211	100.0	42	2	US-09-865-294A-65	Sequence 65, App1
52	211	100.0	42	2	US-09-979-952-34	Sequence 34, App1
53	211	100.0	42	2	US-09-585-817-34	Sequence 34, App1
54	211	100.0	42	2	US-09-962-955D-37	Sequence 37, App1
55	211	100.0	42	2	US-09-706-574A-20	Sequence 20, App1
56	211	100.0	42	2	US-10-934-603-1	Sequence 1, App1
57	211	100.0	42	2	US-10-884-892-1	Sequence 1, App1
58	211	100.0	42	2	US-09-848-616-174	Sequence 174, App
59	211	100.0	42	2	US-10-933-559-1	Sequence 1, App1
60	211	100.0	42	2	US-10-815-400-1	Sequence 1, App1
61	211	100.0	42	3	US-10-816-386-1	Sequence 1, App1
62	211	100.0	42	3	US-10-363-082-1	Sequence 1, App1
63	211	100.0	42	5	PCT-US92-06700-2	Sequence 2, App1
64	211	100.0	42	5	PCT-US93-00335-1	Sequence 1, App1
65	211	100.0	43	1	US-08-235-400-1	Sequence 1, App1
66	211	100.0	43	1	US-08-437-067-1	Sequence 1, App1
67	211	100.0	43	1	US-08-302-808-6	Sequence 6, App1
68	211	100.0	43	1	US-08-079-511-1	Sequence 1, App1
69	211	100.0	43	1	US-08-467-607-1	Sequence 1, App1
70	211	100.0	43	1	US-08-404-831-1	Sequence 1, App1
71	211	100.0	43	1	US-08-602-264A-3	Sequence 3, App1
72	211	100.0	43	1	US-08-469-362-1	Sequence 1, App1
73	211	100.0	43	1	US-08-612-785B-1	Sequence 1, App1
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76	211	100.0	43	1	US-07-737-371E-70	Sequence 70, App1
77	211	100.0	43	1	US-08-986-948-6	Sequence 6, App1
78	211	100.0	43	1	US-08-975-977-1	Sequence 1, App1
79	211	100.0	43	1	US-08-817-423-1	Sequence 1, App1
80	211	100.0	43	2	US-08-920-162A-1	Sequence 1, App1
81	211	100.0	43	2	US-08-461-018A-3	Sequence 3, App1
82	211	100.0	43	2	US-08-976-191-1	Sequence 1, App1
83	211	100.0	43	2	US-08-976-179-1	Sequence 1, App1
84	211	100.0	43	2	US-09-216-958-3	Sequence 3, App1
85	211	100.0	43	2	US-09-356-931-1	Sequence 1, App1
86	211	100.0	43	2	US-08-733-202-1	Sequence 1, App1
87	211	100.0	43	2	US-08-703-675C-1	Sequence 1, App1
88	211	100.0	43	2	US-09-390-692-1	Sequence 1, App1
89	211	100.0	43	2	US-08-617-267C-1	Sequence 1, App1
90	211	100.0	43	2	US-09-303-655-1	Sequence 1, App1
91	211	100.0	43	2	US-08-294-818-1	Sequence 1, App1
92	211	100.0	43	2	US-09-408-283-1	Sequence 1, App1
93	211	100.0	43	2	US-09-280-966-1	Sequence 1, App1
94	211	100.0	43	2	US-09-032-019-1	Sequence 1, App1
95	211	100.0	43	2	US-09-481-980A-1	Sequence 1, App1
96	211	100.0	43	2	US-09-594-366-1	Sequence 1, App1
97	211	100.0	43	2	US-08-665-648-1	Sequence 1, App1
98	211	100.0	43	2	US-09-915-342-1	Sequence 1, App1
99	211	100.0	43	2	US-08-996-422-1	Sequence 1, App1

100 211 100.0 43 2 US-09-984-834-1

ALIGNMENTS

Sequence 1, Appli

RESULT 1

US-07-744-767A-2
Sequence 2, Application US/07744767A

Patent No. 5434050

GENERAL INFORMATION:

APPLICANT: Maggio, John E.

APPLICANT: Mantyla, Patrick W.

TITLE OF INVENTION: Labeled

TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/744,767A

FILING DATE: 13-AUG-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mueeling, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 600,226-US-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-0331

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-744-767A-2

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGVVIA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGVVIA 42

RESULT 2

US-08-179-574-1

Sequence 1, Application US/08179574

Patent No. 5506097

GENERAL INFORMATION:

APPLICANT: Huntington Potter

APPLICANT: Usamah Kayyali

TITLE OF INVENTION: Compounds and Methods for Inhibiting

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/179,574

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/819,361

FILING DATE: 13-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: HU90-03A3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-179-574-1

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGVVIA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGVVIA 42

RESULT 3

US-08-347-144-1

Sequence 1, Application US/08347144

Patent No. 5589154

GENERAL INFORMATION:

APPLICANT: ANDERSON, STEPHEN

TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT

TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWREY & SIMON

STREET: 1299 PENNSYLVANIA AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,144

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: AUERBACH, JEFFREY I.

REGISTRATION NUMBER: 32,680

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 383-7451

TELEFAX: (202) 383-6610

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42

RESULT 4
US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-19

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42

RESULT 5
US-08-123-659A-19
Sequence 19, Application US/08123659A
Patent No. 5636477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5636477el Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-19

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNGKATIGLMVGSVTA 42

RESULT 6
US-08-464-247A-19
Sequence 19, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-19

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 7

US-08-464-248A-19
Sequence 19, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RIDDEL, RUSSELL E.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 9

US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
TITLE OF INVENTION: LABELED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 10
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-5

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11
US-08-268-348A-1
Sequence 1, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobell, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-1

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42

RESULT 12
US-08-433-734-2
Sequence 2, Application US/08433734
Patent No. 5837473

GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: -Amyloid Peptide and Methods
TITLE OF INVENTION: Labelled
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-2

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42

RESULT 13
US-08-609-090-9
Sequence 9, Application US/08609090
Patent No. 5840838

GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA

ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-9

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFFPAEDVGSNKGAIIIGLWGVVIA 42

RESULT 14
US-07-737-371E-72
Sequence 72, Application US/07737371E
Patent No. 5876948

GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 15

US-08-422-333-4
Sequence 4, Application US/08422333
Patent No. 5912410
GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 966-2438
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 16
US-08-682-245A-4
Sequence 4, Application US/08682245A
Patent No. 5919631

GENERAL INFORMATION:
APPLICANT: GOYAL, SHEPALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOCHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-4

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 17
US-08-986-948-5
Sequence 5, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317unhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRB
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-5

Query Match 100.0%; Score 211; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 18
US-08-717-551A-2
Sequence 2, Application US/08717551A
Patent No. 6071493
GENERAL INFORMATION:
APPLICANT: Dana Giulian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSER: & No. 6071493/15 LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,551A
FILING DATE: Sept-20-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-551A-2

Query Match 100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-09-388-890-1
Sequence 1, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/666,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

ORGANISM: AMYLOID PEPTIDE
US-09-388-890-1

Query Match	100.0%	Score 211	DB 2	Length 42
Best Local Similarity	100.0%	Pred. No.	6	2e-25
Matches 41	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGALITGLMVGGVIA 4 22
Db	2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGALITGLMVGGVIA 4 22

RESULT 20
US-09-005-215-20
; Sequence 20, Application US/09005215

GENERAL INFORMATION: Applicant: Ingram, Vernon M.
Applicant: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE CAUSED BY -AMYLOID PEPTIDES
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/035,847
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/960,188
 FILING DATE: 29-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Gates, Edward R.
 REGISTRATION NUMBER: 31,616
 REFERENCE/DOCKET NUMBER: M06566/7035
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 INFORMATION FOR SEO ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 JS-09-005-215-20

Query Match	100.0%	Score 211,	DB 2,	Length 42;
Best Local Similarity	100.0%	Pred. No. 6.2e-25;		
Matches	41;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps
QY	2	AERPHDSGYEHNOKLVEFAEDUSGNKALITGLMVGWVA	42	
Db	2	AERPHDSGYEHNOKLVEFAEDUSGNKALITGLMVGWVA	42	

RESULT 21
US-09-242-724-23
; Sequence 23, Application US/09242724

```

; patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; ADDITIONAL: Rich, David W.

```

TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
 FILE REFERENCE: Cyclosporin Analogs
 CURRENT APPLICATION NUMBER: US/09/242,724
 CURRENT FILING DATE: 1999-02-22
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 23

Query Match	100.0%	Score 211	DB 2	Length 42
Best Local Similarity	100.0%	Pred. No. 6	2e-25	
Matches 41; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

[illegible]

RESULT 22
US-08-922-930-2
; Sequence 2, Application US/08922930
; Patent No. 6451544

APPLICANT: Dana Gullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 6451544ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,930
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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1 REGISTRATION NUMBER: 34,293
2 REFERENCE/DOCKET NUMBER: BTLR-0033
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (215) 568-3100
5 TELEFAX: (215) 568-5439
6 INFORMATION FOR SEQ ID NO: 2:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 42 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: peptide
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Query Match	100.0%;	Score 211;	DB 2;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 6,2e-25;		
Matches 41;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;


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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-961-42

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Query Match          100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      2 AEFRRHDSGYEVHQQKLVFFAEEDVGSNKGAIIGLMVGVVIA 42
Db      2 AEFRRHDSGYEVHQQKLVFFAEEDVGSNKGAIIGLMVGVVIA 42

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RESULT 30
US-09-724-552-1
; Sequence 1, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152700-004740US
; CURRENT APPLICATION NUMBER: US/09/724,552
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-552-1

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Query Match          100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      2 AEFRRHDSGYEVHQQKLVFFAEEDVGSNKGAIIGLMVGVVIA 42
Db      2 AEFRRHDSGYEVHQQKLVFFAEEDVGSNKGAIIGLMVGVVIA 42

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Search completed: September 28, 2006, 06:27:12
 Job time : 30.5695 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: September 28, 2006, 06:58:47 ; Search time 96.2421 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-3
Perfect score: 211
Sequence: 1 XAEFRHDSGYEVHHQKLVEF.....DVGSNKGAITIGMVGWVIA 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	42	2	US-08-922-930-2
2	211	100.0	42	2	US-08-923-055-2
3	211	100.0	42	3	US-09-867-847-1
4	211	100.0	42	3	US-09-956-625-26
5	211	100.0	42	3	US-09-731-460-1
6	211	100.0	42	3	US-09-962-955C-37
7	211	100.0	42	3	US-09-848-616-174
8	211	100.0	42	3	US-09-865-294-65
9	211	100.0	42	3	US-09-792-079-113
10	211	100.0	42	3	US-09-825-242-1
11	211	100.0	42	3	US-09-930-915A-293
12	211	100.0	42	4	US-10-051-496-2
13	211	100.0	42	4	US-10-082-804-7
14	211	100.0	42	4	US-10-217-584-2
15	211	100.0	42	4	US-10-169-580-2
16	211	100.0	42	4	US-10-278-181-1
17	211	100.0	42	4	US-10-143-534-2
18	211	100.0	42	4	US-10-190-548A-1
19	211	100.0	42	4	US-10-051-663-2
20	211	100.0	42	4	US-10-159-279-13
21	211	100.0	42	4	US-10-050-902-220
22	211	100.0	42	4	US-10-050-898-220
23	211	100.0	42	4	US-10-082-014-81
24	211	100.0	42	4	US-10-372-076-82
25	211	100.0	42	4	US-10-455-218-2
26	211	100.0	42	4	US-10-231-298B-15
27	211	100.0	42	4	US-10-231-470C-15

28	211	100.0	42	4	US-10-231-063C-15	Sequence 15, Appl
29	211	100.0	42	4	US-10-366-125-28	Sequence 28, Appl
30	211	100.0	42	4	US-10-411-544-2	Sequence 2, Appl
31	211	100.0	42	4	US-10-231-213D-15	Sequence 15, Appl
32	211	100.0	42	4	US-10-231-114C-15	Sequence 15, Appl
33	211	100.0	42	4	US-10-337-261-2	Sequence 2, Appl
34	211	100.0	42	4	US-10-363-082-1	Sequence 1, Appl
35	211	100.0	42	4	US-10-433-385-6	Sequence 6, Appl
36	211	100.0	42	4	US-10-423-047-1	Sequence 1, Appl
37	211	100.0	42	4	US-10-617-876-7	Sequence 7, Appl
38	211	100.0	42	4	US-10-429-216-1	Sequence 1, Appl
39	211	100.0	42	4	US-10-656-624-5	Sequence 5, Appl
40	211	100.0	42	4	US-10-622-087-91	Sequence 91, Appl
41	211	100.0	42	4	US-10-683-815-11	Sequence 11, Appl
42	211	100.0	42	4	US-10-732-862A-95	Sequence 95, Appl
43	211	100.0	42	4	US-10-806-006-293	Sequence 293, App
44	211	100.0	42	4	US-10-416-262B-6	Sequence 6, Appl
45	211	100.0	42	4	US-10-677-074-82	Sequence 82, Appl
46	211	100.0	42	4	US-10-805-913-293	Sequence 293, App
47	211	100.0	42	4	US-10-816-022-1	Sequence 1, Appl
48	211	100.0	42	4	US-10-816-529-1	Sequence 1, Appl
49	211	100.0	42	4	US-10-815-353-1	Sequence 1, Appl
50	211	100.0	42	4	US-10-815-391-1	Sequence 1, Appl
51	211	100.0	42	4	US-10-772-656-55	Sequence 55, Appl
52	211	100.0	42	4	US-10-478-308-3	Sequence 3, Appl
53	211	100.0	42	4	US-10-478-307-3	Sequence 3, Appl
54	211	100.0	42	4	US-10-402-420-1	Sequence 1, Appl
55	211	100.0	42	4	US-10-771-174A-1	Sequence 1, Appl
56	211	100.0	42	5	US-10-828-548-1	Sequence 1, Appl
57	211	100.0	42	5	US-10-864-107-2	Sequence 2, Appl
58	211	100.0	42	5	US-10-816-380-1	Sequence 1, Appl
59	211	100.0	42	5	US-10-485-310-19	Sequence 19, Appl
60	211	100.0	42	5	US-10-889-999-42	Sequence 42, Appl
61	211	100.0	42	5	US-10-890-070-42	Sequence 42, Appl
62	211	100.0	42	5	US-10-861-614-65	Sequence 65, Appl
63	211	100.0	42	5	US-10-481-387-2	Sequence 2, Appl
64	211	100.0	42	5	US-10-890-000-42	Sequence 42, Appl
65	211	100.0	42	5	US-10-788-666-1	Sequence 1, Appl
66	211	100.0	42	5	US-10-923-471-1	Sequence 1, Appl
67	211	100.0	42	5	US-10-823-463-42	Sequence 42, Appl
68	211	100.0	42	5	US-10-923-469-1	Sequence 1, Appl
69	211	100.0	42	5	US-10-933-559-1	Sequence 1, Appl
70	211	100.0	42	5	US-10-815-404-1	Sequence 1, Appl
71	211	100.0	42	5	US-10-934-609-1	Sequence 1, Appl
72	211	100.0	42	5	US-10-950-018-1	Sequence 1, Appl
73	211	100.0	42	5	US-10-883-150-3	Sequence 3, Appl
74	211	100.0	42	5	US-10-923-474-1	Sequence 1, Appl
75	211	100.0	42	5	US-10-884-892-1	Sequence 1, Appl
76	211	100.0	42	5	US-10-822-968-42	Sequence 42, Appl
77	211	100.0	42	5	US-10-933-206-37	Sequence 37, Appl
78	211	100.0	42	5	US-10-777-792-32	Sequence 32, Appl
79	211	100.0	42	5	US-10-825-958-1	Sequence 1, Appl
80	211	100.0	42	5	US-10-775-562-1	Sequence 1, Appl
81	211	100.0	42	5	US-10-852-950-1	Sequence 1, Appl
82	211	100.0	42	5	US-10-890-071-42	Sequence 42, Appl
83	211	100.0	42	5	US-10-903-279-1	Sequence 1, Appl
84	211	100.0	42	5	US-10-810-881A-50	Sequence 50, Appl
85	211	100.0	42	5	US-10-890-024-42	Sequence 42, Appl
86	211	100.0	42	5	US-10-934-819-1	Sequence 1, Appl
87	211	100.0	42	5	US-10-508-586-1	Sequence 1, Appl
88	211	100.0	42	5	US-10-505-313-27	Sequence 27, Appl
89	211	100.0	42	5	US-10-770-712-35	Sequence 35, Appl
90	211	100.0	42	5	US-10-923-267-1	Sequence 1, Appl
91	211	100.0	42	5	US-10-928-926-42	Sequence 42, Appl
92	211	100.0	42	5	US-10-923-605-1	Sequence 1, Appl
93	211	100.0	42	5	US-10-934-818-1	Sequence 1, Appl
94	211	100.0	42	5	US-10-945-133-1	Sequence 1, Appl
95	211	100.0	42	5	US-10-966-919B-3	Sequence 3, Appl
96	211	100.0	42	6	US-11-058-757-42	Sequence 42, Appl
97	211	100.0	42	6	US-11-004-053-37	Sequence 37, Appl
98	211	100.0	42	6	US-11-007-643-37	Sequence 37, Appl
99	211	100.0	42	6	US-11-007-644-37	Sequence 37, Appl
100	211	100.0	42	6	US-11-007-669-37	Sequence 37, Appl

ALIGNMENTS

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RESULT 1
US-08-922-930-2
; Sequence 2, Application US/08922930
; Publication No. US20010016326A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,930
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-922-930-2

Query Match          100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEFRRHDSGYEVHOKLVFFPADVGSNKGAIIGLMVGVVIA 42
DB      2 AEFRRHDSGYEVHOKLVFFPADVGSNKGAIIGLMVGVVIA 42

RESULT 2
US-08-923-055-2
; Sequence 2, Application US/08923055
; Publication No. US20010016327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
```

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; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US//08/923,055
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-923-055-2

Query Match          100.0%; Score 211; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 AEFRRHDSGYEVHOKLVFFPADVGSNKGAIIGLMVGVVIA 42
DB      2 AEFRRHDSGYEVHOKLVFFPADVGSNKGAIIGLMVGVVIA 42
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RESULT 3
US-09-867-847-1
; Sequence 1, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lisa
; APPLICANT: Kong, Xiangji
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; US-09-867-847-1
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Query Match          100.0%; Score 211; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEFRRHDSGYEVHOKLVFFPADVGSNKGAIIGLMVGVVIA 42
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Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

RESULT 4

US-09-956-625-26

Sequence 26, Application US/09956625

Patent No. US20020119926A1

GENERAL INFORMATION:

APPLICANT: Fraser, Paul

TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof

FILE REFERENCE: 14445-503

CURRENT APPLICATION NUMBER: US/09/956,625

CURRENT FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: 60/233,482

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

LENGTH: 42

TYPE: PRT

ORGANISM: Homo sapiens

US-09-956-625-26

Query Match 100.0%; Score 211; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

RESULT 5

US-09-731-460-1

Sequence 1, Application US/09731460

Patent No. US20020137112A1

GENERAL INFORMATION:

APPLICANT: Buck, Martina

TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's

FILE REFERENCE: CHOUKIER-04302

CURRENT APPLICATION NUMBER: US/09/731,460

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 42

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-731-460-1

Query Match 100.0%; Score 211; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

RESULT 6

US-09-962-955C-37

Sequence 37, Application US/09962955C

Publication No. US20030013648A1

GENERAL INFORMATION:

APPLICANT: Gerardo M. Castillo

APPLICANT: Alan D. Snow

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrick M. Dwyer

STREET: ProteoTech, Inc, 1818 Westlake Avenue N, Suite 114

CITY: Seattle

STATE: WA (Washington)

COUNTRY: United States of America

ZIP: 98109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC

OPERATING SYSTEM: Windows 98

SOFTWARE: Wordperfect 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,955C

FILING DATE: 24-September-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/938,275

FILING DATE: 22-August-2001

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dwyer, Patrick M.

REGISTRATION NUMBER: 32,411

REFERENCE/DOCKET NUMBER: PROTEO.P03CI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 343-7074

TELEFAX: (206) 343-7085

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

ORIGINAL SOURCE:

ORGANISM: MOUSE

FEATURE:

OTHER INFORMATION: Also referred to in the specification as "AB 1-42"

US-09-962-955C-37

Query Match 100.0%; Score 211; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGAVVIA 42

RESULT 7

US-09-848-616-174

Sequence 174, Application US/09848616

Publication No. US20030054010A1

GENERAL INFORMATION:

APPLICANT: Seibel, Peter

APPLICANT: Dunant, Nicolas

APPLICANT: Bachmann, Martin

APPLICANT: Tissot, Alain

APPLICANT: Lechner, Franziska

TITLE OF INVENTION: Molecular Antigen Array

FILE REFERENCE: 1700.0180002

CURRENT APPLICATION NUMBER: US/09/848,616

CURRENT FILING DATE: 2001-05-05

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 174

LENGTH: 42

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Amyloid Beta Peptide

US-09-848-616-174

Query Match 100.0%; Score 211; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 8

US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; PRIORITY FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-65

Query Match 100.0%; Score 211; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 9

US-09-792-079-13
; Sequence 13, Application US/09792079
; Publication No. US20030083277A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Hersh, Louis B.
; APPLICANT: Mukherjee, Atish
; TITLE OF INVENTION: Use of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzhei
; FILE REFERENCE: 05029-0261
; CURRENT APPLICATION NUMBER: US/09/792,079
; PRIORITY FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,826
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-079-13

Query Match 100.0%; Score 211; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 10

US-09-825-242-1
; Sequence 1, Application US/09825242
; Publication No. US20030092000A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuraltab Limited

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/825,242
; PRIORITY FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/201,430
; PRIORITY FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIORITY FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-825-242-1

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11

US-09-930-915A-293
; Sequence 293, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; PRIORITY FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIORITY FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIORITY FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 293
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-915A-293

Query Match 100.0%; Score 211; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 12

US-10-051-496-2
; Sequence 2, Application US/10051496
; Publication No. US20020182660A1
; GENERAL INFORMATION:
; APPLICANT: Kei-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
; Abeta(1-41), Abeta(1-42) and Abeta(1-43)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kei-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US2002018260A1epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183,407
FILING DATE: 18-February-2000
ATTORNEY/AGENT INFORMATION:
NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662
REFERENCE/DOCKET NUMBER: PBI-PT001.1
TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1-42
IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-051-496-2
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity: 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
Db 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
RESULT 13
US-10-082-804-7
Sequence 7, Application US/10082804
Publication No. US20020194632A1
GENERAL INFORMATION:
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Transgenic Knockouts of BACE-1
FILE REFERENCE: MBH 02-329-A
CURRENT APPLICATION NUMBER: US/10/082,804
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/271,092
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/271,514
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/293,762
PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity: 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
Db 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
RESULT 14
US-10-217-584-2
Sequence 2, Application US/10217584
Publication No. US20030077261A1
GENERAL INFORMATION:
APPLICANT: Paris, Daniel
TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
FILE REFERENCE: USF-T161XCI
CURRENT APPLICATION NUMBER: US/10/217,584
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,656
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(42)
OTHER INFORMATION: A-beta 1-42 peptide
US-10-217-584-2
Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity: 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
Db 2 AEFRRDSGYEVHOKLVFFAEDVGSNKGAIIIGLWVGVI 42
RESULT 15
US-10-169-580-2
Sequence 2, Application US/10169580
Publication No. US20030100477A1
GENERAL INFORMATION:
APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR SUPPRESSING B-AMYLOID PRODUCTION
FILE REFERENCE: 070898
CURRENT APPLICATION NUMBER: US/10/169,580
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 2000-131037
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: PCT/JP01/03555
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens

US-10-169-580-2

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 16

US-10-278-181-1
; Sequence 1, Application US/10278181
; Publication No. US20030104488A1
; GENERAL INFORMATION:
; APPLICANT: Choikier, Mario
; APPLICANT: Buck, Matina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOJKIER-04302
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/731,460
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-278-181-1

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 17

US-10-143-534-2
; Sequence 2, Application US/10143534
; Publication No. US20030105152A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M00656/70078
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 10/051,663
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-143-534-2

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 18

US-10-190-548A-1
; Sequence 1, Application US/10190548A
; Publication No. US20030109435A1
; GENERAL INFORMATION:
; APPLICANT: Griswold Premer, Irene
; APPLICANT: Wright, Sarah
; APPLICANT: Yednock, Theodore
; APPLICANT: Rydel, Russell
; TITLE OF INVENTION: Methods of Inhibiting Amyloid Toxicity
; FILE REFERENCE: 08576, 0030-00
; CURRENT FILING DATE: US/10/190,548A
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-548A-1

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19

US-10-051-663-2
; Sequence 2, Application US/10051663
; Publication No. US20030114510A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M0656/7071
; CURRENT FILING DATE: US/10/051,663
; PRIOR APPLICATION NUMBER: 2002-01-18
; PRIOR FILING DATE: US 09/706,574
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-051-663-2

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 20

US-10-159-279-13
; Sequence 13, Application US/10159279
; Publication No. US20030165481A1

GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: Hersch, Louis B.
APPLICANT: Mukherjee, Arish
TITLE OF INVENTION: Use Of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzheimer's Disease
FILE REFERENCE: 050229-0298
CURRENT APPLICATION NUMBER: US/10/159,279
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/184,826
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/792,079
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-159-279-13

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42
Db 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42

RESULT 21

US-10-050-902-220
Sequence 220, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Plosek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 220
LENGTH: 42
TYPE: PRT
ORGANISM: Amyloid Beta Peptide
US-10-050-902-220

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42
Db 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42

RESULT 22
US-10-050-898-220

Sequence 220, Application US/10050898
Publication No. US20030175711A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Plosek, Christine
APPLICANT: Ottmann, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staufendiel, Matthias
APPLICANT: Frey, Peter
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190005
CURRENT APPLICATION NUMBER: US/10/050,898
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 220
LENGTH: 42
TYPE: PRT
ORGANISM: Amyloid Beta Peptide
US-10-050-898-220

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42
Db 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42

RESULT 23

US-10-082-014-81
Sequence 81, Application US/10082014
Publication No. US20030185858A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY.
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 42
TYPE: PRT
ORGANISM: Alzheimer's disease b-Amyloid
US-10-082-014-81

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42
Db 2 AEFPHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGSVIA 42

RESULT 24

US-10-372-076-82
; Sequence 82, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 82
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Alzheimer's disease b-Amyloid
US-10-372-076-82

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42

RESULT 25
US-10-455-218-2
; Sequence 2, Application US/10455218
; Publication No. US20030204051A1
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-218-2

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42

RESULT 26
US-10-231-298B-15
; Sequence 15, Application US/10231298B
; Publication No. US20030219853A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Cross-Linking a Compound
; FILE REFERENCE: SAMG/0006

CURRENT APPLICATION NUMBER: US/10/231,298B
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-298B-15

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42

RESULT 27
US-10-231-470C-15
; Sequence 15, Application US/10231470C
; Publication No. US20030219857A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Having Broad Substrate
; FILE REFERENCE: SAMG/0003
; CURRENT APPLICATION NUMBER: US/10/231,470C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-470C-15

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42
DB 2 AEFRRHDSGYEVHHQKLVFFAEDVGSNNKGAIIGLMVGGVVIA 42

RESULT 28
US-10-231-063C-15
; Sequence 15, Application US/10231063C
; Publication No. US20030224476A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Reactive Compound
; FILE REFERENCE: SAMG/0004
; CURRENT APPLICATION NUMBER: US/10/231,063C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 42

TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-063C-15

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42
DB 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42

RESULT 29

US-10-366-125-28
Sequence 28, Application US/10366125
Publication No. US2003028259A1
GENERAL INFORMATION:
APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: EASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
FILE REFERENCE: 416272003500
CURRENT APPLICATION NUMBER: US/10/366,125
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 60/356,008
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-366-125-28

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42
DB 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42

RESULT 30
US-10-411-544-2
Sequence 2, Application US/10411544
Publication No. US20030232758A1
GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter
TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzhe
TITLE OF INVENTION: Disease
FILE REFERENCE: LI01547
CURRENT APPLICATION NUMBER: US/10/411,544
CURRENT FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-544-2

Query Match 100.0%; Score 211; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42
DB 2 AEFRRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMWGVVIA 42

Search completed: September 28, 2006, 07:09:23
Job time : 96.4088 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 ; Search time 16.3857 Seconds
(without alignments)
199.069 Million cell updates/sec

Title: US-09-731-899-3

Perfect score: 211
Sequence: 1 XAEFRHDSGYEVHQLVLF.....DVGSNGKATIGLWGVVIA 42

Scoring table: BIOSIM62
Gapop 10.0 , Gapept 0.5

Searched: 285145 seqs, 7763843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*
1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	42	1	US-09-731-899-3
2	211	100.0	42	6	US-10-890-071-42
3	211	100.0	42	6	US-10-544-093-1
4	211	100.0	42	6	US-10-546-547-3
5	211	100.0	42	6	US-10-966-645-36
6	211	100.0	42	7	US-11-104-300-2
7	211	100.0	42	7	US-11-297-316-1
8	211	100.0	42	7	US-11-287-157A-49
9	211	100.0	43	1	US-09-731-899-4
10	211	100.0	43	7	US-11-348-091-1
11	211	100.0	56	6	US-10-544-093-16
12	211	100.0	56	6	US-10-544-093-19
13	211	100.0	58	6	US-10-515-919A-30
14	211	100.0	58	6	US-10-544-093-12
15	211	100.0	58	6	US-10-544-093-14
16	211	100.0	58	6	US-10-544-093-27
17	211	100.0	59	1	US-09-731-899-1
18	211	100.0	60	6	US-10-544-093-10
19	211	100.0	64	6	US-10-544-093-13
20	211	100.0	79	6	US-10-544-093-15
21	211	100.0	99	6	US-10-544-093-22
22	211	100.0	99	6	US-10-544-093-24
23	211	100.0	142	6	US-10-544-093-17
24	211	100.0	142	6	US-10-544-093-21
25	211	100.0	142	6	US-10-544-093-23

26	211	100.0	185	6	US-10-544-093-18	Sequence 18, Appl
27	211	100.0	203	6	US-10-544-093-26	Sequence 26, Appl
28	211	100.0	316	6	US-10-544-093-25	Sequence 25, Appl
29	211	100.0	695	6	US-10-515-919A-1	Sequence 1, Appl
30	211	100.0	695	6	US-10-511-269-7	Sequence 7, Appl
31	211	100.0	751	6	US-10-546-547-2	Sequence 2, Appl
32	211	100.0	770	6	US-10-511-269-9	Sequence 9, Appl
33	207	98.1	40	6	US-10-966-645-38	Sequence 38, Appl
34	206	97.6	626	6	US-10-515-919A-13	Sequence 13, Appl
35	206	97.6	626	6	US-10-515-919A-18	Sequence 18, Appl
36	205	97.2	626	6	US-10-515-919A-15	Sequence 15, Appl
37	204	96.7	626	6	US-10-515-919A-20	Sequence 20, Appl
38	204	96.7	42	7	US-11-269-857-5	Sequence 5, Appl
39	204	96.7	626	6	US-10-515-919A-14	Sequence 14, Appl
40	204	96.7	626	6	US-10-515-919A-16	Sequence 16, Appl
41	204	96.7	626	6	US-10-515-919A-19	Sequence 19, Appl
42	204	96.7	626	6	US-10-515-919A-21	Sequence 21, Appl
43	203	96.2	40	1	US-09-731-899-2	Sequence 2, Appl
44	203	96.2	40	6	US-10-966-645-37	Sequence 37, Appl
45	203	96.2	626	6	US-10-515-919A-12	Sequence 12, Appl
46	203	96.2	626	6	US-10-515-919A-17	Sequence 17, Appl
47	202	95.7	40	1	US-09-731-899-5	Sequence 5, Appl
48	199	94.3	38	6	US-10-966-645-39	Sequence 39, Appl
49	198	93.8	42	6	US-10-515-919A-3	Sequence 3, Appl
50	198	93.8	42	6	US-10-515-919A-8	Sequence 8, Appl
51	197	93.4	40	7	US-11-104-300-3	Sequence 3, Appl
52	197	93.4	42	6	US-10-515-919A-5	Sequence 5, Appl
53	197	93.4	42	6	US-10-515-919A-10	Sequence 10, Appl
54	196	92.9	38	6	US-10-966-645-44	Sequence 44, Appl
55	196	92.9	40	7	US-11-269-857-3	Sequence 3, Appl
56	196	92.9	42	6	US-10-515-919A-4	Sequence 4, Appl
57	196	92.9	42	6	US-10-515-919A-6	Sequence 6, Appl
58	196	92.9	42	6	US-10-515-919A-9	Sequence 9, Appl
59	196	92.9	42	6	US-10-515-919A-11	Sequence 11, Appl
60	195	92.4	42	6	US-10-515-919A-2	Sequence 2, Appl
61	195	92.4	42	6	US-10-515-919A-7	Sequence 7, Appl
62	192	91.0	42	6	US-10-515-919A-22	Sequence 22, Appl
63	192	91.0	43	6	US-10-515-919A-23	Sequence 23, Appl
64	192	91.0	695	6	US-10-538-410-96	Sequence 96, Appl
65	192	91.0	770	7	US-11-104-300-1	Sequence 1, Appl
66	185	73.5	32	1	US-09-731-899-6	Sequence 6, Appl
67	146	69.2	28	7	US-11-287-316-2	Sequence 2, Appl
68	125	59.2	26	1	US-09-731-899-7	Sequence 7, Appl
69	110	52.1	21	6	US-10-966-645-42	Sequence 42, Appl
70	106	50.2	19	6	US-10-966-645-43	Sequence 43, Appl
71	103	48.8	19	6	US-10-966-645-45	Sequence 45, Appl
72	84	39.8	19	6	US-10-890-071-75	Sequence 75, Appl
73	61	28.9	10	6	US-10-890-071-13	Sequence 13, Appl
74	61	28.9	10	6	US-10-890-071-14	Sequence 14, Appl
75	60	28.4	13	6	US-10-890-071-72	Sequence 72, Appl
76	59	28.0	10	6	US-10-890-071-12	Sequence 12, Appl
77	58	27.5	10	6	US-10-890-071-15	Sequence 15, Appl
78	58	27.5	624	6	US-10-449-902-33879	Sequence 33879, A
79	56.5	26.8	1046	6	US-10-449-902-51230	Sequence 51230, A
80	56	26.5	10	6	US-10-890-071-10	Sequence 10, Appl
81	56	26.5	10	6	US-10-890-071-11	Sequence 11, Appl
82	56	26.5	10	6	US-10-890-071-16	Sequence 16, Appl
83	56	26.5	10	6	US-10-890-071-17	Sequence 17, Appl
84	56	26.5	10	6	US-10-890-071-18	Sequence 18, Appl
85	56	26.5	11	6	US-10-966-645-40	Sequence 40, Appl
86	55.5	26.3	356	7	US-11-056-355B-51289	Sequence 51289, A
87	55.5	26.3	480	7	US-11-056-355B-51388	Sequence 51388, A
88	55.5	26.3	504	7	US-11-056-355B-51387	Sequence 51387, A
89	55.5	26.3	618	6	US-10-449-902-47542	Sequence 47542, A
90	55	26.1	10	6	US-10-890-071-19	Sequence 19, Appl
91	55	26.1	10	6	US-10-890-071-21	Sequence 21, Appl
92	55	26.1	429	7	US-11-056-355B-53789	Sequence 53789, A
93	55	26.1	556	7	US-11-056-355B-53788	Sequence 53788, A
94	55	26.1	826	7	US-11-056-355B-87461	Sequence 87461, A
95	54.5	25.8	826	7	US-11-056-355B-87460	Sequence 87460, A
96	54.5	25.8	828	7	US-11-056-355B-87459	Sequence 87459, A
97	54.5	25.8	1083	7	US-11-056-355B-87458	Sequence 87458, A
98	54	25.6	10	6	US-10-890-071-20	Sequence 20, Appl

99 53.5 25.4 921 6 US-10-519-135-6 Sequence 6, Appl
100 53 25.1 10 6 US-10-890-071-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-731-899-3

Sequence 3, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa is L-Asp, D-Asp, or L-Iso Asp
US-09-731-899-3

Query Match 100.0%; Score 211; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 2e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42

RESULT 2
US-10-890-071-42

Sequence 42, Application US/10890071
Publication No. US20060121038A9
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Bard, Frederique
APPLICANT: Yednock, Ted
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
FILE REFERENCE: 152701-004760US
CURRENT APPLICATION NUMBER: US/10/890,071
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US/09/580,018
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/322,289
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-890-071-42

Query Match 100.0%; Score 211; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42

Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42

RESULT 3
US-10-544-093-1

Sequence 1, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
PREVENTION AND TREATMENT OF AMYLOIDGENIC DISEASE
FILE REFERENCE: 152701-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-544-093-1

Query Match 100.0%; Score 211; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42

RESULT 4
US-10-546-547-3

Sequence 3, Application US/10546547
Publication No. US20060188951A1
GENERAL INFORMATION:
APPLICANT: Mook, In Hee
APPLICANT: Hurt, Ji Yeun
TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Same
FILE REFERENCE: DE-1646
CURRENT APPLICATION NUMBER: US/10/546,547
CURRENT FILING DATE: 2005-08-23
PRIOR APPLICATION NUMBER: PCT/KR2004/000371
PRIOR FILING DATE: 2004-02-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: 1-42 amino acid of amyloid A4 precursor protein (APP)
US-10-546-547-3

Query Match 100.0%; Score 211; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2e-21;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIA 42
RESULT 5
US-10-966-645-36

; Sequence 36, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFEMANN, TORSTEN
; APPLICANT: NIESTROU, ANDRE JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20486/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-36

Query Match 100.0%; Score 211; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42
Db 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 6
US-11-104-300-2
; Sequence 2, Application US/11104300
; Publication No. US2006099211A1
; GENERAL INFORMATION:
; APPLICANT: Monthe, Carmen
; APPLICANT: Szabo, Paul
; APPLICANT: Weksler, Mark
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treating
; FILE REFERENCE: 1676,027US1
; CURRENT APPLICATION NUMBER: US/11/104,300
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US 60/561,423
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-104-300-2

Query Match 100.0%; Score 211; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42
Db 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 7
US-11-297-316-1
; Sequence 1, Application US/11297316
; Publication No. US2006014602A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE REFERENCE: 01142-0200-00304

; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-1

Query Match 100.0%; Score 211; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42
Db 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 8
US-11-287-157A-49
; Sequence 49, Application US/11287157A
; Publication No. US20060154863A1
; GENERAL INFORMATION:
; APPLICANT: SKJBATCH, HANNA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
; FILE REFERENCE: 32051-701.201
; CURRENT APPLICATION NUMBER: US/11/287,157A
; CURRENT FILING DATE: 2005-11-25
; PRIOR APPLICATION NUMBER: 60/658,859
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/652,287
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/630,880
; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Version 3.3
; SEQ ID NO 49
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-287-157A-49

Query Match 100.0%; Score 211; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42
Db 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 9
US-09-731-899-4
; Sequence 4, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 20555/120343-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Version 3.3
; SEQ ID NO 4
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-731-899-4

Query Match 100.0%; Score 211; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 10
US-11-348-091-1
Sequence 1, Application US/11348091
Publication No. US20060211679A1
GENERAL INFORMATION:

APPLICANT: Ham, Qi
TITLE OF INVENTION: Substituted Lactams as Inhibitors of Abeta Protein Production
FILE REFERENCE: BMS-PH-7164.1(C)
CURRENT APPLICATION NUMBER: US/11/348,091
CURRENT FILING DATE: 2006-02-06
PRIOR APPLICATION NUMBER: US 10/685,031
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 09/832,455
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/196,549
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-11-348-091-1

Query Match 100.0%; Score 211; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11
US-10-544-093-16
Sequence 16, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Padre-A-beta fragment fusion protein
NAME/KEY: MISC_FEATURE
LOCATION: (3)..(3)

OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16

Query Match 100.0%; Score 211; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 15 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 55

RESULT 12

US-10-544-093-19
Sequence 19, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (46)..(46)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-19

Query Match 100.0%; Score 211; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 13

US-10-515-919A-30
Sequence 30, Application US/10515919A
Publication No. US20060160146A1
GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
FILE REFERENCE: 084952
CURRENT APPLICATION NUMBER: US/10/515,919A
CURRENT FILING DATE: 2004-11-29

;; PRIOR APPLICATION NUMBER: PCT/JP03/06319
;; PRIOR FILING DATE: 2003-05-21
;; PRIOR APPLICATION NUMBER: JP 2002-159472
;; PRIOR FILING DATE: 2002-05-31
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 30
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-515-919A-30

Query Match 100.0%; Score 211; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 18 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 58

RESULT 14
US-10-544-093-12
;; Sequence 12, Application US/10544093
;; Publication No. US20060188512A1
;; GENERAL INFORMATION:
;; APPLICANT: Yednock, Ted
;; APPLICANT: Vasquez, Nicki
;; APPLICANT: Bard, Frederique
;; APPLICANT: Seubert, Peter A.
;; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
;; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
;; FILE REFERENCE: 15270J-009820US
;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 12
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)-(43)
;; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12

Query Match 100.0%; Score 211; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 15
US-10-544-093-14
;; Sequence 14, Application US/10544093
;; Publication No. US20060188512A1
;; GENERAL INFORMATION:
;; APPLICANT: Yednock, Ted
;; APPLICANT: Vasquez, Nicki
;; APPLICANT: Bard, Frederique
;; APPLICANT: Seubert, Peter A.
;; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR

;; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
;; FILE REFERENCE: 15270J-009820US
;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 14
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)-(43)
;; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-14

Query Match 100.0%; Score 211; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 16
US-10-544-093-27
;; Sequence 27, Application US/10544093
;; Publication No. US20060188512A1
;; GENERAL INFORMATION:
;; APPLICANT: Yednock, Ted
;; APPLICANT: Vasquez, Nicki
;; APPLICANT: Bard, Frederique
;; APPLICANT: Seubert, Peter A.
;; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
;; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
;; FILE REFERENCE: 15270J-009820US
;; CURRENT APPLICATION NUMBER: US/10/544,093
;; CURRENT FILING DATE: 2005-08-01
;; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
;; PRIOR FILING DATE: 2004-01-31
;; PRIOR APPLICATION NUMBER: US 60/444,150
;; PRIOR FILING DATE: 2003-02-01
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 27
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Fusion protein
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)-(43)
;; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
;; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27

Query Match 100.0%; Score 211; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 2 AEFRRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 17
US-09-731-899-1
; Sequence 1, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-1

Query Match 100.0%; Score 211; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2,9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 42
Db 6 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 46

RESULT 18
US-10-544-093-20

; Sequence 20, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-20

Query Match 100.0%; Score 211; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 42
Db 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 42

RESULT 19
US-10-544-093-13
; Sequence 13, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13

Query Match 100.0%; Score 211; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 3,2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 42
Db 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAITGLMWGVVIA 42

RESULT 20
US-10-544-093-15
; Sequence 15, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

Query Match 100.0%; Score 211; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 3,2e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-544-093-15

Query Match 100.0%; Score 211; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42
DB 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 21

US-10-544-093-22

Sequence 22, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:

APPLICANT: Vaequez, Ted

APPLICANT: Vaequez, Nicki

APPLICANT: Bard, Frederique

APPLICANT: Seubert, Peter A.

TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR

FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093

CURRENT FILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: WO PCT/US2004/002856

PRIOR FILING DATE: 2004-01-31

PRIOR APPLICATION NUMBER: US 60/444,150

PRIOR FILING DATE: 2003-02-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2

SEQ ID NO 22

LENGTH: 99

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Fusion protein

NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (57)..(99)

OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-22

Query Match 100.0%; Score 211; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42
DB 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 22

US-10-544-093-24

Sequence 24, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:

APPLICANT: Vaequez, Ted

APPLICANT: Vaequez, Nicki

APPLICANT: Bard, Frederique

APPLICANT: Seubert, Peter A.

TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR

FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093

CURRENT FILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: WO PCT/US2004/002856

PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 99

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Fusion protein

NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (44)..(86)

OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-24

Query Match 100.0%; Score 211; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42
DB 2 AEFPHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 23

US-10-544-093-17

Sequence 17, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:

APPLICANT: Vaequez, Ted

APPLICANT: Vaequez, Nicki

APPLICANT: Bard, Frederique

APPLICANT: Seubert, Peter A.

TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR

FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093

CURRENT FILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: WO PCT/US2004/002856

PRIOR FILING DATE: 2004-01-31

PRIOR APPLICATION NUMBER: US 60/444,150

PRIOR FILING DATE: 2003-02-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2

SEQ ID NO 17

LENGTH: 142

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: A-beta-A-beta-A-beta- Padre fusion protein

NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (44)..(86)

OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (87)..(129)

OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (137)..(132)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-17

Query Match 100.0%; Score 211; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 24
US-10-544-093-21
Sequence 21, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: US 60/444,150
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-21

Query Match 100.0%; Score 211; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 15 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 55
RESULT 25
US-10-544-093-23
Sequence 23, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted

APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: US 60/444,150
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (87)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-23

Query Match 100.0%; Score 211; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42
DB 2 AEFRRDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 26
US-10-544-093-18
Sequence 18, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: US 60/444,150
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein

NAME/KEY: MISC_FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: X is cyclonexylalanine, tyrosine, or phenylalanine.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (143)..(185)
OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-18

Query Match 100.0%; Score 211; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 42
15 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 55

RESULT 27
US-10-544-093-26
Sequence 26, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: US 60/444,150
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 203
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (81)..(123)
OTHER INFORMATION: Only a contiguous fragment of residues 81-123 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (161)..(203)

OTHER INFORMATION: Only a contiguous fragment of residues 161-203 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-26

Query Match 100.0%; Score 211; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 42
2 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 42

RESULT 28
US-10-544-093-25
Sequence 25, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: US 60/444,150
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 316
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (109)..(151)
OTHER INFORMATION: Only a contiguous fragment of residues 109-151 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (152)..(194)
OTHER INFORMATION: Only a contiguous fragment of residues 152-194 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (195)..(237)
OTHER INFORMATION: Only a contiguous fragment of residues 195-237 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (238)..(280)
OTHER INFORMATION: Only a contiguous fragment of residues 238-280 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-25

Query Match 100.0%; Score 211; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 42
2 AEFRRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIA 42

```
RESULT 29
US-10-515-919A-1
; Sequence 1, Application US/10515919A
; Publication No. US20060160146A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
; FILE REFERENCE: Q84952
; CURRENT APPLICATION NUMBER: US/10/515, 919A
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: PCT/JP03/06319
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: JP 2002-159472
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-515-919A-1

Query Match          100.0%; Score 211; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGGVIA 42
      |||||||
Db      598 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGGVIA 638

RESULT 30
US-10-511-269-7
; Sequence 7, Application US/10511269
; Publication No. US2006020566A1
; GENERAL INFORMATION:
; APPLICANT: MORI, HIROSHI
; TITLE OF INVENTION: GAMMA-SECRETASE INHIBITORS
; FILE REFERENCE: 260276USOPT
; CURRENT APPLICATION NUMBER: US/10/511, 269
; CURRENT FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: PCT/JP03/050117
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: JP2002-121983
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-269-7

Query Match          100.0%; Score 211; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGGVIA 42
      |||||||
Db      598 AEFRRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLMVGGVIA 638
```

Search completed: September 28, 2006, 07:10:55
Job time : 17.3857 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 114.924 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-4
Perfect score: 222
Sequence: 1 DAEFRHDSGYEVHQLVFF.....VGSNKGAICGLMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	43	2	AAR54759 Beta amyl
2	222	100.0	43	2	AAR60367 Beta-amyl
3	222	100.0	43	2	AAR61328 Amyloid b
4	222	100.0	43	2	AAR64165 Beta amyl
5	222	100.0	43	2	ADD11650 Human bet
6	222	100.0	43	2	AAR95673 A-beta.pr
7	222	100.0	43	2	AAR93371 Human bet
8	222	100.0	43	2	AAV17758 Beta-amyl
9	222	100.0	43	2	AAW51316 Natural b
10	222	100.0	43	2	AAV42955 Beta-amyl
11	222	100.0	43	2	AAW21216 Beta-amyl
12	222	100.0	43	2	AAW71378 Beta-amyl
13	222	100.0	43	2	AAW40129 Human amy
14	222	100.0	43	2	AAW89362 Beta-amyl
15	222	100.0	43	3	AAV88390 Beta-amyl
16	222	100.0	43	3	AAV56102 Natural b
17	222	100.0	43	3	AAW27020 Beta-amyl
18	222	100.0	43	3	AAW15372 Human bet
19	222	100.0	43	4	ABW07901 Beta-amyl
20	222	100.0	43	4	AAW84428 Partial s
21	222	100.0	43	4	AAW91811 Amyloid b
22	222	100.0	43	4	AAW91778 Amyloid b
23	222	100.0	43	4	AAW78791 Human bet

24	222	100.0	43	4	AAW6344 Beta-amyl
25	222	100.0	43	4	AAW81193 Beta-amyl
26	222	100.0	43	4	AAW98986 Beta-amyl
27	222	100.0	43	4	AAW47108 Biotinyl a
28	222	100.0	43	4	AAE12508 Beta-amyl
29	222	100.0	43	5	ABW98516 Human bet
30	222	100.0	43	5	ABW71001 Natural l
31	222	100.0	43	5	AAO18457 Human bet
32	222	100.0	43	5	ABW05149 Beta amyl
33	222	100.0	43	5	AAU98701 Human amy
34	222	100.0	43	5	AAW50862 Beta-amyl
35	222	100.0	43	5	ABW78007 Amino aci
36	222	100.0	43	5	AAE26265 Human bet
37	222	100.0	43	6	AAO16064 Neurologi
38	222	100.0	43	6	ABG73456 Natural b
39	222	100.0	43	6	ABU08505 Human amy
40	222	100.0	43	6	ABP96145 Human Abe
41	222	100.0	43	6	ABR39273 Human Amy
42	222	100.0	43	6	ABP97881 Amino aci
43	222	100.0	43	6	ABU62720 Beta-amyl
44	222	100.0	43	6	ADK66003 Human A(b
45	222	100.0	43	7	ADK23549 Human Abe
46	222	100.0	43	7	ADK23549 Human Abe
47	222	100.0	43	8	ADK23549 Human Abe
48	222	100.0	43	8	ADK23549 Human Abe
49	222	100.0	43	8	ADK23549 Human Abe
50	222	100.0	43	8	ADK23549 Human Abe
51	222	100.0	43	8	ADK23549 Human Abe
52	222	100.0	43	8	ADK23549 Human Abe
53	222	100.0	43	8	ADK23549 Human Abe
54	222	100.0	43	9	ADK23549 Human Abe
55	222	100.0	43	9	ADK23549 Human Abe
56	222	100.0	43	9	ADK23549 Human Abe
57	222	100.0	43	9	ADK23549 Human Abe
58	222	100.0	43	9	ADK23549 Human Abe
59	222	100.0	43	10	AEF42416 Beta-amyl
60	222	100.0	43	10	AEF92528 Amylophie
61	222	100.0	43	10	AEF92528 Amylophie
62	222	100.0	45	2	AAW64169 Human b
63	222	100.0	47	2	AAW81475 Synthetic
64	222	100.0	48	4	AAW37523 Amyloid p
65	222	100.0	48	9	ADZ77669 Human amy
66	222	100.0	52	2	AAW64166 Variant b
67	222	100.0	52	2	AAW81476 Synthetic
68	222	100.0	52	6	ABU08712 Amyloid b
69	222	100.0	52	6	ABP97924 Amino aci
70	222	100.0	52	6	ADA90299 Abeta ami
71	222	100.0	52	7	ADJ81404 Self-asse
72	222	100.0	52	7	ADJ81274 Self-asse
73	222	100.0	52	8	ADJ71599 APP770 pe
74	222	100.0	52	8	ADJ71599 APP770 pe
75	222	100.0	52	8	ADJ71599 APP770 pe
76	222	100.0	53	2	AAW55695 Sequence
77	222	100.0	53	2	AAW55695 Sequence
78	222	100.0	53	6	ABU08708 Amyloid b
79	222	100.0	53	6	ABU08708 Amyloid b
80	222	100.0	53	7	ADK23549 Human Abe
81	222	100.0	53	8	ADK23549 Human Abe
82	222	100.0	54	3	AAW32126 Amyloid-b
83	222	100.0	55	4	AAW11482 Human APP
84	222	100.0	55	4	AAW11482 Human APP
85	222	100.0	57	3	AAW10910 Human amy
86	222	100.0	59	2	AAW05375 Amyloid p
87	222	100.0	59	2	AAW05375 Amyloid p
88	222	100.0	59	2	AAW05375 Amyloid p
89	222	100.0	60	3	AAW69701 Beta-amyl
90	222	100.0	61	9	AAW69701 Beta-amyl
91	222	100.0	61	9	AAW69701 Beta-amyl
92	222	100.0	63	2	AAW42976 Beta-amyl
93	222	100.0	63	2	AAW42976 Beta-amyl
94	222	100.0	63	7	ADK23549 Human Abe
95	222	100.0	64	5	ADK23549 Human Abe
96	222	100.0	70	4	AAE09373 Human wil

97	222	100.0	70	4	AAE09374	Aae09374 Human APP
98	222	100.0	70	4	AAE09375	Aae09375 Human tru
99	222	100.0	70	4	AAU05015	Aau05015 Human amy
100	222	100.0	79	2	AAW53981	Aaw53981 Human ALZ

ALIGNMENTS

RESULT 1

AAAR54759 standard; peptide; 43 AA.
AC AAR54759;
XX
XX 25-MAR-2003 (revised)
DT 30-NOV-1994 (first entry)
XX
DE Beta amyloid peptide.
XX
KM Beta amyloid peptide; amyloid plaques; Alzheimer's disease; lesion;
KW brain; senility; dementia; detection; diagnosis.
XX
XX Homo sapiens.
OS
PN WO9410569-A1.
PD 11-MAY-1994.
XX
XX 01-SEP-1993; 93WO-US008264.
PF
XX 26-OCT-1992; 92US-00965972.
PR
XX
XX (SCHE/) SCHENK D B.
PA (SCHL/) SCHLOSSMACHER M G.
PA (SELK/) SELKOE D J.
PA (SEUB/) SEUBERT P A.
PA (VIGO/) VIGO-PELFREY C.
XX
XX Schenk DB, Schlossmacher MG, Selkoe DJ, Seubert PA;
PI Vigo-Pelfrey C;
XX
XX WPI; 1994-167654/20.
DR
XX
PT Detecting soluble beta-amyloid peptide concns. e.g. for diagnosing and
PT assessing progression of Alzheimer's disease - by exposing cultured cells
PT to test cpd. to determine effect of cpd. on produced soluble beta-amyloid
PT peptide.
XX
XX
PS Disclosure; Page 10; 55pp; English.
XX
XX Beta amyloid peptide is the principal chemical constituent of amyloid
CC plaques, lesions found on the brains of Alzheimer's disease patients. The
CC ability to detect beta amyloid peptide in fluid samples provides a means
CC of diagnosing Alzheimer's disease. (Updated on 25-MAR-2003 to correct PN
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 2
AAAR60367 standard; peptide; 43 AA.
ID

AC AAR60367;
XX
XX 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX
XX Beta-amyloid (1-43).
XX
XX
XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.
XX
XX Homo sapiens.
OS
PN WO9417197-A1.
PD 04-AUG-1994.
XX
XX 24-JAN-1994; 94WO-JP000089.
PF
XX
XX 25-JAN-1993; 93JP-00010132.
PR 05-FEB-1993; 93JP-00019035.
PR 16-NOV-1993; 93JP-00286985.
PR 28-DEC-1993; 93JP-00334773.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Suzuki N, Odaka A, Kitada C;
PI
XX
XX WPI; 1994-264110/32.
DR
XX
XX Antibodies recognising specific parts of beta-amyloid - can be used for
PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
PT disease.
XX
XX
XX Disclosure; Page 83; 116pp; Japanese.
PS
XX
XX Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclional) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
CC the C-terminal portion. The antibodies are useful for assaying beta-
CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
CC
XX (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 3
AAR61328 standard; protein; 43 AA.
ID
XX
XX AAR61328;
AC
XX
XX 25-MAR-2003 (revised)
DT 21-APR-1995 (first entry)
XX
XX Amyloid beta-protein, ABP.
DE
XX
XX Amyloid beta-protein; ABP; Tau-protein kinase I enzyme; TPK-I;
KW Alzheimer's disease.
XX
XX Synthetic.
OS
XX
XX EPI61032-A2.
PN
XX
XX 21-SEP-1994.
PD

Query Match	100.0%	Score 222;	DB 2;	Length 43;
Best Local Similarity	100.0%	Pred. No. 6.4e-25;		
Matches	43;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	DAEFRHDSGYEYHOKLVFPAEDVGSNKGATIGLWGGVLTAT	43	
Db	1	DAEFRHDSGYEYHOKLVFPAEDVGSNKGATIGLWGGVLTAT	43	

RESULT	5
ADD11650	
ID	ADD11650 standard; protein; 43 AA.
XX	
AC	ADD11650;
XX	
DT	01-JAN-2004 (first entry)
XX	

DE Human beta-amyloid 1-43 (betal-43).
XX
XX neurotoxic effect; beta-amyloid peptide; neurotoxicity inhibitor;
KW amyloidogenic amylin; beta-2-microglobulin; amylin; Alzheimer's disease;
KW Down's syndrome; beta-amyloid neurotoxicity assay; human;
KW beta-amyloid 1-43; betal-43.
XX
OS Homo sapiens.
XX
XX EP646792-A1.
PD 05-APR-1995.
XX
XX 17-AUG-1994; 94EP-00306053.
PF 19-AUG-1993; 93US-00109782.
PR
XX 19-AUG-1993; 93US-00109782.
XX
XX (ELIL) LILLY & CO ELI.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI May PC, Rydel RE;
XX
DR WPI, 1995-132760/18.
XX
PT Assay for effectiveness of agents used in the treatment of Alzheimer's
PT disease - by incubating potential inhibitor of neurotoxicity with amylin
PT or beta-2-microglobulin and measuring neurotoxic props. of mixt.
XX
PS Disclosure: SEQ ID NO 1; 14pp; English.

The invention describes a method for assaying the effectiveness of agents useful for accumulating the neurotoxic effects of a condition associated with the accumulation of a beta-amyloid peptide. The method comprises:
(a) incubating potential inhibitors of neurotoxicity with an amyloidogenic amylin or beta-2-microglobulin; (b) measuring the neurotoxic properties of each amylin or beta-2-microglobulin/potential inhibitor mixture; and (c) detecting reduction in the neurotoxicity relative to a control. The preferred amyloidogenic amylin is human amylin. The method is especially for assessing the ability of an agent to ameliorate the neurotoxic effects of Alzheimer's disease or Down's syndrome. The method provides a more consistent beta-amyloid neurotoxicity assay and is more sensitive and covers a broader range. This is the amino acid sequence of human beta-amyloid 1-43 (betal-43).

Sequence 43 AA;

Query Match	100.0%;	Score 222;	DB 2;	Length 43;
Best Local Similarity	100.0%;	Pred. No. 6.4e-25;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT	43	
Db	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT	43	
XX				
RESULT 6				
ID	AA95673			
AA95673	standard; peptide; 43 AA.			
XX				
AC	AA95673;			
XX				
DT	24-FEB-1997	(first entry)		
XX				
DE	A-beta protein (43 amino acid version).			
XX				
KM	A-beta protein; beta-amyloid precursor protein; APP; Alzheimer's disease;			
KW	diagnosis; monitor; amyloid plaque; senile.			
XX				
OS	Homo sapiens.			
PN	MO9615452-A1.			
PD				
XX				
PF	13-NOV-1995;	95WO-US014659.		
XX				
PR	14-NOV-1994;	94US-00339141.		
XX				
PR	07-APR-1995;	95US-00419008.		
XX				
PA	(ATHE-) ATHENA NEUROSCIENCES INC.			
XX				
PI	Seubert PA, Vigo-Pelfrey C, Schenk DB, Barbour R;			
XX				
DR	WPI: 1996-260003/26.			
XX				
PT	Diagnosis and monitoring of Alzheimer's disease - by detecting abnormally			
XX	low concentration of A-beta peptide extending beyond amino acid 41 in			
PT	cerebrospinal fluid.			
XX				
PS	Disclosure; Page 16; 57pp; English.			
XX				
CC	The "amyloid-beta peptide" or A-beta is an approx. 4.2 kD protein which,			
CC	in the brains of Alzheimer's disease, Down's Syndrome, HCHWA-D and some			
CC	normal aged subjects, forms the subunit of amyloid filaments comprising			
CC	the senile (amyloid) plaques and the amyloid deposits in small cerebral			
CC	and meningeal blood vessels. A-beta is an approx. 39-43 amino acid			
CC	fragment of a large membrane-spanning glycoprotein, referred to as the			
CC	beta-amyloid precursor protein (APP), encoded by a gene on the long arm			
CC	of human chromosome 21. Detecting the amt. of A-beta is useful in			
CC	diagnosis and monitoring of Alzheimer's disease, when taken together with			
CC	other clinical symptoms. The present sequence is a 43 amino acid version			
CC	of A-beta			
XX				
XX				
Sequence 43 AA;				
Query Match	100.0%;	Score 222;	DB 2;	Length 43;
Best Local Similarity	100.0%;	Pred. No. 6.4e-25;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT	43	
Db	1	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT	43	
XX				
RESULT 7				
ID	AAW93371			
AAW93371	standard; protein; 43 AA.			
XX				

AA93371;
28-MAY-1999 (first entry)
Human beta-amyloid polypeptide.
Cathepsin Y; human; beta-amyloid peptide; BAP; secretion; inhibitor; protease; carboxypeptidase; aliphatic C-terminal amino acid; diagnostic; glycoprotein; cerebral deposition; pathogenesis; Alzheimer's disease; detection; amyloid plaque; angiotensin; brain; Trisomy 21; amyloidosis; Down's syndrome; hereditary cerebral haemorrhage.
Homo sapiens.
MO9639194-A1.
12-DEC-1996.
26-APR-1996; 96WO-US006211.
06-JUN-1995; 95US-00467607.
06-JUN-1995; 95US-00469362.
(ATHE-) ATHENA NEUROSCIENCES INC.
Tung US, Sinha S, Mcconlogue L, Tatsuno G, Anderson J, Semko CMF; Chrysler S;
WPI, 1997-042872/04.
Acylamino and acyl-peptide; amino alcohol and aldehyde derivs. - inhibit beta-amyloid peptide prodn. in cells; use in Alzheimer's disease, also prepn. of cathepsin Y and nucleic acid encoding for it.
Disclosure; Page 11; 90pp; English.

CC also be used for expression of recombinant cathepsin Y, by transfection
 CC of a host cell
 XX
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43
 DB 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 8
 AAY17758
 ID AAY17758 standard; peptide; 43 AA.
 AC AAY17758;
 XX
 DT 10-AUG-1999 (first entry)
 XX
 DE Beta-amyloid peptide.
 XX
 KM Beta-amyloid peptide; beta-amyloid precursor protein; APP;
 XX membrane spanning glycoprotein; Alzheimer's disease.
 XX Homo sapiens.
 OS
 PN WO9822493-A2.
 XX
 PD 28-MAY-1998.
 XX
 PE 20-NOV-1997; 97WO-US018704.
 XX
 PR 22-NOV-1996; 96US-00755334.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 XX (ELIL) LILLY & CO ELI.
 PI Andia JE, Folmer BK, John V, Latimer LH, Nissen JS, Porter WJ;
 XX Thoresett ED, Wu J;
 DR WPI; 1998-322359/28.
 XX
 PT New and known aryl or hetero-aryl amino acid derivatives - useful for
 XX inhibiting beta-amyloid peptide release and/or its synthesis and treating
 PT Alzheimer's disease.
 XX
 PS Disclosure; Page 19; 131pp; English.
 XX
 CC The present invention describes a composition comprising an inert carrier
 CC and an N-(aryl or heteroaryl) amino acid derivative e.g. N-(N-(3,4-
 CC dichlorophenyl)alanine) valine methyl ester. The composition can be used
 CC for inhibiting beta-amyloid peptide release and/or its synthesis in a
 CC cell, for preventing the onset of Alzheimer's disease and for treating
 CC Alzheimer's disease in order to inhibit further deterioration. The dosage
 CC is 0.1-500 mg/kg/day orally, rectally, transdermally, subcutaneously or
 CC intravenously. The present sequence represents the beta-amyloid peptide
 XX
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43
 DB 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 9
 AAW51316

ID AAW51316 standard; peptide; 43 AA.

AC AAW51316;

DT 14-AUG-1998 (first entry)

DE Natural beta-amyloid peptide fragment.

KM Natural beta-amyloid peptide; aggregation; D-amino acid;
 KW Alzheimer's disease; beta-amyloidosis.

OS Homo sapiens.

PN WO9808868-A1.

PD 05-MAR-1998.

PE 27-AUG-1997; 97WO-US015166.

PR 27-AUG-1996; 96US-00703675.

PR 21-JUL-1997; 97US-00897342.

XX (PRAE-) PRAECIS PHARM INC.

PI Findeis MA, Geffter ML, Museo G, Signer ER, Wakefield J;
 PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
 PI Arico-Muendel CC, Phillips K, Hayward NJ;

DR WPI; 1998-216936/19.

XX

PT peptide compounds which are preferably based on beta-amyloid peptide(s) -
 PT are useful in treatment of disorders related to beta-amyloidosis,
 PT especially Alzheimer's disease.

XX

PS Disclosure; Page 8; 92pp; English.

XX The invention relates to peptides that modulate natural beta-amyloid

CC peptide aggregation. The modulators of the invention comprise a peptide

CC preferably based on a beta-amyloid peptide, that is comprised entirely of

CC D-amino acids. Preferably the peptide comprises 3-5 D-amino acid residues

CC and includes at least two D-amino acid residues independently selected

CC from the group consisting of D-leucine, D-phenylalanine and D-valine.

CC Preferred amino-terminal modifying groups include cyclic, heterocyclic,
 CC polycyclic and branched alkyl groups. Preferred carboxy-terminal

CC modifying groups include an amide group, an alkyl amide group, an aryl

CC amide group or a hydroxy group. The peptides may be used to treat

CC disorders associated with beta-amyloidosis, especially Alzheimer's

CC disease. They may also be used in methods for detecting the presence of

CC beta-amyloid peptides in biological samples. The present sequence

CC represents the 43 amino acid long form of natural beta-amyloid peptide

XX

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43
 DB 1 DAERHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 10
 AAY42955
 ID AAY42955 standard; protein; 43 AA.
 AC AAY42955;
 XX
 DT 02-JAN-2000 (first entry)
 XX
 DE Beta-amyloid precursor protein.
 DB Beta-amyloid precursor protein.
 XX
 KW Beta-amyloid precursor protein; APP; release inhibition;

KM Alzheimer's disease.
 XX Homo sapiens.
 OS US5965614-A.
 PN 12-OCT-1999.
 PD 21-NOV-1997; 97US-00975977.
 PE 22-NOV-1996; 96US-00755444.
 PR 22-NOV-1996; 96US-0104593P.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 PA Polymer BK, Audia JE, Latimer LH, Nissen JS, Reel JK, Thorsett ED;
 PI Whitehall CA, John V;
 XX WPI; 1998-348125/30.
 DR N-Aryl- and N-hetero-aryl-amino acid ester(s) and amidoxime ester(s) -
 PT are inhibitors of beta-amyloid peptide synthesis and/or release, used in
 PT treating Alzheimer's disease.
 PS Disclosure; Col 49; 29pp; English.
 XX New chemical compounds are disclosed which inhibit the cellular release
 CC and/or synthesis of beta-amyloid peptide (the present sequence). The
 CC compounds are N-(aryl or heteroaryl) amino acid ester derivatives, of
 CC which N-(3,4-dichlorophenyl)alanine ethyl ester is a specific example.
 CC These compounds can be used for the treatment and prevention of
 CC Alzheimer's disease
 XX Sequence 43 AA;
 SQ

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 11
 AAB21216
 ID AAB21216 standard; peptide; 43 AA.
 XX AAB21216;
 AC AAB21216;
 XX 11-JAN-2001 (first entry)
 DT Beta-amyloid peptide.
 DE Beta-amyloid peptide.
 XX Beta-amyloid peptide; membrane-spanning glycoprotein; analgesic;
 KM nicotinic agonist; beta-amyloid precursor protein; APP;
 KM Alzheimer's disease.
 XX Homo sapiens.
 OS US6117901-A.
 PN 12-SEP-2000.
 PD 21-NOV-1997; 97US-00976179.
 PF 22-NOV-1996; 96US-007554895.
 PR 22-NOV-1996; 96US-0098551P.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 PA (ELIT) Lilly & Co Eli.
 XX Thorsett ED, Nissen JS, Wu J, Latimer LH, John V, Fang LY;

PI Audia JE, Mabry TE;
 XX WPI; 1998-348123/30.
 DR New and use of substituted amino acid ester or thio-ester(s) - as
 PT inhibitors of beta-amyloid peptide release and/or synthesis used in the
 PT treatment and/or prevention of Alzheimer's disease.
 PS Disclosure; Col 11; 32pp; English.
 XX The present sequence is the beta-amyloid peptide, which is part of a
 CC large membrane-spanning glycoprotein, referred to as the beta-amyloid
 CC precursor protein (APP). Aryl substituted olefinic amine (metanilcotine)
 CC compounds which inhibit beta-amyloid peptide release and/or its synthesis
 CC may be useful for treating Alzheimer's disease, both prophylactically and
 CC therapeutically
 XX Sequence 43 AA;
 SQ

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 12
 AAW71378
 ID AAW71378 standard; peptide; 43 AA.
 XX AAW71378;
 AC AAW71378;
 XX 02-DEC-1998 (first entry)
 DT Beta-amyloid precursor protein epitope.
 DE Beta-amyloid precursor protein epitope.
 XX Beta amyloid precursor protein; eukaryotic cell line;
 KM exogenous gene construction; identification; quantification; inhibitor;
 KM beta-amyloid processing; treatment; Alzheimer's disease; brain trauma;
 KM Downs syndrome.
 XX Homo sapiens.
 OS WO9837215-A1.
 PN 27-AUG-1998.
 PD 03-FEB-1998; 98WO-US001899.
 PF 24-FEB-1997; 97US-00804971.
 PR 02-APR-1997; 97US-00825737.
 PR 31-JUL-1997; 97US-00904296.
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 PA (SCIO-) SCIOS INC.
 PI Cordell B, Scardina JM, Mischak RP, Huggins J, Pruss R;
 PI Rautmann G;
 XX WPI; 1998-495368/42.
 DR New eukaryotic cell lines - contain a gene construct containing a beta-
 PT amyloid precursor protein encoding sequence, used for identifying
 PT inhibitors of beta-amyloid processing.
 PS Disclosure; Fig 5; 82pp; English.
 XX The present sequence represents an epitope derived from a beta amyloid
 CC precursor protein, and recognised by antibodies BA#1, 108.1, 1702.1, and
 CC 1101.1. The specification describes an eukaryotic cell line having
 CC exogenous gene construction comprising a cytomegalovirus (CMV) promoter,

CC a strong ribosome binding site (RBS), a beta-amyloid precursor protein
 CC (BAP) nucleic acid sequence, a selectable marker, and a poly-adenylation
 CC signal. The products can be used for identifying or quantifying beta-
 CC amyloid protein and for identifying inhibitors of beta-amyloid
 CC processing. They can be used to develop products for treating
 CC amyloidosis, e.g. Alzheimer's disease, brain trauma or Down's syndrome
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 Db

RESULT 13
 AAM40129
 ID AAM40129 standard; peptide; 43 AA.

AC AAM40129;
 DT 03-JUN-1998 (first entry)
 XX Human amyloid-beta peptide.
 DE
 XX

KM Amyloid-beta peptide; A-beta; senile plaque; angiopathy; brain;
 KM membrane-spanning glycoprotein; beta-amyloid precursor protein; APP;
 KM chromosome 21; human; Alzheimer's disease; AD; amyloid filament;
 KM treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.

XX
 OS Homo sapiens.
 XX
 PN M09748983-A1.
 XX

PD 24-DEC-1997.

XX 18-JUN-1997; 97WO-US010601.

XX 18-JUN-1996; 96US-00665649.

PA (ATHE-) ATHENA NEUROSCIENCES INC.
 PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL.

PI Citron M, Selkoe DJ, Seubert PA, Schenk D;

DR WPI; 1998-063287/06.

PT Identifying compounds that alter cellular production of amyloid-beta 42
 PT fragment - in vitro or in transgenic animal models, potentially useful
 PT for treatment of Alzheimer's and other amyloid deposition diseases.

XX Disclosure; Page 15; 86pp; English.

CC This sequence represents a human amyloid-beta peptide (A-beta) which is a
 CC fragment of the of a large membrane-spanning glycoprotein referred to as
 CC the beta-amyloid precursor protein (APP) encoded by a gene on the long
 CC arm of chromosome 21. This peptide is also known as the beta-AP peptide
 CC and forms the subunit of the amyloid filaments comprising senile
 CC (amyloid) plaques and the amyloid deposits in small cerebral and
 CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be a
 CC 39-43 amino acid fragment. This invention provides methods of screening
 CC compounds for their ability to alter the production of the A-beta
 CC peptide, which is composed of >41 amino acids, alone, or in combination
 CC with the A-beta peptide composed of 40 amino acids or less. Such agents
 CC that reduce the production of the A-beta peptide are potentially useful
 CC for treatment of Alzheimer's disease or other diseases involving amyloid
 CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with
 CC amyloidosis of Dutch type and advanced aging of the brain
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 Db

RESULT 14
 AAM89362
 ID AAM89362 standard; peptide; 43 AA.

AC AAM89362;
 DT 02-MAR-1999 (first entry)
 XX Beta-amyloid peptide derivative A-beta-1-43.
 DE
 XX

KM Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KM familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KM Creutzfeldt-Jakob disease; BAP.

XX Homo sapiens.
 OS Synthetic.
 OS

PN US5854204-A.

PD 29-DEC-1998.

XX 14-MAR-1996; 96US-00612785.

XX 14-MAR-1995; 95US-00404831.

PR 07-JUN-1995; 95US-00475579.

PR 27-OCT-1995; 95US-00548998.

XX (PRAE-) PRAECIS PHARM INC.

XX Hundal A, Gefter ML, Kaeman L, Musso G, Molineaux S, Benjamin H;

PI Findex MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;

PI Garnick MB, Kudasek W, Signer ER;

DR WPI; 1999-094964/08.

XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 PT aggregation - and neurotoxicity, specifically for treatment and
 PT prevention of Alzheimer's disease.

XX Example 1; Col 46; 52pp; English.

CC The present invention describes beta-amyloid peptide (BAP) derivatives.
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
 CC even when BAP is present in molar excess. The present sequence represents
 CC a BAP derivative
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
 Db

RESULT 15
 AAY88390
 ID AAY88390 standard; protein; 43 AA.
 XX
 AC AAY88390;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE Beta-amyloid peptide amino acid sequence.
 XX
 KM Beta-amyloid peptide; Alzheimer's disease; inhibitor; treatment.
 XX
 OS Unidentified.
 XX
 PN WO200019210-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US022684.
 XX
 PR 30-SEP-1998; 98US-0160082P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 PA (ELIL) LILLY & CO ELI.
 PI Audia JE, Hyslop PA, Nissen JS, Thompson RC, Tung JS, Tanner LI;
 XX
 DR WPI; 2000-328743/28.
 XX
 PT New reagents which bind factors involved in production of beta-amyloid
 PT peptide, useful for developing drugs for use in treatment of Alzheimer's
 PT disease.
 XX
 PS Disclosure; Page 14-15; 86pp; English.
 XX
 CC This amino acid sequence represents the beta-amyloid peptide, which is a
 CC fragment of the larger amyloid precursor protein (APP). Brains of
 CC patients with Alzheimer's disease have characteristic lesions termed
 CC senile or amyloid plaques, the principle constituent of which is the beta
 CC -amyloid peptide. The invention relates to biological reagents which
 CC inhibit beta-amyloid release and/or its synthesis. The reagents can be
 CC used to determine the cellular mechanism involved in the generation of
 CC the beta-amyloid peptide. The compounds can also be used to identify
 CC cells which express a cellular agent, such as peptides or proteins
 CC involved with beta-amyloid peptide release and/or its synthesis. Such
 CC methods can be used to provide drug design for agents which target
 CC Alzheimer's disease
 CC
 XX
 SQ Sequence 43 AA;
 Query Match 100.0%; Score 222; DB 3; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIAT 43
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIAT 43
 ||||||||||||||||||||||||||||||||||||||||
 RESULT 16
 AAY56102
 ID AAY56102 standard; peptide; 43 AA.
 XX
 AC AAY56102;
 XX
 DT 04-FEB-2000 (first entry)
 XX
 DE Natural beta amyloid peptide 43 amino acid sequence.
 XX
 KM Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
 KM retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
 XX

KM Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
 KM amyloidosis-Dutch-type.
 XX
 OS Homo sapiens.
 XX
 PN US5985242-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 27-AUG-1997; 97US-00920162.
 XX
 PR 27-OCT-1995; 95US-00548998.
 PR 14-MAR-1996; 96US-00616081.
 PR 27-AUG-1996; 96US-00703675.
 PR 21-JUL-1997; 97US-00897342.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
 PI Musso G, Phillips K, Hayward NJ, Getter ML, Findels MA, Lee J;
 PI Arico-Muendel CC, Chin J;
 XX
 DR WPI; 2000-022266/02.
 XX
 PT Compound comprising a peptidic structure, an amino-terminal modifying
 PT group and a carboxy-terminal modifying group, useful for treating
 PT Alzheimer's disease.
 XX
 PS Disclosure; Col 6; 40pp; English.
 XX
 CC The present invention describes a compound of formula A-(Xaa)-B,
 CC comprising a peptidic structure (Xaa), an amino-terminal modifying group
 CC (A), and a carboxy-terminal modifying group (B). AAY49973 to AAY49994
 CC represent specifically claimed examples of (Xaa). Also described is a
 CC method for inhibiting aggregation of natural beta-amyloid peptides and
 CC treating Alzheimer's disease, comprising contacting the amyloid peptides
 CC with A-(Xaa)-B; and a method for detecting the presence of natural beta-
 CC amyloid peptides in a biological sample by contacting with A-(Xaa)-B. The
 CC compound is useful for treating Alzheimer's disease and for detecting the
 CC presence of natural beta-amyloid peptides in a biological sample. The
 CC compound can also be used prophylactically or therapeutically to treat
 CC other clinical occurrences of beta-amyloid deposition, such as in Down's
 CC syndrome individuals and in patients with hereditary cerebral haemorrhage
 CC with amyloidosis-Dutch-type (HCHWA-D). The present sequence represents
 CC the 43 amino acid long form of the natural beta amyloid peptide from the
 CC present invention
 CC
 XX
 SQ Sequence 43 AA;
 Query Match 100.0%; Score 222; DB 3; Length 43;
 Best Local Similarity 100.0%; Pred. No. 6,4e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIAT 43
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIAT 43
 ||||||||||||||||||||||||||||||||||||||||
 RESULT 17
 AAB27020
 ID AAB27020 standard; protein; 43 AA.
 XX
 AC AAB27020;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Beta-amyloid peptide.
 XX
 KM Beta-amyloid peptide; neurotropic; neuroprotective; Alzheimer's disease.
 KM Unidentified.
 XX
 PN WO200052048-A1.

XX 08-SEP-2000.
PD 03-MAR-2000; 2000WO-US005574.
XX 04-MAR-1999; 99US-0122736P.
XX (PRAE-) PRAECIS PHARM INC.
PI Findels MA, Phillips K, Olson GL, Self C;
XX WPI; 2000-594168/56.
DR WPI; 2000-594168/56.
XX Novel compounds that are useful as modulators of beta-amyloid peptide
PT aggregation in treating amyloidosis, comprises D-amino acids.
XX
XX Disclosure; Page 9; 87pp; English.
XX
XX The present sequence is beta-amyloid peptide. The present invention
CC relates to peptides (see AAB27023-B27046) that modulate beta-amyloid
CC peptide aggregation, and hence inhibit the neurotoxicity of beta-amyloid
CC peptide. The beta-amyloid peptide modulators would be useful for treating
CC disorders associated with beta-amyloidosis for e.g. Alzheimer's disease.
CC The present sequence is derived from amyloid precursor protein via
CC proteolysis. The gene for amyloid precursor protein maps to chromosome 21
XX

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 18

AAB15372
ID AAB15372 standard; peptide; 43 AA.

XX AAB15372;

DT 17-JAN-2001 (first entry)

XX Human beta-amyloid precursor protein A-beta fragment.

XX Human; beta-amyloid precursor protein; beta-APP; Alzheimer's disease;

KW chromosome 21; epitope.

XX Homo sapiens.

XX WO200042166-A2.

XX 20-JUL-2000.

PD 13-JAN-2000; 2000WO-US000872.

XX 13-JAN-1999; 99US-0115749P.

XX (DUPO) DUPONT PHARM CO.

XX Seiffert DA, Mitchell TJ;

XX WPI; 2000-476049/41.

XX A CDNA construct that encodes beta-amyloid precursor protein for
PT identifying compounds which inhibit A-beta peptide release and/or
PT synthesis comprises an epitope tag within the A-beta sequence.
XX Disclosure; Page 13-14; 42pp; English.

XX The present sequence is A-beta fragment of the human beta-amyloid

CC precursor protein (beta-APP). It was used in the production of peptides
CC of the invention. The invention concerns the production, detection and
CC characterisation of epitope-tagged beta-APP proteins, and their use in
CC identifying modulators of beta-APP which can be used to treat diseases
CC associated with an altered metabolism of the protein, in particular
CC Alzheimer's disease

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 19

ABB07901
ID ABB07901 standard; protein; 43 AA.

XX ABB07901;

DT 30-JUL-2002 (first entry)

XX Beta-amyloid peptide (Abeta) sequence.

XX Abeta peptide; lactam; amyloid precursor protein; APP; beta-amyloid;

KW neuroprotective; nootropic; cerebroprotective; gamma-secretase;

XX Alzheimer's disease; Down's syndrome.

XX Unidentified.

XX WO200174784-A1.

XX 11-OCT-2001.

PD 03-APR-2001; 2001WO-US010773.

XX 03-APR-2000; 2000US-0194302P.

XX (DUPO) DUPONT PHARM CO.

XX Yang MG, Liu H;

XX WPI; 2001-626367/72.

XX New cyclic lactam compounds are gamma-secretase inhibitors, useful for
PT treating neurological disorders associated with beta-amyloid production
PT e.g. Alzheimer's disease and Down's syndrome.

XX Disclosure; Page 62; 16pp; English.

XX The invention relates to cyclic lactam compounds of specified formula.

XX These novel compounds inhibit the processing of amyloid precursor protein

CC (APP), more specifically inhibit the production of beta-amyloid (Abeta)

CC peptide. The compounds are useful in treatment of neurological disorders

CC associated with beta-amyloid production e.g. Alzheimer's disease and

CC Down's syndrome. The present sequence represents the beta-amyloid (Abeta)

XX peptide sequence

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

```
RESULT 20
AAB84428
ID AAB84428 standard; peptide; 43 AA.
XX
AC AAB84428;
XX
DT 22-AUG-2001 (first entry)
XX
DE Partial sequence of a human beta-amyloid precursor protein.
XX
KM Beta-amyloid precursor protein; APP, chimeric peptide; B cell epitope;
KM vaccine.
XX
OS Homo sapiens.
XX
PN MO200142306-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033203.
XX
PR 08-DEC-1999; 99US-0169687P.
XX
PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
XX
PI Chain B;
XX
DR WPI; 2001-381648/40.
XX
PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
PT epitope from naturally occurring internal peptide cleavage product (such
PT as beta amyloid peptide) of a precursor protein, joined to T cell
PT epitope.
XX
PS Claim 3; Page 42; 47pp; English.
XX
CC The present sequence represents a partial sequence of a human beta-
CC amyloid precursor protein (APP). The peptide is used to create chimeric
CC peptides of the invention. The chimeric peptides contain a N- or C-
CC terminal end-specific B cell epitope from a naturally occurring internal
CC peptide cleavage product of a precursor or mature protein, as a free N-
CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
CC reduce or prevent the accumulation of amyloid beta peptide in the
CC extracellular space, interstitial fluid and cerebrospinal fluid of the
CC brain, and aggregation into senile amyloid deposits or plaques. They also
CC block the interaction of amyloid beta peptides with other molecules that
CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
CC useful for immunizing humans against the free N- or C-terminus of an
CC internal self peptide cleavage product (e.g. APP peptide) derived from a
CC precursor protein or a mature protein. The internal peptide cleavage
CC product is the self molecule of the mammal
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
RESULT 21
AAB91811
ID AAB91811 standard; peptide; 43 AA.
XX
AC AAB91811;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:987.
```

```
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 517; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
RESULT 22
AAB91778
ID AAB91778 standard; peptide; 43 AA.
XX
AC AAB91778;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:954.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidy; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
```

OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX
XX PF 17-MAY-2000; 2000WO-US013576.
XX
XX PR 17-MAY-1999; 99US-0134406P.
XX PR 10-SEP-1999; 99US-0134406P.
XX PR 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity.
XX
XX PS Disclosure; Page 505; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity in
XX vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specifically as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention
XX
XX SQ Sequence 43 AA;
XX
XX Query Match 100.0%; Score 222; DB 4; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-25;
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
XX 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
XX
XX Db
XX
XX RESULT 23
XX AAG78791
XX ID AAG78791 standard; protein; 43 AA.
XX
XX AC AAG78791;
XX
XX DT 15-JAN-2002 (first entry)
XX
XX DE Human beta amyloid protein.
XX
XX Human, beta amyloid; Alzheimer's disease; cyclic malonamide; nootropic;
XX neurotoxic deposit; Down's syndrome; cyclic lactam; neuroprotective;
XX cerebroprotective.
XX
XX OS Homo sapiens.
XX
XX PN WO200174783-A1.
XX
XX PD 11-OCT-2001.
XX
XX PF 03-APR-2001; 2001WO-US010657.

XX 03-APR-2000; 2000US-0194503P.
XX
XX PA (DUPO) DUPONT PHARM CO.
XX
XX FI Olson RE, Yang MG;
XX WPI; 2001-639338/73.
XX
XX DR WPI; 2001-639338/73.
XX
XX New cyclic lactam compounds are gamma-secretase inhibitors, useful for
XX treating neurological disorders associated with beta-amyloid production
XX e.g. Alzheimer's disease and Down's syndrome.
XX
XX PS Disclosure; Page 98; 245pp; English.
XX
XX The present invention relates to novel cyclic lactam compounds, more
XX specifically malonamides, which are capable of inhibiting the processing
XX of amyloid precursor protein, thus preventing the formation of amyloid
XX beta deposits. They can be used in the treatment of neurological
XX disorders such as Alzheimer's disease and Down's syndrome. The present
XX sequence is the beta amyloid protein
XX
XX SQ Sequence 43 AA;
XX
XX Query Match 100.0%; Score 222; DB 4; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-25;
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
XX 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
XX
XX Db
XX
XX RESULT 24
XX AAB48344
XX ID AAB48344 standard; peptide; 43 AA.
XX
XX AC AAB48344;
XX
XX DT 20-APR-2001 (first entry)
XX
XX DE Beta-amyloid peptide (Abeta1-43).
XX
XX Beta-amyloid; nootropic; neuroprotective; vaccine; antibody; brain;
XX amyloid plaque; Alzheimer's disease; antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO200077178-A1.
XX
XX PD 21-DEC-2000.
XX
XX PF 15-JUN-2000; 2000WO-US016551.
XX
XX PR 16-JUN-1999; 99US-0139408P.
XX
XX PA (BOST-) BOSTON BIOMEDICAL RES INST.
XX
XX RA Rao V;
XX
XX WPI; 2001-112220/12.
XX
XX New antibodies which catalyze hydrolysis of beta-amyloid at a
XX predetermined amide linkage, useful for e.g. sequestering or reducing
XX free beta-amyloid in the bloodstream and brain and preventing formation
XX of amyloid plaques.
XX
XX PS Example 1; Fig 1; 82pp; English.
XX
XX The invention relates to an antibody which catalyzes the hydrolysis of
XX beta-amyloid at a predetermined amide linkage. The antibodies are useful
XX for sequestering free beta-amyloid in the bloodstream of an animal,
XX reducing beta-amyloid levels in the brain, preventing formation of

CC amyloid plaques, and disaggregating amyloid plaques present in the brain,
CC thus may be used in treating patients diagnosed with or at risk for
CC Alzheimer's disease. The present sequence represents a beta-amyloid
CC peptide sequence from which antigenic peptides were designed to be tested
CC for suitability to antibody-mediated therapy

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
Db

RESULT 25
AAB81193
ID AAB81193 standard; peptide; 43 AA.

XX AAB81193;

XX 23-JUL-2001 (first entry)

XX Beta-amyloid peptide.

XX Amino lactam sulfonylamides; neuroprotective; cerebroprotective; nootropic;
KW Abeta; beta-amyloid; Beta/A4; amyloid plaque; Alzheimer's disease;
KW Down's syndrome; gamma-secretase inhibitor; cerebrovascular disorder;
KW neurological disorder.

XX OS Unidentified.

XX WO200127091-A1.

XX 19-APR-2001.

XX 07-OCT-2000; 2000WO-US027665.

XX 08-OCT-1999; 99US-0158565P.

XX (DUPO) DU PONT PHARM CO.

XX Thompson LA;

XX WPI; 2001-328423/34.

XX New amino lactam sulfonylamides, useful as inhibitors of Abeta peptide
PT production and gamma secretase activity for treating neurological
PT disorders including Alzheimer's disease and Down's syndrome.

XX Disclosure; Page 53; 161pp; English.

XX This invention relates to amino lactam sulfonylamides, their salts and
CC prodrugs. Pharmaceutical compositions containing the amino lactam
CC sulfonylamides have neuroprotective, cerebroprotective, and nootropic
CC activity. The present sequence represents the beta amyloid peptide (also
CC referred to as Abeta or Beta/A4), which is found in amyloid plaques
CC associated with Alzheimer's disease. The novel lactams of the invention
CC inhibit the processing of amyloid precursor protein, and more
CC specifically, are inhibitors of the production of Abeta-peptide, thereby
CC preventing the formation of neurological deposits of amyloid protein. The
CC lactams are also inhibitors of gamma-secretase activity. The amino lactam
CC sulfonylamides can be used for treating neurological disorders and
CC Alzheimer's disease especially associated with Abeta amyloid production;
CC and for inhibiting gamma-secretase activity. The lactams may also be used
CC in the treatment of Down's syndrome and cerebrovascular disorders

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
Db

RESULT 26
AAB98986
ID AAB98986 standard; protein; 43 AA.

XX AAB98986;

XX 20-AUG-2001 (first entry)

XX Beta-amyloid peptide.

XX Beta-amyloid peptide; amyloid precursor protein; APP; beta amino acid;
KW Alzheimer's disease.

XX Homo sapiens.

XX WO200134571-A1.

XX 17-MAY-2001.

XX 26-OCT-2000; 2000WO-US026278.

XX 09-NOV-1999; 99US-0164399P.

XX (EHL) LILLY & CO ELI.

XX Audia JE, Porter WJ, Scott WL, Stack DR, Thompson RC;

XX WPI; 2001-343586/36.

XX New beta-aminoacid derivatives are approximately-b-amyloid peptide release
PT and/or synthesis inhibitors useful for preventing or treating Alzheimer's
PT disease.

XX Disclosure; Page 8; 70pp; English.

XX The present invention provides a number of beta-amino acid derivatives
CC which can be used to inhibit beta-amyloid peptide release or synthesis.
CC Beta-amyloid peptide is a fragment of the amyloid precursor protein and
CC is found deposited in the brains of patients with Alzheimer's disease.
CC The compounds of the invention can thus be used in the prevention and
CC treatment of Alzheimer's disease. The present sequence is the beta-
CC amyloid peptide

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
Db

RESULT 27
AAB47108
ID AAB47108 standard; peptide; 43 AA.

XX AAB47108;

XX 04-JUN-2001 (first entry)

XX Biotinylated beta-amyloid peptide.

XX Human; prion protein; plaque forming disease; display vehicle; kuru;
KW aggregating protein; amyloid plaque; brain; early onset; senility;

KW	Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis;
KM	hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD;
KX	bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FFI;
KV	Gerstmann-Strausler-Sheinker Disease; GSS; fatal familial insomnia.
XX	
OS	Synthetic.
PX	
PN	WO200118169-A2.
PD	
PD	15-MAR-2001.
XX	
PF	31-AUG-2000; 2000WO-IL000518.
PR	03-SEP-1999; 99US-0152417P.
PR	29-DEC-1999; 99US-00473653.
PR	31-JUL-2000; 2000US-00629971.
XX	
PA	(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PI	
PI	Solomon B, Frenkel D, Hanan E;
DR	WPI; 2001-244564/25.
XX	
PT	Treating amyloidogenic disease such as Alzheimer's disease, BSE or CJD
PT	comprises presentation of plaque derived antigens or epitopes on a
XX	display vehicle, and introducing the vehicle into the recipient.
PS	
PS	Example; Page 116; 120pp; English.
CC	This peptide represents beta amyloid peptide. Fragments of this peptide
CC	may be used in the method of the invention. The invention provides an
CC	agent for treating a plaque forming disease. The polypeptide is displayed
CC	on a display vehicle and is capable of eliciting antibodies capable of
CC	disaggregating the aggregating protein and/or of preventing aggregation
CC	of the aggregating protein. This reduces formation of amyloid plaques in
CC	the brain of victims of plaque forming diseases, e.g. early onset
CC	Alzheimer's disease, late onset Alzheimer's disease, pre-symptomatic
CC	Alzheimer's disease, SAA amyloidosis, hereditary Icelandic syndrome,
CC	senility, multiple myeloma, scrapie, bovine spongiform encephalopathy
CC	(BSE), kuru, Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strausler-
CC	Sheinker Disease (GSS) and fatal familial insomnia (FFI)
XX	
SQ	Sequence 43 AA;
Query Match	100.0%; Score 222; DB 4; Length 43;
Best Local Similarity	100.0%; Pred. No. 6.4e-25;
Matches 43; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 DAEFRHDSGYEVHHOKLVFPAEDVGSNNKGAIIGLWVGVIAT 43 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNNKGAIIGLWVGVIAT 43
Db	1 DAEFRHDSGYEVHHOKLVFPAEDVGSNNKGAIIGLWVGVIAT 43
RESULT 28	
ID	AAE12508
XX	AAE12508 standard; peptide; 43 AA.
AC	AAE12508;
DT	
DT	03-JAN-2002 (first entry)
DE	Beta-amyloid peptide (AP) of beta-amyloid precursor protein (APP-770).
KM	Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis;
KM	Alzheimer's disease; neuroprotective; beta-amyloid precursor protein;
XX	APP-770; nootropic.
OS	Unidentified.
XX	
FN	US6277826-B1.
XX	
PD	21-AUG-2001.
XX	

PF	19-JUL-1999;	99US-00356931.
PX	27-AUG-1996;	96US-00703675.
PR	27-AUG-1997;	97US-00920162.
PX		
PA	(PRAE-) PRAECIS PHARM INC.	
PX		
PI	Pindeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;	
PI	Molineux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;	
PI	Arico-Muendel CC, Phillips K, Hayward NJ;	
XX		
DR	WPI, 2001-637856/73.	
XX		
PT	Modulator compound for treating disorders associated with beta-	
PT	amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid peptide	
PT	containing D-amino acids.	
XX		
PS	Example 11; Col 6; 41pp; English.	
XX		
CC	The patent discloses compounds and pharmaceutical compositions thereof,	
CC	that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide),	
CC	modulate the aggregation of natural beta-AP and/or inhibit the cyto-	
CC	toxicity of natural beta-APs. The beta-amyloid modulator compounds of the	
CC	invention comprise a peptide, preferably based on beta-AP, that is	
CC	composed entirely of D-amino acids. The modulators of the invention are	
CC	useful for treating a disorder associated with beta-amyloidosis such as	
CC	Alzheimer's disease. The present sequence is a natural beta-amyloid	
CC	peptide of beta amyloid precursor protein (APP-770)	
XX		
SQ	Sequence 43 AA;	
	Query Match	100.0%; Score 222; DB 4; Length 43;
	Best Local Similarity	100.0%; Pred. No. 6,4e-25;
	Matches	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 DAERHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVAT 43	
DB	1 DAERHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVAT 43	
RESULT 29		
ABB98516		
ID	ABB98516 standard; protein; 43 AA.	
XX		
AC	ABB98516;	
XX		
DT	25-NOV-2002 (first entry)	
XX		
DE	Human beta-amyloid precursor protein, APP.	
XX		
KM	Human; tau; neurotropic; neuroprotective; antiparkinsonian; amyloid plaque;	
KM	Alzheimer's disease; dementia; neurodegenerative disease; Pick's disease;	
KM	Progressive Supranuclear Palsy; Corticobasal Degeneration;	
KM	Down's Syndrome; Frontotemporal dementia; Parkinson's disease;	
KM	beta-amyloid precursor protein; APP; A-beta peptide.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Region	1..43
FT	/note=	"This sequence is specifically claimed in Claim 9"
FT	Region	1..42
FT	/note=	"This region is specifically claimed in Claim 8"
FT	Region	1..41
FT	/note=	"This region is specifically claimed in Claim 7"
FT	Region	1..40
FT	/note=	"This region is specifically claimed in Claim 6"
FT	Region	1..39
FT	/note=	"This region is specifically claimed in Claim 5"
XX		
FN	EPI234835-A2.	
XX		
XX	28-AUG-2002.	

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XX 18-FEB-2002; 2002EP-00251083.
PF 23-FEB-2001; 2001US-0271102P.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Rank KB, Sharma SK;
XX WPI; 2002-668446/72.
XX
XX A method for identifying agents that are inhibitors of tau-beta amyloid
PT complex formation useful for discovering agents potentially useful in the
PT treatment and prevention of neurodegenerative diseases.
XX
XX Claim 9; Page 6; 34pp; English.
XX
XX The present sequence is human beta-amyloid precursor protein, APP, also
CC known as A-beta peptide. In Alzheimer's disease (AD), A-beta peptide and
CC hyperphosphorylated tau are found in amyloid plaques and neurofibrillary
CC tangles respectively. This sequence was used in the method of the
CC invention, which is for identifying agents that are inhibitors of tau-
CC beta amyloid complex formation. The method comprises: (a) contacting a
CC tau protein-derived polypeptide and an aggregated beta-amyloid peptide in
CC the presence and absence of a test compound; and (b) determining and
CC comparing the respective amounts of tau-beta amyloid complex formed in
CC the presence and absence of the test agent, where a test agent which
CC decreases the amount of tau-beta amyloid complex formed is an inhibitor.
CC The method of the invention is useful for discovering agents potentially
CC useful in the treatment and prevention of neurodegenerative diseases,
CC including Alzheimer's disease, Progressive Supranuclear Palsy,
CC Corticobasal Degeneration, Down's Syndrome, Frontotemporal dementia,
CC Parkinsons, and Pick's Disease
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
RESULT 30
ABG71001
ID ABG71001 standard; protein; 43 AA.
XX
AC ABG71001;
XX
DT 05-DEC-2002 (first entry)
XX
XX Natural long form beta-amyloid protein.
XX
XX Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
XX familial amyloid polynuropathy; familial amyloid cardiomyopathy;
XX isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
XX bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
XX adult onset diabetes; Gestmann-Straussler-Scheinker syndrome;
XX insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
XX macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
XX primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
XX hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
XX hereditary non-neuropathic systemic amyloidosis;
XX familial Mediterranean Fever.
XX Homo sapiens.
XX
XX US2002098173-A1.
XX
XX 25-JUL-2002.
XX

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PF 04-OCT-2001; 2001US-00972475.
XX 14-MAR-1995; 95US-00404831.
XX 07-JUN-1995; 95US-00475579.
PR 27-OCT-1995; 95US-00548898.
PR 14-MAR-1996; 96US-00617267.
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Benjamin H, Garnick MB, Gelfer ML, Hundal A;
PI Kaaman L, Musco G, Signer ER, Wakefield J, Reed MJ;
XX WPI; 2002-697709/75.
XX
XX Amyloid modulator useful for treating a disorder associated with
PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
PT coupled to a modifying group.
XX
XX Example 1; Page 5; 41pp; English.
XX
XX The invention describes an amyloid modulator comprising an amyloidogenic
CC protein and/or peptide fragment coupled to a modifying group so that the
CC compound modulates the aggregation of natural amyloid proteins or
CC peptides. The modulator is used for treating a disorder associated with
CC amyloidosis e.g. familial amyloid polynuropathy (Portuguese, Japanese
CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
CC diabetes, Gestmann-Straussler-Scheinker syndrome, insulinoma, isolated
CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
CC nodular amyloidosis associated with Sjogren's syndrome, reactive
CC (secondary) amyloidosis, familial Mediterranean Fever and familial
CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
CC amyloidosis associated with long term haemodialysis, hereditary non-
CC neuropathic systemic amyloidosis (familial amyloid polynuropathy III),
CC familial amyloidosis of Finnish type, amyloidosis associated with
CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
CC renal amyloidosis and lysosome-associated hereditary systemic
CC amyloidosis. The compound is capable of altering and inhibiting beta-
CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents the long form of
CC natural beta-amyloid
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

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Search completed: September 28, 2006, 06:10:48
 Job time : 119.924 secs

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OW protein - protein search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 17.7399 Seconds
(without alignments)
233.221 Million cell updates/sec

Title: US-09-731-899-4
Perfect score: 222
Sequence: 1 DAEPFHDSGVHGHQKLVFF.....VGSNKGAIIIGMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	57	2 A60045	Alzheimer's disease
2	222	100.0	57	2 F60045	Alzheimer's disease
3	222	100.0	57	2 D60045	Alzheimer's disease
4	222	100.0	57	2 B60045	Alzheimer's disease
5	222	100.0	57	2 G60045	Alzheimer's disease
6	222	100.0	57	2 B60045	Alzheimer's disease
7	222	100.0	82	2 P00438	Alzheimer's disease
8	222	100.0	695	1 A49795	Alzheimer's disease
9	222	100.0	770	1 Q0R0U4	Alzheimer's disease
10	217	97.7	42	2 PN0512	Alzheimer's disease
11	203	91.4	695	2 A27485	Alzheimer's disease
12	203	91.4	695	2 S00550	Alzheimer's disease
13	203	91.4	747	2 JH0773	Alzheimer's disease
14	133	59.9	33	2 S23094	Alzheimer's disease
15	64	28.8	755	2 A13228	Alzheimer's disease
16	62	27.9	755	1 O0AGWT	Alzheimer's disease
17	62	27.9	755	1 O0AGWT	Alzheimer's disease
18	57	25.7	327	2 S73843	Alzheimer's disease
19	57	25.7	327	2 S73843	Alzheimer's disease
20	56.5	25.5	378	2 S61992	Alzheimer's disease
21	55.5	25.0	297	2 G69525	Alzheimer's disease
22	55.5	25.0	621	2 AF3016	Alzheimer's disease
23	55.5	25.0	642	2 B98268	Alzheimer's disease
24	55.5	25.0	678	2 G71526	Alzheimer's disease
25	55	24.8	291	2 F95015	Alzheimer's disease
26	55	24.8	317	2 H97888	Alzheimer's disease
27	55	24.8	488	2 S27652	Alzheimer's disease
28	55	24.8	738	2 C95936	Alzheimer's disease
29	55	24.8	3063	2 J50166	Alzheimer's disease

30	54.5	24.5	678	2 C81683	3-methyl-2-oxobuta
31	54.5	24.5	832	2 H84848	phospholipase D (1
32	54.5	24.3	77	2 C97027	feoa-like protein,
33	54	24.3	284	2 S04723	genome polypeptide
34	54	24.3	316	2 D97865	hypothetical prote
35	54	24.3	322	2 E71647	hypothetical prote
36	54	24.3	763	2 A13443	Na+/H+ antiporter
37	53.5	24.1	245	2 A11098	a probable phospho
38	53.5	24.1	245	2 AG1461	probable phospho-b
39	53.5	24.1	708	2 T24727	hypothetical prote
40	53.5	24.1	971	2 D70128	conserved hypothet
41	53	23.9	256	2 G96774	hypothetical prote
42	53	23.9	390	2 C75103	na+/h+ antiporter
43	53	23.9	422	2 D72302	hypothetical prote
44	53	23.9	601	2 T02581	nodulin-like prote
45	53	23.9	1555	2 J70959	polypeptide - pote
46	52.5	23.6	314	2 P86805	cation transporter
47	52.5	23.6	678	2 C66495	hypothetical prote
48	52.5	23.6	678	2 H72128	3-methyl-2-oxobuta
49	52.5	23.4	272	2 F70979	hypothetical prote
50	52	23.4	339	2 A81351	signal transductio
51	52	23.4	417	2 F70132	conserved hypothet
52	52	23.4	527	2 T18232	conserved hypothet
53	52	23.4	611	2 S19434	probable transport
54	51.5	23.2	1036	2 T18530	phospholipase D (E
55	51.5	23.2	1068	2 T48756	mitochondrial, nico
56	51.5	23.2	1364	2 T51920	probable xanthine
57	51	23.0	103	2 D75449	SAGE protein - Del
58	51	23.0	257	2 ACl024	probable dimethyl
59	51	23.0	494	2 C70940	probable cobq prot
60	51	23.0	763	2 A49321	amyloid beta (A4)
61	51	23.0	769	1 JC1121	leukocyte adhesio
62	50.5	22.7	165	2 H90519	ABC transporter at
63	50.5	22.7	292	2 H87260	asparaginase faml
64	50.5	22.7	519	2 PCl072	nuclear inclusion
65	50.5	22.7	833	2 T01547	probable phospholi
66	50.5	22.7	1014	2 T17275	hypothetical prote
67	50.5	22.7	1345	2 S55659	legume protein 7
68	50	22.5	234	2 G95989	hypothetical glyci
69	50	22.5	263	2 H85376	hypothetical prote
70	50	22.5	263	2 T04634	hypothetical prote
71	50	22.5	285	1 B64105	naphthoate synthas
72	50	22.5	296	2 A69856	polyubiquitin
73	50	22.5	390	2 H71083	probable Na+/H+-ex
74	50	22.5	441	2 T31482	hypothetical prote
75	50	22.5	487	2 T49424	hypothetical prote
76	50	22.5	674	2 S39476	kinase-like trans
77	50	22.5	946	1 JC5667	multidrug resistanc
78	50	22.5	1286	2 T02187	probable ABC trans
79	50	22.5	1292	2 T48007	P-glycoprotein hom
80	50	22.5	2178	2 S55805	alpha-toxin - Clos
81	49.5	22.3	311	2 G86324	hypothetical prote
82	49.5	22.3	1162	2 S07421	hypothetical prote
83	49	22.1	82	2 AF3441	E2 glycoprotein pr
84	49	22.1	193	2 B95340	hypothetical prote
85	49	22.1	246	2 S29716	tirosine-phosphate i
86	49	22.1	403	2 T36019	phosphoglycerate k
87	49	22.1	469	2 C30446	permease, multicitr
88	49	22.1	489	2 F82085	glutamate synthase
89	49	22.1	511	2 JC1404	CDEI-box DNA-bind
90	49	22.1	527	2 A43938	Pseudomonas cytoch
91	49	22.1	533	2 B84858	phosphoprotein pho
92	49	22.1	542	2 C70732	probable integral
93	49	22.1	568	1 O8PSA	pseudomonas cytoch
94	49	22.1	577	2 A84681	nodulin-like prote
95	49	22.1	649	2 S88064	hdc protein - fru
96	49	22.1	701	2 S64599	storage membrane
97	49	22.1	704	2 A44287	storage protein 2
98	49	22.1	751	2 A9974	beta-amyloid precu
99	49	22.1	891	2 G96636	hypothetical prote
100	49	22.1	1150	2 A80064	probable membrane

ALIGNMENTS

RESULT 1

A60045 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 2

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIDN:CAA39592.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 3

D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 4

B60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 5

G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 6

B60045 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
C:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>

A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 43
Db 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 48

RESULT 7

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MUID:93075180; PMID:1445331

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R:Jomstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; amyloid; Down's syndrome
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 222; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.8e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 43
Db 17 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 59

RESULT 8

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795

R:Podlasky, M.B.; Toland, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p

A:Reference number: A49795; MUID:91273117; PMID:1905108

A:Accession: A49795

A:Molecule type: Preliminary

A:Status: preliminary

A:Residues: 1-695 <POD>

A:Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing

Query Match 100.0%; Score 222; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 4e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 43
Db 597 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMWGVVIT 639

RESULT 9

ORF0U4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP (770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3

R:LeMay, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466

A:Note: alternative splice form APP (695)

R:LeMay, H.G.

Submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: UNIPARC:UPI000016A5FC; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:
A:Note: alternative splice form APP (695)

R:La Paul, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAP>

A:Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:g341202; PIDN:AA13

R:Jomstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:g178663; PIDN:AA51768.1; PID:
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bos, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A:Cross-references: UNIPARC:UPI0000148176

A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 87, 257-263, 1990

A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105

A:Accession: I39451

A:Molecule type: DNA

A:Residues: 1-770 <YOS1>

A:Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:g178613; PIDN:AA859502.1; PID:
A:Accession: I39451

A:Molecule type: DNA

A:Residues: 1-530, 'QWLMPIPAWEAKVR', <YOS2>

A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AA859501.1; PID:
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 102, 291-292, 1991

A:Reference number: A59020; MUID:91340168; PMID:1908403

A:Accession: A59020

A:Molecule type: DNA

A:Residues: 1-530, 'QWLMPIPAWEAKVR', <YOS2>

A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AA859501.1; PID:
A:Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine

Science 248, 1124-1126, 1990
A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: 139453; MUID:90260663; PMID:2111584
A:Accession: 139453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G176816; PIDN:AAA51727.1; PID:
A>Note: a mutation with 693-gln is presented
R:Murrell, U.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A:Reference number: 159562; MUID:92022553; PMID:1925564
A:Accession: 159562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MOR>
A:Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:G236720; PIDN:AA819991.1; PID:
R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonzo, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:G257377; PIDN:AA823645.1; PID:
A:Experimental source: familial Alzheimer disease family 88
A>Note: sequence extracted from NCBI Backbone (NCBI:P115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: UNIPARC:UPI000016B394; GB:S45135; NID:G257379; PIDN:AA823646.1; PID:
A:Experimental source: familial Alzheimer disease family LIT
A>Note: sequence extracted from NCBI Backbone (NCBI:P115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G
R:ROBakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:G178539; PIDN:AAA51722.1; PID:
A>Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:
R:Dyckes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muehle
EMBO J. 7, 949-957, 1988

A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
A:Cross-references: UNIPARC:UPI0000035AB0
R:Tanzi, R.E.; McClatchey, A.I.; Lampertl, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 528-532, 1988
A>Title: A new A4 amyloid-mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA3
A>Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: UNIPARC:UPI000014553B; GB:X06961; NID:G28816; PIDN:CAA30041.1; PID:G
A:Experimental source: glioblastoma cell line
A>Note: alternative splice form APP(770)
R:Vitek, M.P.; Raoou, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
A:Cross-references: UNIPARC:UPI0000174094
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4, 5e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGVYEHQKLVFAEDVGSNKGALIGMGVVIAT 43
|||||
DB 672 DAEFRHDSGVYEHQKLVFAEDVGSNKGALIGMGVVIAT 714
|||||

RESULT 10
PNO512
beta-amyloid protein - guinea pig (fragment)

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C/Species: Cavia porcellus (guinea pig)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: P00512
R/Shimomigishi, Y.; Matsumoto, H.; Takano, Y.; Saio, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A/Reference number: P00512; MUID:93290653; PMID:7685598
A/Accession: P00512
A/Molecule type: protein
A/Residues: 1-42 <SH>
A/Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C/Keywords: alternative splicing; amyloid

Query Match          97.7%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 42

RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N/Alternate names: proteinase nexin II
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C/Accession: A27485; S19727; I49485
R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A/Reference number: A27485; MUID:86106489; PMID:3322280
A/Accession: A27485
A/Molecule type: mRNA
A/Residues: 1-695 <YMA>
A/Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:9191568; PIDN:
A/Experimental source: brain
R/de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A/Reference number: S19727; MUID:92096458; PMID:1756177
A/Accession: S19727
A/Molecule type: mRNA
A/Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A/Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R/Iizumi, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A/Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A/Reference number: I49485; MUID:92209998; PMID:1555768
A/Accession: I49485
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-19 <RES>
A/Cross-references: UNIPARC:UPI0000003B7; GB:D10603; NID:9220328; PIDN:BA01456.1; PID:
C/Genetics: 16C3
A/Map position: 16C3
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C/Keywords: alternative splicing; amyloid; transmembrane protein

Query Match          91.4%; Score 203; DB 2; Length 695;
Best Local Similarity 93.0%; Pred. No. 1.3e-18;
Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 639

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat

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N/Alternate names: beta-A4 amyloid protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: S00550; A41245; A39820; S46251
R/Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A/Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A/Reference number: S00550; MUID:88312583; PMID:2900758
A/Accession: S00550
A/Molecule type: mRNA
A/Residues: 1-695 <SH>
A/Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:955616; PIDN:
R/Schubert, D.; Schroeder, R.; Lachbriere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A/Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core 1
A/Reference number: A41245; MUID:88264430; PMID:2968652
A/Accession: A41245
A/Molecule type: protein
A/Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A/Cross-references: UNIPARC:UPI00001777FD
A/Note: evidence for heparan sulfate attachment
R/Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A/Title: The beta-A4 amyloid precursor protein binding to copper.
A/Reference number: S46251; MUID:94320627; PMID:7913895
A/Contents: annotation; copper binding sites
A/Note: rat peptides were isolated but not sequenced
R/Potempsky, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A/Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A/Reference number: A39820; MUID:91217087; PMID:1673681
A/Accession: A39820
A/Status: preliminary
A/Molecule type: protein
A/Residues: 18-32 <POT>
A/Cross-references: UNIPARC:UPI00001777FE
A/Experimental source: brain
C/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch.
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match          91.4%; Score 203; DB 2; Length 695;
Best Local Similarity 93.0%; Pred. No. 1.3e-18;
Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 639

RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C/Accession: JH0773
R/Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A/Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A/Reference number: JH0773; MUID:91129227; PMID:11282805
A/Accession: JH0773
A/Molecule type: mRNA
A/Residues: 1-747 <OKA>
A/Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:9263150; PIDN:AA24653.1; PID:
A/Experimental source: larva
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C/Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          91.4%; Score 203; DB 2; Length 747;
Best Local Similarity 88.4%; Pred. No. 1.4e-16;
Matches 38; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```


Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A:Authors: Uteerback, T.; Cotton, M.D.; Springs, T.; Attlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Moese, C.R.; Venter, J.C.

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeal
A:Reference number: Ae9250; MUID:98049343; PMID:9389475

A:Accession: GG59525

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-297 <KLE>

A:Cross-references: UNIPROT:O28076; UNIPARC:UPI0000056A22; GB:AEO09553; GB:AEO00782; NITD
R.Schworer, B.; Breitling, J.; Klein, A.R.; Stetter, K.O.; Thauer, R.K.

Rsch. Microbiol. 159, 225-232, 1993

A>Title: Formylmethanofuran: tetrahydromethanopterin formyltransferase and N5,N10-methyl-
enzymes from methanogenic Archaea.

A:Reference number: A48369; MUID:93243884; PMID:841089

A:Accession: AA8369

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-31,33,'1',35-42,'T',44-49 <SCH>

A:Cross-references: UNIPARC:UPI0000178B9D

A>Note: sequence extracted from NCBI Bankone (NCBI:P130602)

C:Superfamily: formylmethanofuran:tetrahydromethanopterin formyltransferase

C:Keywords: acyltransferase

Query Match 25.0%; Score 55.5; DB 2; Length 297;
Best Local Similarity 34.0%; Pred. No. 12;
Matches 16; Conservative 8; Mismatches 12; Indels 11; Gaps 2;

Oy 1 DAEFHDSGYEVHHQKVFFPAE-----DGSNGKAIIGLMVGGVI 41
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 110 DAEEKFDGTG----KLKFADGYKEVEVGGRKCWAVPMMEGDFII 151
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

RESULT 22

AF3016

N+/H+ antiporter Atut3738 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AF3016

R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Bidle, P.; Jung, M.; Krepsan, W.; Perry, M.; Gordon-Kamm,
ser, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AF3016

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-621 <KUS>

A:Cross-references: UNIPROT:O8UJ0; UNIPARC:UPI0000164865; GB:AEO08689; PIDN:AAI44548.1;
A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atut3738

A:Map position: linear chromosome

Query Match 25.0%; Score 55.5; DB 2; Length 621;
Best Local Similarity 43.2%; Pred. No. 28;
Matches 16; Conservative 7; Mismatches 5; Indels 9; Gaps 3;

Oy 7 DSGYEVHHQKLVFAEDVGSNKAIIGLMVGGVIAT 43
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 185 DSGF-----LLFIEMKG--LGVIFGLI-GSLMIAT 212
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

RESULT 23

B98268

Possible sodium/hydrogen antiporter PA5021 [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: B98268

[illegible]

A:Gene: SP0136
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 24.8% Score 55; DB 2; Length 291;
Best Local Similarity 37.9% Pred. No. 14;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 6 HDGVEVHHOKLVFAEDVGSNKGAIIG 34
Db 58 HFGYTHRIKILISNEDLGATNANIGI 86

RESULT 26

H97888
glycosyl transferase, family 2 (imported) - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: H97888
R:Hoekings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: H97888
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 <KUR>

A:Cross-references: UNIPROT:Q8DRG7; UNIPARC:UPI00000E33BF; GB:AE007317; PIDN:AAK98940.1;
C:Genetics:

A:Gene: glycosyltransferase
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 24.8% Score 55; DB 2; Length 317;
Best Local Similarity 37.9% Pred. No. 15;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 6 HDGVEVHHOKLVFAEDVGSNKGAIIG 34
Db 58 HFGYTHRIKILISNEDLGATNANIGI 86

RESULT 27

S27652
probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) - Pseudomonas sp.

C:Species: Pseudomonas sp.
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: C42971; S27652
R:Peterson, J.A.; Lu, J.Y.; Geisselsoder, J.; Graham-Lorence, S.; Carmona, C.; Witney, F

J. Biol. Chem. 267, 14193-14203, 1992
A:Title: Cytochrome P-450cyp. Isolation and purification of the protein and cloning and
A:Reference number: A42971; MUID:92332528; PMID:1629218

A:Accession: C42971
A:Molecule type: nucleic acid; protein

A:Status: preliminary; not compared with conceptual translation

A:Residues: 1-488 <PER>
A:Cross-references: UNIPROT:P33008; UNIPARC:UPI000012928E; EMBL:M91440; NID:g151584; PID

A:Title: sequence extracted from NCBI backbone (NCBI:P108473)
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

C:Keywords: NAD; oxidoreductase

Query Match 24.8% Score 55; DB 2; Length 488;
Best Local Similarity 40.6% Pred. No. 25;
Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

Qy 6 HDGVEVHHOKLVFAEDV----GSKNGAIIG 33
Db 305 HESTYAFRDKLVAAQNVVIGDSQPGVTMG 336

RESULT 28

C95936

conserved hypothetical membrane protein, similar to Y1058 SMD21251 (imported) - Sinorhiz

C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: C95936
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,663-kb pSymB megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95936

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-738 <KUR>

A:Cross-references: UNIPROT:Q92VFL; UNIPARC:UPI00000CB649; GB:AL591985; PIDN:CAC49155.1,
A:Experimental source: strain 1021, megaplasmid pSymB

R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,

L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation
C:Genetics: SMD21251
A:Gene: SMD21251
A:Genome: plasmid

Query Match 24.8% Score 55; DB 2; Length 738;
Best Local Similarity 50.0% Pred. No. 39;
Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 20 FAEDVGSNKGAIIGLVGVVIAT 43
Db 300 FPEVDRNLTGAVLGLVVIAGLAIDT 323

RESULT 29

JS0166
genome polyprotein - potato virus Y (strain N)

N:Contains: 31k protein; 38k protein; capsid protein; cytoplasmic inclusion protein; gen
olymerase (EC 2.7.7.48) core, nuclear inclusion protein a

C:Species: potato virus Y, PVY
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Feb-2001

C:Accession: JS0166; PS0317
R:Robaglia, C.; Durand-Tardif, M.; Tronchet, M.; Boudazin, G.; Asstier-Manificier, S.; Ca

J. Gen. Virol. 70, 935-947, 1989
A:Title: Nucleotide sequence of potato virus Y (N strain) genomic RNA.
A:Reference number: JS0166; MUID:89279275; PMID:2732709

A:Accession: JS0166
A:Molecule type: mRNA

A:Residues: 1-1063 <ROB>
A:Cross-references: UNIPARC:UPI0000178735

A:Accession: PS0317
A:Molecule type: protein

A:Residues: 1158-1163; 2797-2812, 'O', 2814-2816 <RO2>
A:Cross-references: UNIPARC:UPI0000178735

C:Keywords: ATP; cysteine protease; genome-linked protein; glycoprotein; hydrolase; nu

F:1-275/Product: 31k protein #status predicted <31k>
F:276-824/Product: helper component #status predicted <HPC>

F:309-340/Product: zinc binding #status predicted
F:825-1157/Product: 38k protein #status predicted <38k>

F:1158-1791/Product: cytoplasmic inclusion protein #status predicted <CIP>
F:1242-1250/Product: nucleotide-binding motif A (P-loop)

F:1327-1332/Product: nucleotide-binding motif B
F:1331-1334/Product: DXH motif

F:1792-1843/Product: genome-linked protein #status predicted <GLP>
F:1844-2275/Product: nuclear inclusion protein a #status predicted <NIA>

F:2276-2796/Product: nuclear inclusion protein b #status predicted <NIB>
F:2797-3063/Product: capsid protein #status predicted <CAP>

F:450-744/Product: carboxylate (Asn) (covalent) #status predicted
F:1907/Product: binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

F:2182-2198/Product: Cys, His #status predicted

Query Match 24.8%; Score 55; DB 2; Length 3063;
Best Local Similarity 53.1%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAERFDHSGYEVHHOKLVFPAEDV---GSNK 28
DB 2783 DDEFELDS-YEVHHQ-----ANDRIDAGGSNK 2808

RESULT 30

C81683 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC061
N;Alternate names: oxoisovalerate dehydrogenase
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81683
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: AB1500; MUID:20150255; PMID:10684935
A;Accession: C81683
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-678 <TER>
A;Cross-references: UNIPROT:O9PKS4; UNIPARC:UPI00000579C3; GB:AE002330; GB:AE002160; NID
A;Experimental source: Strain Nig9 (MoPn)
C;Genetics:
A;Gene: TC0618
C;Keywords: oxidoreductase

Query Match 24.5%; Score 54.5; DB 2; Length 678;
Best Local Similarity 44.0%; Pred. No. 41;
Matches 11; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 11 EVHHQK-LVFPADVGSNKGAIGL 34
DB 364 EMHRDPGVVFGEDVAGNKGGVFGV 388

Search completed: September 28, 2006, 06:24:33
Job time : 18.7399 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:51 ; Search time 139.991 Seconds
(without alignments)
284.110 Million cell updates/sec

Title: US-09-731-899-4
Perfect score: 222
Sequence: 1 DAERFHDGVEVHHOKLVFF.....VGSNKGAIIIGMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	57	1 A4_URDMA	Q29149 u amyloid b
2	222	100.0	58	1 A4_CANFA	Q28280 o amyloid b
3	222	100.0	58	1 A4_RABIT	Q28748 o amyloid b
4	222	100.0	58	1 A4_SHEEP	Q28757 o amyloid b
5	222	100.0	59	1 A4_BOVIN	Q28053 b amyloid b
6	222	100.0	113	2 O8JH58_CHESE	Q8JH58 chelydra se
7	222	100.0	534	2 O93296_CHICK	Q93296 gallus gall
8	222	100.0	695	2 O2XQAO_PIG	Q2XQAO sus scrofa
9	222	100.0	695	2 O56UK3_CANFA	Q56UK3 canis faml
10	222	100.0	695	2 O5R477_PONPY	Q5R477 pongo pygma
11	222	100.0	695	2 O6RH29_CANFA	Q6RH29 canis faml
12	222	100.0	695	2 O9DGJ8_CHICK	Q9DGJ8 gallus gall
13	222	100.0	714	2 O56UK4_CANFA	Q56UK4 canis faml
14	222	100.0	749	2 O56UK2_STRECO	Q56UK2 strella co
15	222	100.0	751	1 A4_SATSC	Q95241 s amyloid b
16	222	100.0	751	2 O6GSC0_HUMAN	Q6GSC0 homo sapien
17	222	100.0	751	2 O4R4R8_MACFA	Q4R4R8 macaca faec
18	222	100.0	751	2 O56UK5_CANFA	Q56UK5 canis faml
19	222	100.0	751	2 O6RH28_CANFA	Q6RH28 canis faml
20	222	100.0	751	2 O2XQ99_PIG	Q2XQ99 sus scrofa
21	222	100.0	751	2 O9DGJ7_CHICK	Q9DGJ7 gallus gall
22	222	100.0	770	1 A4_CAVFO	Q60495 g amyloid b
23	222	100.0	770	1 A4_HUMAN	P05067 h amyloid b
24	222	100.0	770	1 A4_MACFA	P53560 m amyloid b
25	222	100.0	770	1 A4_PANTR	Q51880 p amyloid b
26	222	100.0	770	1 A4_PIG	P79307 s amyloid b
27	222	100.0	770	2 O56UK6_CANFA	Q56UK6 canis faml
28	222	100.0	770	2 O6RH30_CANFA	Q6RH30 canis faml
29	217	97.7	42	2 O56UK6_GPRGR	Q56UK6 grampus gri
30	217	97.7	42	2 O56UK7_TURTR	Q56UK7 turlops tr
31	217	97.7	42	2 Q7M088_CAVFO	Q7M088 cavia porce

32	217	97.7	52	2	Q6WZ99_HUMAN	Q6WZ99 homo sapien
33	217	97.7	569	2	Q9PVL1_CHICK	Q9PVL1 gallus gall
34	212	95.5	64	2	Q3M025_ANTST	Q3M025 antechinus
35	203	91.4	79	2	O35463_CRIGR	O35463 cricetus
36	203	91.4	218	2	O8BPV5_MOUSE	O8BPV5 mus musculus
37	203	91.4	384	2	O8BPC7_MOUSE	O8BPC7 mus musculus
38	203	91.4	695	2	Q98SG0_XENLA	Q98SG0 xenopus lae
39	203	91.4	695	2	O6GR78_MOUSE	O6GR78 mus musculus
40	203	91.4	733	2	O6P605_RAT	O6P605 rattus norv
41	203	91.4	747	2	O91963_PPIPI	O91963 xenopus . ap
42	203	91.4	749	2	O6NRP1_XENLA	O6NRP1 xenopus lae
43	203	91.4	750	2	O6DU86_XENTR	O6DU86 xenopus tro
44	203	91.4	752	2	O3TW83_MOUSE	O3TW83 mus musculus
45	203	91.4	752	2	O3TXI9_MOUSE	O3TXI9 mus musculus
46	203	91.4	770	1	A4_MOUSE	P12023 m amyloid b
47	203	91.4	770	1	A4_RAT	P08592 r amyloid b
48	203	91.4	770	2	O53ZT3_MOUSE	O53ZT3 mus musculi
49	203	91.4	770	2	O547B7_RAT	O547B7 rattus norv
50	200	90.1	695	2	O7ZXQ0_XENLA	O7ZXQ0 xenopus lae
51	200	90.1	695	2	O98SP9_XENLA	O98SP9 xenopus lae
52	193	86.9	699	2	O57394_NARJA	O57394 narke japon
53	180	81.1	754	2	O4RYJ3_TETNG	O4RYJ3 tetradon n
54	180	81.1	780	1	A4_TETFL	O73683 tetradon f
55	176	79.3	33	2	Q9UC33_HUMAN	Q9UC33 homo sapien
56	176	79.3	737	1	A4_FUGRU	O93279 fugu rubrip
57	176	79.3	759	2	Q4SOU4_TETNG	Q4SOU4 tetradon n
58	163.5	73.2	357	2	O8UUI8_BRARE	O8UUI8 brachydanto
59	163.5	73.2	472	2	O8UUS0_BRARE	O8UUS0 brachydanto
60	162.5	73.2	612	2	O919E7_BRARE	O919E7 brachydanto
61	162.5	73.2	678	2	O7ZZT1_BRARE	O7ZZT1 brachydanto
62	162.5	73.2	738	2	O6NUZ1_BRARE	O6NUZ1 brachydanto
63	162.5	73.2	738	2	O90WZ8_BRARE	O90WZ8 brachydanto
64	161	72.5	239	2	O8UUI7_BRARE	O8UUI7 brachydanto
65	161	72.5	362	2	O5XIY5_BRARE	O5XIY5 brachydanto
66	161	72.5	694	2	O8UUR9_BRARE	O8UUR9 brachydanto
67	126	56.8	49	2	O97917_BOVIN	O97917 bos taurus
68	126	56.8	49	2	O2XQ98_PIG	O2XQ98 sus scrofa
69	64	28.8	328	2	O9RPS4_ENTFA	O9RPS4 enterococcu
70	64	28.8	755	2	O9R472_9RHIZ	O9R472 agrobacteri
71	64	28.8	755	2	O9R694_9RHIZ	O9R694 agrobacteri
72	64	28.8	755	2	O9R717_9RHIZ	O9R717 agrobacteri
73	64	28.8	755	2	O8U6A3_AGRIS	O8U6A3 agrobacteri
74	63	28.4	321	2	O8RG41_GLOVN	O8RG41 gloobacteri
75	62.5	28.2	545	2	O7NGT4_GLOVI	O7NGT4 gloobacteri
76	62	27.9	755	1	TR2M_AGRU4	P043V2 agrobacteri
77	62	27.9	755	1	TR2M_AGRU4	P043V3 agrobacteri
78	62	27.9	755	1	TR2N_AGRU1	P25017 agrobacteri
79	62	27.9	755	2	Q4388_9RHIZ	Q4388 agrobacteri
80	61	27.5	755	2	O6LJ99_PHOTO	O6LJ99 photobacteri
81	60.5	27.3	252	2	O40M73_DESAC	Q40M73 desulfuromo
82	60	27.0	300	2	O8HMH7_SQUAC	Q8HMH7 squallus aca
83	60	27.0	351	2	O44IM9_SOLUS	Q44IM9 solibacter
84	60	27.0	419	2	O4DBL7_TRYCR	Q4DBL7 trypanosoma
85	60	27.0	3011	2	O8IKEL_PLAF7	O8IKEL plasmodium
86	60	27.0	3336	2	O5K514_VITRU	O5K514 bacterioph
87	59	26.6	362	2	O44IH4_CHRSU	Q44IH4 chromohalob
88	58	26.1	288	2	O7P4H7_FUSNV	Q7P4H7 fusobacteri
89	58	26.1	320	2	O6G2C8_BRUSU	Q6G2C8 bruceella su
90	58	26.1	368	2	O41IH0_GIBZE	Q41IH0 gibberella
91	58	26.1	491	2	O6Z4F2_ORYSA	Q6Z4F2 oryza sativ
92	58	26.1	624	1	O2YMB3_BRUA2	Q2YMB3 bruceella ab
93	58	26.1	763	2	O4UES6_THEAN	Q4UES6 theileria a
94	57.5	25.9	323	2	Q4NSD6_THRPA	Q4NSD6 theileria p
95	57.5	25.9	405	2	O3CTU1_AUTAT	Q3CTU1 pseudaltier
96	57.5	25.9	495	2	O3IER1_PSEHT	Q3IER1 pseudaltier
97	57.5	25.9	496	2	O9AMB6_LYCES	Q9AMB6 lycopersico
98	57.5	25.9	895	2	O6EXB0_SPOCV	Q6EXB0 potato viru
99	57	25.7	182	2	O22662_ARATH	Q22662 arabidopsis
100	57	25.7	195	2		

ALIGNMENTS

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RESULT 1
A4_URSMA STANDARD; PRT; 57 AA.
AC Q25149;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-MAR-2006, entry version 36.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalartos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1556157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DE EMBL: X56128; CA39593.1; -; mRNA.
DR PIR: B60045; B60045.
DR HSSP: P08592; 1NMJ.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETRAYMLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1> 57
FT FTID=PRO_0000226244.
FT FTID=PRO_0000226244.
FT CHAIN <1> 5 Soluble APP-beta (By similarity).
FT FTID=PRO_0000000191.
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT FTID=PRO_0000000192.
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT FTID=PRO_0000000193.
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT FTID=PRO_0000000194.
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT FTID=PRO_0000000195.
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT FTID=PRO_0000000196.
FT CHAIN 47 >58 Extracellular (Potential).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT CHAIN 49 >58 Extracellular (Potential).
FT TOPO_DOM <1> 33
FT TRANSMEM 34 57
FT NON_TER 1 1
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SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLVGQVIAI 43
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLVGQVIAI 48

RESULT 2
A4_CANFA STANDARD; PRT; 58 AA.
AC Q25280;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-MAR-2006, entry version 37.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1556157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DE EMBL: X56125; CA39590.1; -; mRNA.
DR HSSP: P08592; 1NMJ.
DR Ensembl: ENSGAFG00000008557; Canis familiaris.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETRAYMLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
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FT FTID=PRO_0000226241.
FT CHAIN <1> 6 Soluble APP-beta (By similarity).
FT FTID=PRO_0000000070.
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT FTID=PRO_0000000071.
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT FTID=PRO_0000000072.
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT FTID=PRO_0000000073.
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT FTID=PRO_0000000074.
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT CHAIN 49 >58 Extracellular (Potential).
FT TOPO_DOM <1> 34
FT TRANSMEM 35 58
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48BA2E12DFA CRC64;

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Query Match 100.0%; Score 222; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.8e-21;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLVGSGVIAT 43
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 DB 7 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLVGSGVIAT 49

RESULT 3
 A4_RABIT STANDARD; PRT; 58 AA.
 ID A4_RABIT
 AC Q28748;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 37.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 protein.
 CC -1- SIMILARITY: Belongs to the APP family.
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EMBL; X56129; CA39594.1; -; mRNA.
 DR HSSP; P08592; 1NMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
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 FT Soluble APP-beta (By similarity).
 FT /FTID=PRO_0000000153.
 FT CTF-alpha (By similarity).
 FT /FTID=PRO_0000000154.
 FT Beta-amyloid protein 42 (By similarity).
 FT /FTID=PRO_0000000155.
 FT Beta-amyloid protein 40 (By similarity).
 FT /FTID=PRO_0000000156.
 FT Gamma-CTF(59) (By similarity).
 FT /FTID=PRO_0000000157.
 FT Gamma-CTF(57) (By similarity).
 FT /FTID=PRO_0000000158.
 FT Extracellular (Potential).
 FT /FTID=PRO_0000000159.
 FT Potential.
 FT TOPO_DOM <1> 33
 FT TRANSMEM 34 57
 FT TOPO_DOM 58 >58 Cytoplasmic (Potential).

FT NON TER 1 1
 FT NON TER 58 58
 FT SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.8e-21;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLVGSGVIAT 43
 |||||
 DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAIIIGLVGSGVIAT 48

RESULT 4
 A4_SHEEP STANDARD; PRT; 58 AA.
 ID A4_SHEEP
 AC Q28757;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Heart;
 RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 protein.
 CC -1- SIMILARITY: Belongs to the APP family.
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EMBL; X56130; CA39595.1; -; mRNA.
 DR HSSP; P08592; 1NMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
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 FT Soluble APP-beta (By similarity).
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 FT CTF-alpha (By similarity).
 FT /FTID=PRO_0000000186.
 FT Beta-amyloid protein 42 (By similarity).
 FT /FTID=PRO_0000000187.
 FT Beta-amyloid protein 40 (By similarity).
 FT /FTID=PRO_0000000188.
 FT Gamma-CTF(59) (By similarity).
 FT /FTID=PRO_0000000189.
 FT Gamma-CTF(57) (By similarity).
 FT CHAIN 48 >58

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FT  TOPO_DOM <1 33 /FTid=PRO_0000000190.
FT  TRANSMEM 34 57 Extracellular (Potential).
FT  TOPO_DOM 58 >58 Potential.
FT  NON_TER 1 1 Cytoplasmic (Potential).
FT  NON_TER 58 58
SQ  SEQUENCE 58 AA; 6300 MW; F434209D8BEA82D CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 48

RESULT 5
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DE 07-FEB-2006, entry version 36.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=9901079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
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CC
DR EMBL: X56124; CA39589.1; -; mRNA.
DR EMBL: X56126; CA39591.1; -; mRNA.
DR HSSP: P08592; INMJ
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
DR Amyloid; Membrane; Transmembrane.
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FT  CHAIN 7 48 CTF-alpha (By similarity).
FT  CHAIN 7 48 /FTid=PRO_0000000065.
FT  CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT  CHAIN 7 46 /FTid=PRO_0000000066.
FT  CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT  CHAIN 7 46 /FTid=PRO_0000000067.

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FT  CHAIN 47 >59 Gamma-CTF(59) (By similarity).
FT  CHAIN 49 >59 /FTid=PRO_0000000068.
FT  CHAIN 49 >59 Gamma-CTF(57) (By similarity).
FT  CHAIN 49 >59 /FTid=PRO_0000000069.
FT  TOPO_DOM <1 34 Extracellular (Potential).
FT  TRANSMEM 35 58 Potential.
FT  TOPO_DOM 59 >59 Cytoplasmic (Potential).
FT  NON_TER 1 1
FT  NON_TER 59 59
SQ  SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 222; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 49

RESULT 6
ID Q8UH58 CHESE PRELIMINARY; PRT; 113 AA.
AC Q8UH58;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Amyloid beta protein (Fragment).
DE Chalydya serpentina serpentina (common snapping turtle).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=114619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina."
RL Environ. Health Perspect. 110:269-275 (2002).
CC
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CC
DR EMBL: AF541917; AA04908.1; -; mRNA.
DR HSSP: Q16019; IYT.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00320; A4_INTRA; 1.
FT  NON_TER 1 1
SQ  SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 15 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 57

RESULT 7
ID Q93296 CHICK PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.

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OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Manbult R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RU Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CR861380; CAH93439.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR012282; Cytochrome_C_R.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMAMLOID.
DR SMART: SM00066; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 78627 MW; 0BF5DD9BA213E49 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 43
DB 597 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 639

RESULT 11
ID O6RH29_CANFA PRELIMINARY; PRT; 695 AA.
AC O6RH29_ CANFA
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Beta amyloid protein isoform APP695.
GN Name=beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AY498707; AAR97727.1; -; mRNA.
DR HSSP: Q16019; IBA4.
DR SMR: O6RH29; 28-123, 124-189, 385-494.
DR Ensemble: ENSGALG0000008557; Canis familiaris.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.

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DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMAMLOID.
DR SMART: SM00066; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F956C10 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 43
DB 597 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 639

RESULT 12
ID O9DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
AC O9DGJ8_ CHICK
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:16039787; DOI=10.1016/j.neuroscience.2005.05.020;
RA Carrodeguez J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,
RA Perez-Pe R., Iacosta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RA Sorribas V., Sarsa M.;
RT "The chick embryo appears as a natural model for research in beta-
RT amyloid precursor protein processing.";
RL Neuroscience 134:1285-1300(2005).
CC -----
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CC -----
DR EMBL: AF289218; AAG00593.1; -; mRNA.
DR HSSP: Q16019; IYT.
DR SMR: O9DGJ8; 28-123, 124-189, 385-494.
DR Ensemble: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMAMLOID.
DR SMART: SM00066; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78566 MW; F201BD02AEC6D95 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 43
DB 597 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMVGGVAT 639

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RESULT 13
ID 056JK2 CANFA PRELIMINARY; PRT; 714 AA.
AC 056JK2
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RL "Relationship between canine dementia and Alzheimer's disease.";
Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY926581; AAX81912.1; -; mRNA.
DR SMR; 056JK2; 28-123, 124-189, 404-513.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome c R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4-EXTRA; 1.
DR PRINTS; PR0203; AMYLOIDA4.
DR PRINTS; PR0204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 714 AA; 80827 MW; 50DDE51FB9E90EC5 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 714;
Best Local Similarity 100.0%; Pred. No. 3.8e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 616 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 658

RESULT 14
ID 056JK2 STECO PRELIMINARY; PRT; 749 AA.
AC 056JK2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Beta-amyloid protein 749.
OS Stenella coeruleoalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
NCBI_TaxID=9737;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RL "The molecular machinery of Alzheimer's disease in the dolphin.";
Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY926583; AAX81912.1; -; mRNA.
DR SMR; 056JK2; 28-123, 124-189, 457-566.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome c R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4-EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPASE.
DR PRINTS; PR0204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84543 MW; 42659987C2A95D6 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 749;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 651 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 693

RESULT 15
ID A4_SAIISC STANDARD; PRT; 751 AA.
AC 095241;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1997, sequence version 1.
DT 07-MAR-2006, entry version 60.
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE Amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN Name=APP;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
NCBI_TaxID=99521;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX TISSUE=Kidney, and Liver;
RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RL "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
RT amyloid angiopathy.";
RN Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Trip6 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(i) and JIP (By
CC similarity). Inhibits G(i) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
```

transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metalated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FRL1, APPB1, IBL, KMS2 (via its TPR domains) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAP7 via the MT-binding domains (By similarity). Associates with microtubules in the presence of APP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP770;
IsoId=Q95241-1; Sequence=Displayed;
Name=APP695;
IsoId=Q95241-2; Sequence=Not described;

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/increasein-mediated gamma-secretase processing of C99 releases the Amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

PTM: N- and O-glycosylated (By similarity).

PTM: Phosphorylation in the C-terminal on tyrosine, threonine and

serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

SIMILARITY: Belongs to the APP family.

-1 SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: S81024; A0D14347.1; -; mRNA.
PDB: 1RW6; X-ray; A=346-551.
DR SMR: Q95241; 28-123, 124-189, 287-342.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083.SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTAS.
DR PRINTS: PR00204; BETAAMYLOID.
DR PRODOM: PR000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR 3D-structure: Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.
KW Transmembrane; Zinc.
KW SIGNAL
FT 1 17 By similarity.
FT CHAIN 1 751 Amyloid beta A4 protein.
FT 18 751 /FTid=PRO_0000000172.
FT /FTid=PRO_0000000172. Soluble APP-alpha (Potential).
FT CHAIN 18 668 /FTid=PRO_0000000173.
FT /FTid=PRO_0000000173. Soluble APP-beta (Potential).
FT CHAIN 18 652 /FTid=PRO_0000000174.
FT /FTid=PRO_0000000174. C99 (Potential).
FT CHAIN 653 751 /FTid=PRO_0000000175.
FT /FTid=PRO_0000000175. Beta-amyloid protein 42 (Potential).
FT CHAIN 653 694 /FTid=PRO_0000000176.
FT /FTid=PRO_0000000176. Beta-amyloid protein 40 (Potential).
FT CHAIN 653 692 /FTid=PRO_0000000177.
FT /FTid=PRO_0000000177. C83 (Potential).
FT CHAIN 669 751 /FTid=PRO_0000000178.
FT /FTid=PRO_0000000178. P3(42) (Potential).
FT PEPTIDE 669 694 /FTid=PRO_0000000179.
FT /FTid=PRO_0000000179. P3(40) (Potential).
FT CHAIN 669 692 /FTid=PRO_0000000180.
FT /FTid=PRO_0000000180. Gamma-CTF(59) (Potential).
FT CHAIN 693 751 /FTid=PRO_0000000181.
FT /FTid=PRO_0000000181. Gamma-CTF(57) (Potential).
FT CHAIN 695 751 /FTid=PRO_0000000182.
FT /FTid=PRO_0000000182. Gamma-CTF(50) (Potential).
FT CHAIN 702 751 /FTid=PRO_0000000183.
FT /FTid=PRO_0000000183. C31 (Potential).
FT CHAIN 721 751 /FTid=PRO_0000000184.
FT /FTid=PRO_0000000184. Extracellular (Potential).
FT TOPO DOM 18 680 Extracellular (Potential).
FT TRANSMEM 681 704 Potentail.
FT TOPO DOM 705 751 Cytoplasmic (Potential).
FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
FT REGION 96 110 Heparin-binding (By similarity).
FT REGION 181 188 Zinc-binding (By similarity).

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FT REGION 316 344 Heparin-binding (By similarity).
FT REGION 363 428 Heparin-binding (By similarity).
FT REGION 504 521 Collagen-binding (By similarity).
FT REGION 713 732 Interaction with G(O)-alpha (By
FT MOTIF 705 715 Basolateral sorting signal (By
FT MOTIF 740 743 NPXY motif; contains endocytosis signal.
FT COMBINS 230 260 Asp/Glu-rich (acidic).
FT COMBINS 274 280 Poly-Thr.
FT METAL 137 137 Copper (By similarity).
FT METAL 147 147 Copper (By similarity).
FT METAL 149 149 Copper (By similarity).
FT METAL 151 151 Copper (By similarity).
FT METAL 658 658 Copper or zinc (By similarity).
FT METAL 662 662 Copper or zinc (By similarity).
FT METAL 665 665 Copper or zinc (By similarity).
FT METAL 666 666 Copper or zinc (By similarity).

Query Match 100.0%; Score 222; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 695

RESULT 16
OGGSCO HUMAN PRELIMINARY; PRT; 751 AA.
ID OGGSCO
AC OGGSCO
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Amyloid beta A4 protein,, isoform b.
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavalet T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.D.,
RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schain J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye.
RG NIH MGC Project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC

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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: BC065529; AAH65529.1; -, mRNA.
DR SMR: OGGSCO: 28-123, 124-189, 287-342, 441-550.
DR Ensembl: ENSG00000142192; Homo sapiens.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR012282; Cytochrome C R.
DR InterPro: IPR002223; Prot. inh. Kunitz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz BPTI; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAAMYLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 751 AA; 84819 MW; C987C557C5A3714E CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 695

RESULT 17
Q4R4R8 MACFA PRELIMINARY; PRT; 751 AA.
ID Q4R4R8
AC Q4R4R8
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Brain cDNA, clone: Qf1A-13524, similar to human amyloid beta (A4)
DE protein (protease nexin-II, Alzheimer disease) (APP), transcript
DE variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/me187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.,
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs."
RT Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
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CC

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CC -----
DR EMBL: AB169826; BAB01907.1; -; mRNA.
DR SMR: Q4R48; 28-123, 124-189, 287-342, 441-550.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0020037; F: heme binding; IEA.
DR GO: GO:0008233; F: peptidase activity; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_EXTRA.
DR InterPro: IPR012825; Beta-APP.
DR InterPro: IPR012882; Cytochrome C_R.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYL0ID.
DR PRODOM: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROTEASE.
SQ SEQUENCE 751 AA; 84817 MW; 83C1CD96AD355158 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 695

RESULT 18
Q56JK5 CANFA PRELIMINARY; PRT; 751 AA.
ID Q56JK5
AC Q56JK5
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL: AY926580; AAX81909.1; -; mRNA.
DR SMR: Q56JK5; 28-123, 124-189, 287-342, 441-550.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0020037; F: heme binding; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_EXTRA.
DR InterPro: IPR012825; Beta-APP.
DR InterPro: IPR012882; Cytochrome C_R.
DR InterPro: IPR002222; Prot_inh_Kunz-m; 1.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROTEASE.
SQ SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;
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DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYL0ID.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROTEASE.
SQ SEQUENCE 751 AA; 84920 MW; C1CD20377DFF8550 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 695

RESULT 19
Q6RH28 CANFA PRELIMINARY; PRT; 751 AA.
ID Q6RH28 CANFA
AC Q6RH28
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Beta amyloid protein isoform APP751.
CN Name-beta APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL: AY498708; AAR9728.1; -; mRNA.
DR SMR: Q16019; 1AAP.
DR SMR: Q6RH28; 28-123, 124-189, 287-342, 441-550.
DR EMBL: ENSCAFG0000008557; Canis familiaris.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_EXTRA.
DR InterPro: IPR012825; Beta-APP.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROTEASE.
SQ SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;
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Query Match          100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 43
Db 653 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 695

RESULT 20
Q2XQ99_PIG PRELIMINARY; PRT; 751 AA.
ID Q2XQ99_PIG
AC Q2XQ99;
RT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DE 07-MAR-2006, entry version 4.
DE Amyloid protein variant 2.
GN Name=APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus;
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein. APP: Cloning and characterization
RT of cDNAs."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; DQ267685; ABB82034.1; -; mRNA.
SQ SEQUENCE 751 AA; 84799 MW; 37868743880C369F CRC64;

Query Match          100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 43
Db 653 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 695

RESULT 21
Q9DGJ7_CHICK PRELIMINARY; PRT; 751 AA.
ID Q9DGJ7_CHICK
AC Q9DGJ7;
RT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 22.
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus;
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16039787; DOI=10.1016/j.neuroscience.2005.05.020;
RX Carodégnus J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,
RX Perez-Pe R., Iacosta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RX Sorribes V., Sarsa M.;
RT "The chick embryo appears as a natural model for research in beta-
RT amyloid precursor protein processing."
RL Neuroscience 134:1285-1300(2005).
CC -I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; AF289219; AAG00594.1; -; mRNA.
DR HSSP; Q16019; 11YT.
DR SMR; Q9DGJ7; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSGALG00000015770; Gallus gallus.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004867; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDP4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU_1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84706 MW; E78E9413A8033D84 CRC64;

Query Match          100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 43
Db 653 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVVIAT 695

RESULT 22
A4_CAVPO STANDARD; PRT; 770 AA.
ID A4_CAVPO
AC Q60495; Q60496;
DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
DT 23-APR-2003, sequence version 2.
DE 07-FEB-2006, entry version 56.
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE amyloid protein homolog) [contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN Name=APP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Liver;
RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;
RX Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing."
RL Biochim. Biophys. Acta 1351:17-21(1997).
RN [2]
RP INTERACTION OF BETA-APP40 WITH APOE.
RX MEDLINE=98007700; PubMed=9349544;
RX Marcel C.L., Maccic J.B., Matsubara E., Governale S., Miguel C.,
RX Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT cerebral capillary sequestration and blood-brain barrier transport of
RT circulating Alzheimer's amyloid beta."
RL J. Neurochem. 69:1995-2004(1997).

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RN [3]
 CC PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein.";
 RL Neuroscience 95:243-254(2000).
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;
 RA Pimpli I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative C-
 RT terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possesses protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins E and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Apolipans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, PPRL1, APPBP1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via Bass) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of Arp and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC ApoB3 appears to be the preferred amyloid binding isoform, while
 CC the ApoB1 isoform-beta-ApA40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature Arp (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to

CC exist. The L-isoforms, missing exon 15, are referred to as
 CC apolipans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides. S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta protein, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).
 CC -1- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).
 CC -1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the apolipans (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.
 CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/kunitz inhibitor domain.
 CC -----
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 CC License (CC BY-NC 4.0).
 CC -----
 CC EMBL: X97631; CA66230.1; -; mRNA.
 CC EMBL: X99198; CA67589.1; -; mRNA.
 CC HSSP: P08592; INMW.
 CC SMR: Q60495; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4 APP.
 CC InterPro: IPR008154; A4 extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Prot_inh_Kunz-m.
 CC PANTHER: PTHR10083:SF6; Beta-APP; 6.
 CC Pfam: PF02177; A4 EXTRA; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz BPTI; 1.
 CC PRINTS: PR00203; AMYLOID4.
 CC PRINTS: PR00759; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunz-m; 1.

DR SMART; SM00006; A4 EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4 EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
 KW Metal-binding; Notch signaling pathway; Phosphorylation;
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KW Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 /FTid=PRO_0000000076.
 FT CHAIN 18 671 /FTid=PRO_0000000077.
 FT CHAIN 18 671 /FTid=PRO_0000000078.
 FT CHAIN 672 770 /FTid=PRO_0000000079.
 FT FT
 Query Match 100.0%; Score 222; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.1e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEPHDSGEYHOKLVPFAEDVGSNGKGAIIIGLMVGVIAT 43
 DB 672 DAEPHDSGEYHOKLVPFAEDVGSNGKGAIIIGLMVGVIAT 714
 RESULT 23
 A4_HUMAN STANDARD. PRT: 770 AA.
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9B738; Q9UC49; Q9UCB6; Q9UC88; Q9UCD1; Q9U058;
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1991, sequence version 3.
 DT 07-MAR-2006, entry version 111.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CVA-P) (Protease
 DE nexin-11) (PN-11) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C93; P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59);
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN Name:APP; Synonyms:A4, AD1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RP TISSUE=Brain;
 RC MEDLINE=8714472; PubMed=2881207; DOI=10.1038/325733a0;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Greschick K.-H., Multhaup G., Beyreuther K., Moller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor".
 RL Nature 325:733-736(1987).
 RN [2]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RP TISSUE=Brain;
 RC MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;
 RA Ponte P., Gonzalez-Dewitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors".
 RL Nature 331:525-527(1988).

RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayre R.M.,
 RA Unterbeck A., Beyreuther K., Moller-Hill B.;
 RT "The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is
 RT encoded by 16 exons".
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;
 RA Yoshikaki S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene".
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM.
 RX PubMed=1908403; DOI=10.1016/0378-1119(91)90093-Q;
 RA Yoshikaki S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells".
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;
 RA Hattori M., Tsukunaga F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukunaga S., Sasaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus".
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639".
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT LYS-501.
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gilderleeve H., Cassidy C.M., Johnson E.J.,
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORMS APP305 AND APP751).
 RC TISSUE=Eye, and Pancreas;
 RX MEDLINE=22386257; PubMed=12477933; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Useti T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-10.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP ERRATUM, AND SEQUENCE REVISION.
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 1-75.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Faucei G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [14]
 RP PROTEIN SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=2597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [15]
 RP PROTEIN SEQUENCE OF 18-40.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [16]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [17]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [18]
 RP NUCLEOTIDE SEQUENCE OF 286-366.
 RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
 RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
 RA Gueella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [19]
 RP NUCLEOTIDE SEQUENCE OF 287-367.
 RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
 RT inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [20]

RP NUCLEOTIDE SEQUENCE OF 507-770.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marcote C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [21]
 RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
 RA Behr D., Heese L., Masters C.L., Multhaup G.;
 RA
 Query Match 100.0%; Score 222; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
 DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 714
 RESULT 24
 A4 MACFA STANDARD; PRT; 770 AA.
 ID A4 MACFA
 AC P53601; O60HH7; O95KN7;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 22-FEB-2003, sequence version 3.
 DT 07-FEB-2006, entry version 55.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homolog) [containing: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 DE Name=APP; ORFNames=QCE-15949;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS APP695 AND APP770).
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlasky M.B., Tolian D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease.";
 RL Am. J. Pathol. 138:1423-1435(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
 RC TISSUE=Brain cortex;
 RA Kusuda J., Oada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;
 RT "Isolation and characterization of cDNA for macaque neurological
 RT disease genes.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPB1/Tipe6 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptotic-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-

density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APB family members, the APPA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPR, PPR1, APPB1, IBL, KMS2 (via its TPR domains) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of APP and in a kinesin-dependent manner (By similarity).

- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

- ALTERNATIVE PRODUCTS:

- Event-Alternative splicing: Named isoforms-3; Comment=Additional isoforms seen to exist; Name=APP770; IsoId=PS3601-1; Sequence=Displayed; Name=APP695; IsoId=PS3601-2; Sequence=VSP_000010, VSP_000011; Name=3; IsoId=PS3601-3; Sequence=VSP_013360, VSP_013361; **- DOMAIN:** The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides. S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/increasein-mediated gamma-secretase processing of C99 releases the amyloid-beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

- PTM: N- and O-glycosylated (By similarity).

- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other

proteins (By similarity).

- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

- SIMILARITY: Belongs to the APP family.

- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M58726; AAA36828.1; -; mRNA.
 DR EMBL; M58727; AAA36829.1; -; mRNA.
 DR EMBL; AB125150; BAD51938.1; -; mRNA.
 DR HSSP; P08592; 1NMJ
 DR SMR; PS3601; 28-123, 124-189, 287-342, 460-569.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot inh_Kunz-m.
 DR PANTHER; PTHR10083:SP6; Beta-APP; 6.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot inh_Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.

FT SIGNAL 1 17 By similarity.
 FT CHAIN 1 770 Amyloid beta A4 protein.
 FT FT /FTid=PRO_0000000101.
 FT CHAIN 18 687 Soluble APP-alpha (Potential).
 FT FT /FTid=PRO_0000000102.
 FT CHAIN 18 671 Soluble APP-beta (Potential).
 FT FT /FTid=PRO_0000000103.
 FT CHAIN 672 770 C99 (Potential).
 FT FT /FTid=PRO_0000000104.
 FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
 FT FT /FTid=PRO_0000000105.
 FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
 FT FT /FTid=PRO_0000000106.
 FT CHAIN 688 770 C83 (Potential).
 FT FT /FTid=PRO_0000000107.
 FT CHAIN 688 713 P3(42) (Potential).
 FT FT /FTid=PRO_0000000108.
 FT PEPTIDE 688 711 P3(40) (Potential).
 FT FT /FTid=PRO_0000000109.
 FT CHAIN 712 770 Gamma-CTF(59) (Potential).
 FT FT /FTid=PRO_0000000110.
 FT CHAIN 714 770 Gamma-CTF(57) (Potential).
 FT FT /FTid=PRO_0000000111.
 FT CHAIN 721 770 Gamma-CTF(50) (Potential).
 FT FT /FTid=PRO_0000000112.
 FT CHAIN 740 770 C31 (Potential).
 FT FT /FTid=PRO_0000000113.
 FT TOPO_DOM 18 699 Extracellular (Potential).
 FT TRANSMEM 700 723 Potential.
 FT TOPO_DOM 724 770 Cytoplasmic (Potential).
 FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
 FT REGION 96 110 Heparin-binding (By similarity).
 FT REGION 181 188 Zinc-binding (By similarity).

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FT REGION 391 423 Heparin-binding (By similarity).
FT REGION 491 522 Heparin-binding (By similarity).
FT REGION 523 540 Collagen-binding (By similarity).
FT REGION 732 751 Interaction with G(O)-alpha (By
FT MOTIF 724 734 Basolateral sorting signal (By
Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4,1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAERFHDSGEVHHQKLVFAEDVGSNGAIIIGLVGCVIAT 43
Db 672 DAERFHDSGEVHHQKLVFAEDVGSNGAIIIGLVGCVIAT 714

RESULT 25
A4_PANTR STANDARD; PRT; 770 AA.
AC 051580;
DT 15-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 16.
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE Name=APP;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed15620360; DOI=10.1016/j.cell.2004.11.040;
RA Dornus S., Vallender B.U., Evans P.D., Anderson J.R., Gilbert S.L.,
RA Malowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo
RT sapiens."
RL Cell 119:1027-1040(2004).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(2+)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPT1 domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APPA
CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also

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CC interacts with GPCR-like protein BPT, FPR1, APPB1, IB1, KNS2
CC (via its TPR domains) (By similarity). APPB2 (via BASS) and DBB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acid either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields p3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of beta-amyloid peptides (By similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -!- SIMILARITY: Belongs to the APP family.
CC -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
DR SML: AY665248; AAV74286.1; -; mRNA.
DR SMR: 051580; 28-123, 124-189, 287-342, 460-569.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4-extra.
DR InterPro: IPR001253; Beta-APP.
DR InterPro: IPR012282; Cytochrome C R.
DR InterPro: IPR002223; Prot. inh. Kunitz-m.
DR PANTHER: PTHR10083-SF6; Beta-APP; 6.
DR Pfam: PF02177; A4-extra; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz BPT1; 1.
DR PRINTS: PR00203; AMYLOIDA4.

```

DR	PRINTS,	P000759;	BASICPTASE.
DR	PRINTS,	P000204;	BETRAYALOID.
DR	PRODOM,	P0000222;	Prot Inh_Kunz-m; 1.
DR	SMART,	S000006;	A4_EXTRA; 1.
DR	SMART,	S000131;	KU; 1.
DR	PROSITE,	PS00319;	A4_EXTRA; 1.
DR	PROSITE,	PS00320;	A4_INTRA; 1.
DR	PROSITE,	PS00280;	BPTI_KUNITZ_1; 1.
DR	PROSITE,	PS50279;	BPTI_KUNITZ_2; 1.
KM	Amyloid;	Apoptosis;	Cell adhesion; Coated pits; Copper; Endocytosis;
KM	Glycoprotein;	Heparin-binding;	Iron; Membrane; Metal-binding;
KW	Notch signaling pathway;	Phosphorylation;	Protease inhibitor;
KW	Proteoglycan;	Serine protease inhibitor;	Signal; Transmembrane; Zinc
FT	SIGNAL	1	17
FT	CHAIN	18	770
FT	CHAIN	18	687
FT	CHAIN	18	671
FT	CHAIN	672	770
FT	CHAIN	672	713
FT	CHAIN	672	711
FT	CHAIN	688	770
FT	PEPTIDE	688	713
FT	PEPTIDE	688	711
FT	CHAIN	712	770
FT	CHAIN	714	770
FT	CHAIN	721	770
FT	CHAIN	740	770
FT	TOPO_DOM	18	699
FT	TRANSMEM	700	723
FT	TOPO_DOM	724	770
FT	DOMAIN	291	341
FT	REGION	96	110
FT	REGION	181	188
FT	REGION	391	423
FT	REGION	491	522
FT	REGION	523	540
FT	REGION	732	751
FT	MOTIF	724	734
FT	MOTIF	759	762
FT	COMPBIAS	230	260
FT	COMPBIAS	274	280
FT	METAL	137	137
FT	METAL	147	149
FT	METAL	149	149
FT	METAL	151	151
FT	METAL	677	677
FT	METAL	681	681
FT	METAL	684	684
FT	METAL	685	685
FT	SITE	144	144
FT	SITE	301	302
FT	SITE	671	672
FT	SITE	672	673
FT	SITE	687	688

Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4,1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps

0y. 1 DAEFRDSDGYEYHHQKLVFPAEDVGSNGKAIITGLMGVVIAT 43
Db 672 DAEFRDSDGYEYHHQKLVFPAEDVGSNGKAIITGLMGVVIAT 714

RESULT 26

A4_PIG STANDARD; PRT; 770 AA.
ID A4_PIG
AC P75307: 029023; O9TUD;
DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
DT 23-APR-2003, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE Soluble amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P2(42); P3(40);
DE Gamma-CTF(15) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31).
GN Name-APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_Taxid=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.
RC TISSUE=Small intestine;
RA Whitehouse A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 667-723.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and jip (By
CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(2+)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity).
CC -I- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -I- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal

apoptosis (By similarity).
 SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APB family members, the APPA family, MAPKIP1, and SHC1. Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FRL1, APPB1, IBI, KNS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAP7 via the MT-binding domain (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).
 SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CRF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).
 DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).
 DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).
 PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).
 PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).
 PTM: N- and O-glycosylated (By similarity).
 PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).
 PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).
 MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).
 Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).
 SIMILARITY: Belongs to the APP family.
 SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.

DR SMR; P79307; 28-123, 124-189, 287-342, 460-569.
 DR InterPro; IPR008155; A4 APP.
 DR InterPro; IPR008154; A4 extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot_inh_Kunz-m.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPT1; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASR.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
 KW Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 KM Setine protease inhibitor; Signal; Transmembrane; Zinc.
 FT SIGNAL 1 17
 FT CHAIN 1 770
 FT FT
 FT CHAIN 18 687
 FT FT
 FT CHAIN 18 671
 FT FT
 FT CHAIN 672 770
 FT FT
 FT CHAIN 672 713
 FT FT
 FT CHAIN 672 711
 FT FT
 FT CHAIN 688 770
 FT FT
 FT CHAIN 688 713
 FT FT
 FT PEPTIDE 688 711
 FT FT
 FT CHAIN 712 770
 FT FT
 FT CHAIN 714 770
 FT FT
 FT CHAIN 721 770
 FT FT
 FT CHAIN 740 770
 FT FT
 FT CHAIN 740 770
 FT FT
 FT TOPO DOM 18 699
 FT TRANSMEM 700 723
 FT TOPO DOM 724 770
 FT DOMAIN 291 341
 FT REGION 96 110
 FT REGION 135 155
 FT REGION 181 188
 FT REGION 391 423
 FT REGION 491 522
 FT REGION 523 540
 FT REGION 732 751
 FT MOTIF 724 734
 FT MOTIF 759 762
 FT COMBINS 230 260

Query Match 100.0%; Score 222; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.1e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFAEDYGSNGKALITGLMGVGVAT 43
 DB 672 DAEFRHDSGYEVHHQKLVFAEDYGSNGKALITGLMGVGVAT 714

DR EMBL; AB032550; BA84580.1; -; mRNA.
 DR EMBL; Z84022; CA806313.1; -; mRNA.
 DR EMBL; X56127; CAA39592.1; -; mRNA.
 DR HSSP; P08592; INMW.

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 CC

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RESULT 27
056J06 CANFA PRELIMINARY; PRT; 770 AA.
AC 056J06;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 770.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AY926579; AAX81908.1; -; mRNA.
DR SMR; 056J06; 28-123, 124-189, 287-342, 460-569.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_c_r.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU_1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 770 AA; 86598 MW; 81ADDE2D3FB8DC6D CRC64;

Query Match 100.0%; Score 222; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 714

RESULT 28
06RH30 CANFA PRELIMINARY; PRT; 770 AA.
AC 06RH30;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Beta amyloid protein isoform APP770.
GN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AY989706; AAR9726.1; -; mRNA.
DR HSP; Q16019; IAAP.
DR SMR; 06RH30; 28-123, 124-189, 287-342, 460-569.
DR EMBL; ENSCAFG000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAMLOID.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 770 AA; 86529 MW; 4560E18B8405F588 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 714

RESULT 29
056J06 GRAGR PRELIMINARY; PRT; 42 AA.
AC 056J06;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AY926589; AAX81918.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.

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DR PRINTS; PR00204; BETAMYL0ID.
 FT NON_TER 1
 FT NON_TER 42
 SO SEQUENCE 42 AA; 4514 MM; 3AC85563D7858C37 CRC64;

Query Match 97.7%; Score 217; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGVIA 42
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 Db 1 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGVIA 42

RESULT 30

OS6J7 TURTR PRELIMINARY; PRT; 42 AA.
 ID OS6J7 TURTR
 AC OS6J7
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Amyloid beta protein (Fragment).
 OS Tursiops truncatus (Atlantic bottlenose dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Tursiops.
 OX NCBI_TaxID=9739;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarasa M.,
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";

Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AY926588; AAX81917.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAMYL0ID.
 FT NON_TER 1
 FT NON_TER 42
 SQ SEQUENCE 42 AA; 4514 MM; 3AC85563D7858C37 CRC64;

Query Match 97.7%; Score 217; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGVIA 42
 |||
 Db 1 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGVIA 42

Search completed: September 28, 2006, 06:22:57
 Job time : 140.991 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:23:21 ; Search time 30.2735 Seconds
(without alignments)
124.327 Million cell updates/sec

Title: US-09-731-899-4
Perfect score: 222
Sequence: 1 DAERHDSGYVHHQKLVF.....VGSNKGAIIQLMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :
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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS.COMB.pep.*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	222	100.0	43	1 US-08-437-067-1	Sequence 1, Appli
3	222	100.0	43	1 US-08-302-808-6	Sequence 6, Appli
4	222	100.0	43	1 US-08-079-511-1	Sequence 1, Appli
5	222	100.0	43	1 US-08-467-607-1	Sequence 1, Appli
6	222	100.0	43	1 US-08-404-831-1	Sequence 1, Appli
7	222	100.0	43	1 US-08-602-264A-3	Sequence 1, Appli
8	222	100.0	43	1 US-08-469-362-1	Sequence 1, Appli
9	222	100.0	43	1 US-08-612-785B-1	Sequence 1, Appli
10	222	100.0	43	1 US-08-475-579A-1	Sequence 1, Appli
11	222	100.0	43	1 US-08-850-392-1	Sequence 1, Appli
12	222	100.0	43	1 US-08-986-948-6	Sequence 6, Appli
13	222	100.0	43	1 US-08-975-977-1	Sequence 1, Appli
14	222	100.0	43	1 US-08-817-423-1	Sequence 1, Appli
15	222	100.0	43	1 US-08-920-162A-1	Sequence 1, Appli
16	222	100.0	43	2 US-08-461-018A-3	Sequence 3, Appli
17	222	100.0	43	2 US-08-976-191-1	Sequence 1, Appli
18	222	100.0	43	2 US-08-976-179-1	Sequence 1, Appli
19	222	100.0	43	2 US-09-216-958-3	Sequence 3, Appli
20	222	100.0	43	2 US-09-356-931-1	Sequence 1, Appli
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22	222	100.0	43	2 US-08-703-675C-1	Sequence 1, Appli
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28	222	100.0	43	2 US-09-280-966-1	Sequence 1, Appli
29	222	100.0	43	2 US-09-032-019-1	Sequence 1, Appli
30	222	100.0	43	2 US-09-481-980A-1	Sequence 1, Appli
31	222	100.0	43	2 US-09-594-366-1	Sequence 1, Appli
32	222	100.0	43	2 US-08-655-649-1	Sequence 1, Appli
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34	222	100.0	43	2 US-08-996-422-1	Sequence 1, Appli
35	222	100.0	43	2 US-09-984-834-1	Sequence 1, Appli
36	222	100.0	43	2 US-09-027-258-2	Sequence 2, Appli
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39	222	100.0	43	2 US-10-314-221-1	Sequence 1, Appli
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46	222	100.0	43	2 US-09-425-956-1	Sequence 1, Appli
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50	222	100.0	52	1 US-08-609-090-11	Sequence 1, Appli
51	222	100.0	53	2 US-09-173-887-5	Sequence 5, Appli
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56	222	100.0	63	1 US-08-462-859A-4	Sequence 4, Appli
57	222	100.0	63	1 US-08-123-659A-4	Sequence 4, Appli
58	222	100.0	63	1 US-08-464-247A-4	Sequence 4, Appli
59	222	100.0	63	1 US-08-464-248A-4	Sequence 4, Appli
60	222	100.0	70	3 US-09-155-076-14	Sequence 14, Appli
61	222	100.0	82	2 US-09-848-616-173	Sequence 173, App
62	222	100.0	99	1 US-08-442-333-3	Sequence 3, Appli
63	222	100.0	99	2 US-08-339-708A-4	Sequence 8, Appli
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65	222	100.0	100	7 5187153-10	Patent No. 5187153
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67	222	100.0	100	7 5223482-10	Patent No. 5223482
68	222	100.0	103	1 US-08-404-831-2	Sequence 2, Appli
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70	222	100.0	103	1 US-08-475-579A-2	Sequence 2, Appli
71	222	100.0	103	2 US-08-920-162A-2	Sequence 2, Appli
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73	222	100.0	103	2 US-08-339-708A-12	Sequence 12, Appli
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75	222	100.0	103	2 US-08-703-675C-2	Sequence 2, Appli
76	222	100.0	103	2 US-08-617-267C-2	Sequence 2, Appli
77	222	100.0	103	2 US-09-519-019A-2	Sequence 2, Appli
78	222	100.0	103	2 US-09-895-443A-2	Sequence 2, Appli
79	222	100.0	103	2 US-10-395-290-2	Sequence 2, Appli
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83	222	100.0	117	2 US-09-823-153-2	Sequence 2, Appli
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85	222	100.0	487	1 US-08-462-859A-9	Sequence 9, Appli
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87	222	100.0	487	1 US-08-464-247A-9	Sequence 9, Appli
88	222	100.0	487	1 US-08-464-248A-9	Sequence 9, Appli
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91	222	100.0	492	1 US-08-464-247A-7	Sequence 7, Appli
92	222	100.0	492	1 US-08-464-248A-7	Sequence 7, Appli
93	222	100.0	506	1 US-08-659-984A-21	Sequence 21, Appli
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96	222	100.0	506	2 US-09-404-578-21	Sequence 21, Appli
97	222	100.0	537	1 US-08-453-552-4	Sequence 4, Appli
98	222	100.0	537	1 US-08-710-637-4	Sequence 4, Appli
99	222	100.0	537	5 PCT-US93-00907-4	Sequence 4, Appli

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Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-08-235-400-1

Sequence 1, Application US/08235400

Patent No. 5552426

GENERAL INFORMATION:

APPLICANT: Lunn, William H.

APPLICANT: Monn, James A.

APPLICANT: Zimmerman, Dennis M.

TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL

TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/1104

CITY: Indianapolis

STATE: Indiana

COUNTRY: United States of America

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,400

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-9507

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756

TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-235-400-1

Query Match 100.0%; Score 222; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 9.8e-27; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 2

US-08-437-067-1

Sequence 1, Application US/08437067

Patent No. 5593846

GENERAL INFORMATION:

APPLICANT: Schenk, Dale B.

APPLICANT: Selkoe, Dennis J.

APPLICANT: Schlossmacher, Michael G.

APPLICANT: Seubert, Peter A.

APPLICANT: Vigna-Pelfrey, Carmen

TITLE OF INVENTION: Methods and Compositions for

TITLE OF INVENTION: Detection

TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,067

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/965,972

FILING DATE: 26-OCT-1992

APPLICATION NUMBER: US 07/911,647

FILING DATE: 10-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15270-6-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-437-067-1

Query Match 100.0%; Score 222; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 9.8e-27; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 3

US-08-302-808-6

Sequence 6, Application US/08302808

Patent No. 5750349

GENERAL INFORMATION:

APPLICANT: SUZUKI, No. 5750349unhiro

APPLICANT: ODAKA, Asano

APPLICANT: KITADA, Chieko

TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

TITLE OF INVENTION: DERIVATIVES AND USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02019

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,808

FILING DATE: 15-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 01032/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-302-808-6

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 4
US-08-079-511-1
Sequence 1, Application US/08079511
Patent No. 5766846
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Selkoe, Dennis J.
APPLICANT: Schlossmacher, Michael G.
APPLICANT: Seubert, Peter A.
APPLICANT: Vingo-Pelfrey, Carmen
TITLE OF INVENTION: Methods and Compositions for Detection
TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,511
FILING DATE: 19930617
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,972
FILING DATE: 26-OCT-1992
ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-6-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-079-511-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 5
US-08-467-607-1
Sequence 1, Application US/08467607
Patent No. 5783434
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: TATSUNO, GWEN
APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,607
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 33,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-8370
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-607-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 6

US-08-404-831-1
; Sequence 1, Application US/08404831
; Patent No. 5817626
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis, Howard Benjamin, Marc B. Garnick,
; APPLICANT: Malcolm L. Gelfer, Arvind Hundal, Laura Kasman,
; APPLICANT: Gary Musso, Ethan R. Signer, and James Makefield
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-amyloid peptide Aggrega
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,831
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A. (EAM)
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: PPI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-404-831-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 7
US-08-602-264A-3
; Sequence 3, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington

COUNTRY: D.C.
ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-602-264A-3

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 8
US-08-469-362-1
; Sequence 1, Application US/08469362
; Patent No. 5849711
; GENERAL INFORMATION:
; APPLICANT: TUNG, JAY S.
; APPLICANT: SINHA, SUKANTO
; APPLICANT: MCCONLOGUE, LISA
; APPLICANT: SEMKO, CHRISTOPHER M.F.
; TITLE OF INVENTION: NOVEL CATHERSIN AND METHODS AND
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES
; STREET: 800 F. Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,362
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUVAL, JEAN M.
; REGISTRATION NUMBER: 32,731
; REFERENCE/DOCKET NUMBER: 002010-005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-362-1

Query Match 100.0%; Score 222, DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 9

US-08-612-785B-1
Sequence 1, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-1

Query Match 100.0%; Score 222, DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 10
US-08-475-579A-1
Sequence 1, Application US/08475579A
Patent No. 5854215
GENERAL INFORMATION:

APPLICANT: Mark A. Findeis et al.
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide Aggrega
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,579A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: PPI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-475-579A-1

Query Match 100.0%; Score 222, DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 11
US-08-850-392-1
Sequence 1, Application US/08850392
Patent No. 5858982
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCOLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHESPIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES

STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUVAL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-850-392-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 12
US-08-986-948-6
Sequence 6, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317unhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatetsO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-6

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 13
US-08-975-977-1
Sequence 1, Application US/08975977
Patent No. 5965614
GENERAL INFORMATION:
APPLICANT: JAMES E. AUDIA
APPLICANT: BEVERLY K. FOLMER
APPLICANT: VARGHESE JOHN
APPLICANT: LEE H. LATIMER
APPLICANT: JEFFREY S. NISSEN
APPLICANT: JON K. REEL
APPLICANT: EUGENE D. THORSETT
APPLICANT: CELIA A. WHITESITT
TITLE OF INVENTION: N-(ARYL/HETEROARYL) AMINO
TITLE OF INVENTION: ACID ESTERS, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS
TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
ADDRESSEE: Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,977
FILING DATE: Unassigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,444
FILING DATE: 22 No. 596561ember 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-975-977-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 14
US-08-817-423-1
Sequence 1, Application US/08817423
Patent No. 5972634
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH E.
APPLICANT: BUSH, ASHLEY I.
APPLICANT: MOIR, ROBERT D.
TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's
TITLE OF INVENTION: Disease: Assessment of A Abnormalities
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,423
FILING DATE: 4-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/11895
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4110000/REF/JUK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
US-08-817-423-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 15
US-08-920-162A-1
Sequence 1, Application US/08920162A
Patent No. 5985242
GENERAL INFORMATION:
APPLICANT: Fideis, M. et al.
TITLE OF INVENTION: Modulators of {SYMBOL 98 \{ "symbol" }-Amyloid Peptide
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,162A
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-920-162A-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 16
US-08-461-018A-3
Sequence 3, Application US/08461018A
Patent No. 6071694
GENERAL INFORMATION:
APPLICANT: AKIHIKO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-461-018A-3

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVAT 43

RESULT 17
US-08-976-191-1
Sequence 1, Application US/08976191
Patent No. 6096782
GENERAL INFORMATION:
APPLICANT: BEVERLY K. FOLMER
APPLICANT: VARGHESE JOHN
APPLICANT: LEE H. LATIMER
APPLICANT: EUGENE D. THORSETT
APPLICANT: JING WU
APPLICANT: JAMES E. AUDIA
APPLICANT: JEFFREY S. NISSEN
APPLICANT: WARREN PORTER
TITLE OF INVENTION: N-(ARYL/HETEROARYL) AMINO
TITLE OF INVENTION: ACID DERIVATIVES, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS

TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burne, Doane, Swecker &
ADDRESSEE: Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,191
FILING DATE: 21 NOVEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 No. 6096782ember 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-191-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVAT 43

RESULT 18
US-08-976-179-1
Sequence 1, Application US/08976179
Patent No. 6117901
GENERAL INFORMATION:
APPLICANT: JING WU
APPLICANT: EUGENE D. THORSETT
APPLICANT: JEFFREY S. NISSEN
APPLICANT: THOMAS E. MABRY
APPLICANT: LEE H. LATIMER
APPLICANT: VARGHESE JOHN
APPLICANT: LAWRENCE Y. FANG
APPLICANT: JAMES E. AUDIA
TITLE OF INVENTION: N-(ARYL/HETEROARYL) ACETYL
TITLE OF INVENTION: AMINO ACID ESTERS, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS
TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
ADDRESSEE: Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,179
FILING DATE: 21 No. 6117901ember 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/098,551
FILING DATE: 22 No. 6117901ember 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-179-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAERHDGSEVHHQKLVFPAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAERHDGSEVHHQKLVFPAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 19
US-09-216-958-3
Sequence 3, Application US/09216958
Patent No. 6248559
GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-216-958-3

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAERHDGSEVHHQKLVFPAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAERHDGSEVHHQKLVFPAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 20
US-09-356-931-1
Sequence 1, Application US/09356931
Patent No. 6277826
GENERAL INFORMATION:
APPLICANT: Finkel, M. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1784
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/356,931
FILING DATE: 19-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/920,162
FILING DATE: 27-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/897,342
FILING DATE: 21-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Jr., Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PFI-016CP4CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-09-356-931-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 21

US-08-733-202-1
Sequence 1, Application US/08733202
Patent No. 6284221
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Selkoe, Dennis J.
APPLICANT: Schlossmacher, Michael G.
APPLICANT: Seubert, Peter A.
APPLICANT: Vigo-Pelfrey, Carmen
TITLE OF INVENTION: Methods and Compositions for Detection
TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,202
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,972
FILING DATE: 26-OCT-1992
APPLICATION NUMBER: US 08/437,067
FILING DATE: 09-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,972
FILING DATE: 26-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/911,647
FILING DATE: 10-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-6-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-202-1

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 22

US-08-703-675C-1
Sequence 1, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Finkels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kaia, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-703-675C-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGCVIAT 43

RESULT 23

US-09-390-692-1
Sequence 1, Application US/09390692
Patent No. 6313152
GENERAL INFORMATION:
APPLICANT: JING WU
EUGENE D. THORSETT
JEFFREY S. NISSEN
THOMAS E. MABRY

LEE H. LATIMER
VARGHESE JOHN
LAWRENCE Y. FANG
JAMES E. AUDIA
TITLE OF INVENTION: N-(ARYL/HETEROARYL)ACETYL
AMINO ACID ESTERS, PHARMACEUTICAL
COMPOSITIONS COMPRISING SAME, AND
METHODS FOR INHIBITING BETA-AMYLOID
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/390,692
FILING DATE: 07-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,179
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-050
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-390-692-1
Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGVIAT 43
Db 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGVIAT 43
RESULT 24
US-08-617-267C-1
Sequence 1, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findex, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-1
Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGVIAT 43
Db 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGVIAT 43
RESULT 25
US-09-303-655-1
Sequence 1, Application US/09303655
Patent No. 6333351
GENERAL INFORMATION:
APPLICANT: JING WU
EUGENE D. THORSETT
JEFFREY S. NISSEN
THOMAS E. MABRY
LEE H. LATIMER
VARGHESE JOHN
LAWRENCE Y. FANG
JAMES E. AUDIA
TITLE OF INVENTION: N-(ARYL/HETEROARYL)ACETYL
AMINO ACID ESTERS, PHARMACEUTICAL
COMPOSITIONS COMPRISING SAME, AND
METHODS FOR INHIBITING BETA-AMYLOID
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,655

FILING DATE: 03-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,179
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: <Unknown>
US-09-303-655-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 26
US-08-294-819-1
Sequence 1, Application US/08294819
Patent No. 6365414
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bush, Ashley I.
TITLE OF INVENTION: An In Vitro System for Determining
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,819
FILING DATE: 26-AUG-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4100000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-294-819-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 27
US-09-408-283-1
Sequence 1, Application US/09408283
Patent No. 6486350
GENERAL INFORMATION:
APPLICANT: AUDIA, James
APPLICANT: HYSLIP, Paul
APPLICANT: NISSEN, Jeffrey
APPLICANT: THOMPSON, Richard
APPLICANT: TUNG, Jay
APPLICANT: TANNER, Laura
TITLE OF INVENTION: BIOLOGICAL REAGENTS AND METHODS FOR DETERMINING THE MECHANISM
FILE REFERENCE: 002010-354
CURRENT APPLICATION NUMBER: US/09/408,283
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 09/164,390
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1
LENGTH: 43
TYPE: PRT
ORGANISM: beta-amyloid precursor protein
US-09-408-283-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 28
US-09-280-966-1
Sequence 1, Application US/09280966
Patent No. 6495693
GENERAL INFORMATION:
APPLICANT: JAMES E. AUDIA
BEVERLY K. FOLMER
VARGHESE JOHN
JEFFREY S. NISSEN
WARREN J. PORTER
EUGENE D. THORSETT
JING WU
TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL) AMINO
ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
COMPRISING SAME, AND METHODS FOR INHIBITING
-AMYLOID PEPTIDE RELEASE AND/OR ITS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/280,366
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,191
FILING DATE: 21 NOV 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 NOV 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-280-966-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 29
US-09-032-019-1
Sequence 1, Application US/09032019
Patent No. 6506782
GENERAL INFORMATION:
APPLICANT: EUGENE D. THORSETT
APPLICANT: WARREN J. PORTER
APPLICANT: JEFFREY S. NISSEN
APPLICANT: LEE H. LATIMER
APPLICANT: JAMES E. AUDIA
APPLICANT: JAMES DROSTE
TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
TITLE OF INVENTION: SAME, AND METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS SYNTHESIS BY
TITLE OF INVENTION: USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Machis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,019
FILING DATE: 27 February 1998 (27.02.98)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/093,056
FILING DATE: 28 February 1997 (28.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-081

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-019-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 30
US-09-481-980A-1
Sequence 1, Application US/09481980A
Patent No. 6518011
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING CELLULAR PROCESSING OF EP
TITLE OF INVENTION: TAGGED BETA-AMYLOID
FILE REFERENCE: DM-6978
CURRENT APPLICATION NUMBER: US/09/481,980A
CURRENT FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/115,749
PRIOR FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 43
TYPE: PRT
ORGANISM: Human
US-09-481-980A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGSVIAT 43

Search completed: September 28, 2006, 06:27:13
Job time : 31.2735 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:58:47 ; Search time 98.5336 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-4
Perfect score: 222
Sequence: 1 DAERFRHDSGYEVHHQKLVF.....VGSNKGAIIGIMVGVIAT 43

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	43	3	US-09-280-966-1
2	222	100.0	43	3	US-09-904-987-1
3	222	100.0	43	3	US-09-808-037-3
4	222	100.0	43	3	US-09-866-712-3
5	222	100.0	43	3	US-09-972-475-1
6	222	100.0	43	3	US-09-992-800-1
7	222	100.0	43	3	US-09-895-443-1
8	222	100.0	43	3	US-09-915-342-1
9	222	100.0	43	3	US-09-996-357-1
10	222	100.0	43	3	US-09-992-994-1
11	222	100.0	43	3	US-09-984-834-1
12	222	100.0	43	3	US-09-425-956-1
13	222	100.0	43	3	US-09-942-253-1
14	222	100.0	43	4	US-10-041-605-1
15	222	100.0	43	4	US-10-076-708-7
16	222	100.0	43	4	US-10-051-496-1
17	222	100.0	43	4	US-10-217-459-1
18	222	100.0	43	4	US-10-162-889-3
19	222	100.0	43	4	US-10-217-584-1
20	222	100.0	43	4	US-10-326-049-1
21	222	100.0	43	4	US-10-190-548A-2
22	222	100.0	43	4	US-10-335-035-1
23	222	100.0	43	4	US-10-267-017-1
24	222	100.0	43	4	US-10-314-221-1
25	222	100.0	43	4	US-10-437-706-2
26	222	100.0	43	4	US-10-385-065-1
27	222	100.0	43	4	US-10-463-729-1

28	222	100.0	43	4	US-10-355-700-1	Sequence 1, Appli
29	222	100.0	43	4	US-10-384-788-3	Sequence 3, Appli
30	222	100.0	43	4	US-10-618-856-3	Sequence 3, Appli
31	222	100.0	43	4	US-10-415-383-2	Sequence 2, Appli
32	222	100.0	43	4	US-10-619-454-2	Sequence 2, Appli
33	222	100.0	43	4	US-10-250-581-1	Sequence 1, Appli
34	222	100.0	43	4	US-10-699-517-3	Sequence 33, Appli
35	222	100.0	43	4	US-10-796-522-1	Sequence 1, Appli
36	222	100.0	43	4	US-10-663-815-12	Sequence 12, Appli
37	222	100.0	43	4	US-10-698-099-33	Sequence 33, Appli
38	222	100.0	43	5	US-10-915-214-33	Sequence 33, Appli
39	222	100.0	43	5	US-10-749-522-3	Sequence 3, Appli
40	222	100.0	43	5	US-10-831-524-1	Sequence 1, Appli
41	222	100.0	43	5	US-10-934-819-6	Sequence 6, Appli
42	222	100.0	43	5	US-10-777-247-1	Sequence 1, Appli
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47	222	100.0	43	6	US-11-073-526-3	Sequence 3, Appli
48	222	100.0	43	6	US-11-066-697-954	Sequence 954, App
49	222	100.0	43	6	US-11-066-697-987	Sequence 987, App
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51	222	100.0	43	6	US-11-194-989-17	Sequence 17, Appli
52	222	100.0	43	6	US-11-195-207-17	Sequence 17, Appli
53	222	100.0	43	6	US-11-185-907-33	Sequence 33, Appli
54	222	100.0	43	6	US-10-485-310-20	Sequence 20, Appli
55	222	100.0	43	5	US-10-848-686-1	Sequence 1, Appli
56	222	100.0	43	5	US-10-490-799-129	Sequence 129, App
57	222	100.0	43	5	US-10-505-313-414	Sequence 414, App
58	222	100.0	53	3	US-09-797-543-5	Sequence 5, Appli
59	222	100.0	53	4	US-10-016-717-1	Sequence 1, Appli
60	222	100.0	53	5	US-10-485-310-7	Sequence 7, Appli
61	222	100.0	55	5	US-10-849-423-6	Sequence 6, Appli
62	222	100.0	56	4	US-10-771-174A-16	Sequence 16, Appli
63	222	100.0	56	4	US-10-771-174A-19	Sequence 19, Appli
64	222	100.0	58	4	US-10-771-174A-12	Sequence 12, Appli
65	222	100.0	58	4	US-10-771-174A-14	Sequence 14, Appli
66	222	100.0	58	4	US-10-771-174A-27	Sequence 27, Appli
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68	222	100.0	60	4	US-10-771-174A-20	Sequence 20, Appli
69	222	100.0	64	4	US-10-771-174A-13	Sequence 13, Appli
70	222	100.0	70	3	US-09-155-076-14	Sequence 14, Appli
71	222	100.0	79	4	US-10-771-174A-15	Sequence 15, Appli
72	222	100.0	79	5	US-10-700-922-3	Sequence 3, Appli
73	222	100.0	82	3	US-09-848-616-173	Sequence 173, App
74	222	100.0	82	4	US-10-050-902-219	Sequence 219, App
75	222	100.0	82	4	US-10-050-888-219	Sequence 219, App
76	222	100.0	82	4	US-10-622-087-93	Sequence 93, Appli
77	222	100.0	99	4	US-10-183-119-2	Sequence 2, Appli
78	222	100.0	99	4	US-10-771-174A-22	Sequence 22, Appli
79	222	100.0	99	5	US-10-771-174A-24	Sequence 24, Appli
80	222	100.0	99	5	US-10-486-285-3	Sequence 3, Appli
81	222	100.0	100	3	US-09-794-975-4	Sequence 4, Appli
82	222	100.0	100	4	US-10-275-025-1	Sequence 1, Appli
83	222	100.0	100	4	US-10-275-025-2	Sequence 2, Appli
84	222	100.0	100	4	US-10-275-025-3	Sequence 3, Appli
85	222	100.0	100	4	US-10-275-025-4	Sequence 4, Appli
86	222	100.0	100	4	US-10-275-025-5	Sequence 5, Appli
87	222	100.0	100	5	US-10-849-423-4	Sequence 4, Appli
88	222	100.0	100	5	US-10-486-265-5	Sequence 5, Appli
89	222	100.0	100	6	US-11-243-578-1	Sequence 1, Appli
90	222	100.0	100	6	US-11-243-578-2	Sequence 2, Appli
91	222	100.0	100	6	US-11-243-578-3	Sequence 3, Appli
92	222	100.0	100	6	US-11-243-578-4	Sequence 4, Appli
93	222	100.0	100	6	US-11-243-578-5	Sequence 5, Appli
94	222	100.0	103	3	US-09-972-475-2	Sequence 2, Appli
95	222	100.0	103	3	US-09-895-443-2	Sequence 2, Appli
96	222	100.0	103	4	US-10-395-290-2	Sequence 2, Appli
97	222	100.0	103	4	US-10-463-729-2	Sequence 2, Appli
98	222	100.0	103	5	US-10-989-763-2	Sequence 2, Appli
99	222	100.0	103	5	US-10-677-076-2	Sequence 2, Appli
100	222	100.0	108	4	US-10-275-025-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-280-966-1
Sequence 1, Application US/09280966
Patent No. US20010020097A1

GENERAL INFORMATION:

APPLICANT: JAMES E. AUDIA
BEVERLY K. FOLMER
VARGHESE JOHN
JEFFREY S. NISSEN
WARREN J. PORTER
EUGENE D. THORSETT
JING WU

TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL) AMINO
ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
COMPRISING SAME, AND METHODS FOR INHIBITING
-AMYLOID PEPTIDE RELEASE AND/OR ITS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22113-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/280,966
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/976,191
FILING DATE: 21 NOV 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 NOV 1996

ATTORNEY/AGENT INFORMATION:

NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-280-966-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

RESULT 2

US-09-904-987-1
Sequence 1, Application US/09904987
Patent No. US20020037908A1

GENERAL INFORMATION:

APPLICANT: No. US20020037908A1actyl, Inc.

TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathic

FILE REFERENCE: 42108/26146

CURRENT APPLICATION NUMBER: US/09/904,987

CURRENT FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 43

TYPE: PRT

ORGANISM: homo sapiens

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRRUA4

DATABASE ENTRY DATE: 2000-09-15

RELEVANT RESIDUES: (672)..(714)

US-09-904-987-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

RESULT 3

US-09-808-037-3
Sequence 3, Application US/09808037
Patent No. US20020052311A1

GENERAL INFORMATION:

APPLICANT: HANAN, Elia
APPLICANT: SOLOMON, Beki
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
FILE REFERENCE: SOLOMON-2D

CURRENT APPLICATION NUMBER: US/09/808,037

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/629,971

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/473,653

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: US 60/152,417

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0

SEQ ID NO 3

LENGTH: 43

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic peptide

US-09-808-037-3

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVAT 43

RESULT 4

US-09-866-712-3
Sequence 3, Application US/09866712
Patent No. US20020058637A1

GENERAL INFORMATION:

APPLICANT: AKIHiko TAKASHIMA et al.

TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY

INHIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S DIS

KINASE I (AS AMENDED)

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/866,712
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/216,958
FILING DATE: December 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)721-8200
TELEFAX: (202)721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-866-712-3

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 5
US-09-972-475-1
Sequence 1, Application US/09972475
Patent No. US20020098173A1
GENERAL INFORMATION:
APPLICANT: Findex, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,475
FILING DATE: 04-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,267
FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-972-475-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 6
US-09-992-800-1
Sequence 1, Application US/09992800
Patent No. US20020102261A1
GENERAL INFORMATION:
APPLICANT: Raso, Victor
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
FILE REFERENCE: BBRI-2006
CURRENT APPLICATION NUMBER: US/09/992,800
FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/594,366
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,408
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 43
TYPE: PPT
ORGANISM: Homo sapiens
US-09-992-800-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 7
US-09-895-443-1
Sequence 1, Application US/09895443
Patent No. US20020103134A1
GENERAL INFORMATION:
APPLICANT: Findex, M. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street

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; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,443
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/356,931
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CPACN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-895-443-1
Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 8
US-09-915-342-1
; Sequence 1, Application US/09915342
; Publication No. US20020123486A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Jing
; APPLICANT: Tung, Jay S.
; APPLICANT: Thorseth, Eugene D.
; APPLICANT: Nissen, Jeffrey S.
; APPLICANT: Neitz, Jeffrey
; APPLICANT: Lattimer, Lee H.
; APPLICANT: John, Varghese
; APPLICANT: Britton, Thomas C.
; APPLICANT: Audia, James A.
; APPLICANT: Reel, Jon K.
; APPLICANT: Madry, Thomas E.
; APPLICANT: Cwi, Cynthia L.
; APPLICANT: McDaniel, Stacey L.
; APPLICANT: Scott, William Leonard
; TITLE OF INVENTION: Cycloalkyl, Lactam, Lactone and Related Compounds,
; TITLE OF INVENTION: Pharmaceutical Compositions Comprising Same, and
; TITLE OF INVENTION: Methods of Inhibiting Beta-Amyloid Peptide Release
; TITLE OF INVENTION: and/or its Synthesis by Use of Such Compounds
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; FILE REFERENCE: 002010-062
; CURRENT APPLICATION NUMBER: US/09/915,342
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US/08/996,422
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/064,851
; PRIOR FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: beta-amyloid precursor protein (APP)
US-09-915-342-1
Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 9
US-09-996-357-1
; Sequence 1, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Geffter, Malcolm L
; APPLICANT: Israel, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-1
Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 10
US-09-992-994-1
; Sequence 1, Application US/09992994
; Patent No. US20020136718A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRT-1005
; CURRENT APPLICATION NUMBER: US/09/992,994
; CURRENT FILING DATE: 2001-11-06
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PRIOR APPLICATION NUMBER: 09/594,366
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,408
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-994-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 11
US-09-984-834-1
Sequence 1, Application US/09984834
Patent No. US20020137743A1
GENERAL INFORMATION:
APPLICANT: JING WU
EUGENE D. THORSETT
JEFFREY S. NISSEN
THOMAS E. MABRY
LEE H. LATIMER
VARGHESE JOHN
LAWRENCE Y. FANG
JAMES E. AUDIA
TITLE OF INVENTION: N-(ARYL/HETEROARYL)ACETYL
AMINO ACID ESTERS, PHARMACEUTICAL
COMPOSITIONS COMPRISING SAME, AND
METHODS FOR INHIBITING BETA-AMYLOID
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,834
FILING DATE: 31-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,179
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-984-834-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 12
US-09-425-956-1
Sequence 1, Application US/09425956
Publication No. US2003073074A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH E.
APPLICANT: BUSH, ASHLEY I.
APPLICANT: MOIR, ROBERT D.
TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's
TITLE OF INVENTION: Disease: Assessment of A Abnormalities
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,956
FILING DATE: Herewith (25-OCT-1999)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/817,423
FILING DATE: 04-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/11895
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4110001/REF/JUK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-425-956-1

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 13
US-09-942-253-1
Sequence 1, Application US/09942253

```

; Publication No. US20030082191A1
; GENERAL INFORMATION:
; APPLICANT: Poduslo, Joseph F.
; APPLICANT: Curran, Geoffrey L.
; TITLE OF INVENTION: TREATMENT FOR CENTRAL NERVOUS SYSTEM DISORDERS
; FILE REFERENCE: 07039-351001
; CURRENT APPLICATION NUMBER: US/09/942,253
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-942-253-1

Query Match      100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 14
US-10-041-605-1
; Sequence 1, Application US/10041605
; Publication No. US20020115223A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bush, Ashley I.
; TITLE OF INVENTION: An In Vitro System For Determining Formation of A Amyloid
; FILE REFERENCE: 0609 4100001
; CURRENT APPLICATION NUMBER: US/10/041,605
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 08/294,819
; PRIOR FILING DATE: 1994-08-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-041-605-1

Query Match      100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 15
US-10-076-708-7
; Sequence 7, Application US/10076708
; Publication No. US20020164657A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Satish
; APPLICANT: Rank, Kenneth
; TITLE OF INVENTION: Assays for Accessing Aa-Tau Aggregation
; FILE REFERENCE: 6322
; CURRENT APPLICATION NUMBER: US/10/076,708
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-076-708-7
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Query Match      100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 16
US-10-051-496-1
; Sequence 1, Application US/10051496
; Publication No. US20020182660A1
; GENERAL INFORMATION:
; APPLICANT: Kei-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
; Abeta(1-41), Abeta(1-42) and Abeta(1-43)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Kei-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC Compatibles
; OPERATING SYSTEM: Windows
; SOFTWARE: MS No. US20020182660A1epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051,496
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,854A
; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 60/183,407
; FILING DATE: 18-February-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Koenig, C. Frederick III
; REGISTRATION NUMBER: 29,662
; REFERENCE/DOCKET NUMBER: PRI-PT001.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-6400
; TELEFAX: (215) 568-6499
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 Amino Acid
; TYPE: Amino Acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHEetical: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; CELL TYPE: <Unknown>
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: <Unknown>
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 43
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-051-496-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 17
US-10-217-459-1
Sequence 1, Application US/10217459
Publication No. US2003006945A1
GENERAL INFORMATION:
APPLICANT: AUDIA, James
APPLICANT: HYSLOP, Paul
APPLICANT: NISEN, Jeffrey
APPLICANT: THOMPSON, Richard
APPLICANT: TUNG, Jay
APPLICANT: TANNER, Laura
TITLE OF INVENTION: BIOLOGICAL REAGENTS AND METHODS FOR DETERMINING THE
TITLE OF INVENTION: MECHANISM IN THE GENERATION OF BETA-AMYLOID PEPTIDE
FILE REFERENCE: 002010-354
CURRENT APPLICATION NUMBER: US/10/217,459
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 09/164,390
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: beta-amyloid precursor protein
US-10-217-459-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 18
US-10-162-889-3
Sequence 3, Application US/10162889
Publication No. US20030077252A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beke
APPLICANT: HANAN, Eliat
TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
TITLE OF INVENTION: USEFUL IN DIAGNOSING
TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
FILE REFERENCE: SOLOMON=28
CURRENT APPLICATION NUMBER: US/10/162,889
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US/09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: synthetic peptide
US-10-162-889-3

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 19
US-10-217-584-1
Sequence 1, Application US/10217584
Publication No. US20030077261A1
GENERAL INFORMATION:
APPLICANT: Paris, Daniel
APPLICANT: Mullian, Michael
TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
FILE REFERENCE: USF-T161XC1
CURRENT APPLICATION NUMBER: US/10/217,584
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,656
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1) ..(43)
OTHER INFORMATION: A-beta 1-43 peptide
US-10-217-584-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 20
US-10-326-049-1
Sequence 1, Application US/10326049
Publication No. US20030091983A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING CELLULAR PROCESSING OF EP
FILE REFERENCE: DM-6978
CURRENT APPLICATION NUMBER: US/10/326,049
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/115,749
PRIOR FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Human
US-10-326-049-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 21

US-190-548A-2

Sequence 2, Application US/10190548A

Publication No. US20030109435A1

GENERAL INFORMATION:

APPLICANT: Griswold Premier, Irene

APPLICANT: Wright, Sarah

APPLICANT: Yednock, Theodore

APPLICANT: Rydel, Russell

TITLE OF INVENTION: Methods of Inhibiting Amyloid Toxicity

FILE REFERENCE: 08576, 0030-00

CURRENT APPLICATION NUMBER: US/10/190,548A

CURRENT FILING DATE: 2002-12-09

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 2

LENGTH: 43

TYPE: PRT

ORGANISM: Homo sapiens

US-190-548A-2

Query Match 100.0%; Score 222; DB 4; Length 43;

Best Local Similarity 100.0%; Pred. No. 1e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 22

US-10-335-035-1

Sequence 1, Application US/10335035

Publication No. US20030148392A1

GENERAL INFORMATION:

APPLICANT: CITRON, MARTIN

APPLICANT: SELKOE, DENNIS J.

APPLICANT: SEUBERT, PETER A.

APPLICANT: SCHEINK, DALE

TITLE OF INVENTION: SCREENING COMPOUNDS FOR THE ABILITY TO ALTER THE PRODUCTION OF AMYLOID-BETA PEPTIDE (X-T41)

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,035

FILING DATE: 30-Dec-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/665,649

FILING DATE: 18-JUN-1996

APPLICATION NUMBER: US 08/437,067

FILING DATE: 09-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: STORELLA ESQ., JOHN R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 15270-000650

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 576-0300

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 23

US-10-267-017-1

Sequence 1, Application US/10267017

Publication No. US20030153550A1

GENERAL INFORMATION:

APPLICANT: Audia, James E.

APPLICANT: Thompson, Richard C.

APPLICANT: Wilkie, Stephen

APPLICANT: Britton, Thomas C.

APPLICANT: Potter, Warren J.

APPLICANT: Hufman, George W.

APPLICANT: Lacimer, Lee H.

TITLE OF INVENTION: Deoxyamino Acid Compounds, Pharmaceutical Compositions

TITLE OF INVENTION: Compiling Same, and Methods for Inhibiting

TITLE OF INVENTION: Beta-Amyloid Peptide Release and/or its Synthesis by

TITLE OF INVENTION: Use of Such Compounds

FILE REFERENCE: 002010-776

CURRENT APPLICATION NUMBER: US/10/267,017

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: 09/337,484

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 60/155,265

PRIOR FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1

LENGTH: 43

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Beta-Amyloid

US-10-267-017-1

Query Match 100.0%; Score 222; DB 4; Length 43;

Best Local Similarity 100.0%; Pred. No. 1e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 24

US-10-314-221-1

Sequence 1, Application US/10314221

Publication No. US2003019119A1

GENERAL INFORMATION:

APPLICANT: Wu, Jing

APPLICANT: Thorsett, Eugene D.

APPLICANT: Nissen, Jeffrey S.

APPLICANT: Mabry, Thomas B.

APPLICANT: Lacimer, Lee H.

APPLICANT: John, Vargheese

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-335-035-1

Query Match 100.0%; Score 222; DB 4; Length 43;

Best Local Similarity 100.0%; Pred. No. 1e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

APPLICANT: Fang, Lawrence Y.
APPLICANT: Audia, James E.
TITLE OF INVENTION: N-(Ary1/Heteroarylaceyl) Amino Acid Esters,
TITLE OF INVENTION: Pharmaceutical Compositions Comprising Same, and
TITLE OF INVENTION: Methods for Inhibiting Beta-Amyloid Peptide Release
TITLE OF INVENTION: and/or Its Synthesis by Use of Such Compounds
FILE REFERENCE: 002010-789
CURRENT APPLICATION NUMBER: US/10/314,221
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 09/984,834
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 09/303,655
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: 08/976,179
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/098,551
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Beta-Amyloid
US-10-314-221-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 25
US-10-437-706-2
Sequence 2, Application US/10437706
Publication No. US20030199094A1
GENERAL INFORMATION:
APPLICANT: Pruss, Rebecca
Huggins, John
Rautmann, Guy
Cordell, Barbara
Scardina, Jan
Mischak, Ron
TITLE OF INVENTION: IMPROVED ASSAYS FOR BETA-AMYLOID
PROCESSING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/437,706
FILING DATE: 14-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/027,258
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marsh, David R
REGISTRATION NUMBER: P-41,182

REFERENCE/DOCKET NUMBER: 03561.0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6904
TELEFAX: 202 383-6610
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030199094A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-437-706-2

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 26
US-10-385-065-1
Sequence 1, Application US/10385065
Publication No. US20030235897A1
GENERAL INFORMATION:
APPLICANT: Rao, Victor
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
FILE REFERENCE: BBRI-2004
CURRENT APPLICATION NUMBER: US/10/385,065
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US/09/594,366
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,408
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-10-385-065-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 27
US-10-463-729-1
Sequence 1, Application US/10463729
Publication No. US20040005307A1
GENERAL INFORMATION:
APPLICANT: Finkel, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,729
FILING DATE: 17-JUNE-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConci, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-10-463-729-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 28
US-10-355-700-1
Sequence 1, Application US/10355700
Publication No. US20040006085A1
GENERAL INFORMATION:
APPLICANT: Tung, Jay S.
APPLICANT: Gulnm, Ashley C.
APPLICANT: Thorsette, Gene
APPLICANT: Pleiss, Mike A.
TITLE OF INVENTION: Hydroxyalkanoyl Aminopyrazoles and Related Compounds
FILE REFERENCE: 02351,0002.NPUS01
CURRENT APPLICATION NUMBER: US/10/355,700
PRIOR FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 60/353,214
PRIOR FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: human
US-10-355-700-1

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 29
US-10-384-788-3
Sequence 3, Application US/10384788
Publication No. US20040013647A1
GENERAL INFORMATION:
APPLICANT: FRENKEL, Dan
APPLICANT: SOLOMON, Beka
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
FILE REFERENCE: SOLOMON-2D.2
CURRENT APPLICATION NUMBER: US/10/384,788
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/371,735
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 09/808,037
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/830,954
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 10/162,889
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/152,417
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/IL00/00518
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-384-788-3

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 30
US-10-618-856-3
Sequence 3, Application US/10618856
Publication No. US20040052766A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
APPLICANT: FRENKEL, Dan
TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
FILE REFERENCE: SOLOMON-2A
CURRENT APPLICATION NUMBER: US/10/618,856
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/09/473,653A
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-618-856-3

Query Match 100.0%; Score 222; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 ; Search time 16.7758 Seconds

(without alignments)
199.069 Million cell updates/sec

Title: US-09-731-899-4

Perfect score: 222

Sequence: 1 DAEPFRHDSGYEVHHQKLVF.....VGSNKGAIGLMGVVIAT 43

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 285145 seqs, 7763843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubppa/US06_NEW_PUB pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppa/US07_NEW_PUB pep:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	43	1	US-09-731-899-4
2	222	100.0	43	7	US-11-348-091-1
3	222	100.0	56	6	US-10-544-093-16
4	222	100.0	56	6	US-10-544-093-19
5	222	100.0	58	6	US-10-544-093-12
6	222	100.0	58	6	US-10-544-093-14
7	222	100.0	58	6	US-10-544-093-27
8	222	100.0	59	1	US-09-731-899-1
9	222	100.0	60	6	US-10-544-093-20
10	222	100.0	64	6	US-10-544-093-13
11	222	100.0	79	6	US-10-544-093-15
12	222	100.0	99	6	US-10-544-093-22
13	222	100.0	99	6	US-10-544-093-24
14	222	100.0	142	6	US-10-544-093-21
15	222	100.0	142	6	US-10-544-093-17
16	222	100.0	142	6	US-10-544-093-23
17	222	100.0	185	6	US-10-544-093-18
18	222	100.0	203	6	US-10-544-093-26
19	222	100.0	316	6	US-10-544-093-25
20	222	100.0	695	6	US-10-515-919A-1
21	222	100.0	695	6	US-10-511-269-7
22	222	100.0	751	6	US-10-546-547-2
23	222	100.0	770	6	US-10-511-269-9
24	217	97.7	42	6	US-10-890-071-42
25	217	97.7	42	6	US-10-544-093-1

26	217	97.7	42	6	US-10-546-547-3	Sequence 3, Appli
27	217	97.7	42	6	US-10-966-645-36	Sequence 36, Appli
28	217	97.7	42	6	US-11-104-300-2	Sequence 2, Appli
29	217	97.7	42	7	US-11-297-316-1	Sequence 1, Appli
30	217	97.7	42	7	US-11-287-157A-49	Sequence 49, Appli
31	217	97.7	58	6	US-10-515-919A-30	Sequence 30, Appli
32	217	97.7	626	6	US-10-515-919A-13	Sequence 13, Appli
33	217	97.7	626	6	US-10-515-919A-18	Sequence 18, Appli
34	216	97.3	626	6	US-10-515-919A-15	Sequence 15, Appli
35	216	97.3	626	6	US-10-515-919A-20	Sequence 20, Appli
36	215	96.8	626	6	US-10-515-919A-14	Sequence 14, Appli
37	215	96.8	626	6	US-10-515-919A-16	Sequence 16, Appli
38	215	96.8	626	6	US-10-515-919A-19	Sequence 19, Appli
39	215	96.8	626	6	US-10-515-919A-21	Sequence 21, Appli
40	214	96.4	626	6	US-10-515-919A-12	Sequence 12, Appli
41	214	96.4	626	6	US-10-515-919A-17	Sequence 17, Appli
42	211	95.0	42	1	US-09-731-899-3	Sequence 1, Appli
43	210	94.6	42	7	US-11-269-857-5	Sequence 5, Appli
44	209	94.1	40	1	US-09-731-899-2	Sequence 2, Appli
45	209	94.1	40	6	US-10-966-645-37	Sequence 37, Appli
46	207	93.2	42	6	US-10-966-645-38	Sequence 38, Appli
47	204	91.9	42	6	US-10-515-919A-3	Sequence 3, Appli
48	204	91.9	42	6	US-10-515-919A-8	Sequence 8, Appli
49	203	91.4	42	7	US-11-104-300-3	Sequence 3, Appli
50	203	91.4	42	6	US-10-515-919A-5	Sequence 5, Appli
51	203	91.4	42	6	US-10-515-919A-10	Sequence 10, Appli
52	203	91.4	695	6	US-10-538-410-96	Sequence 96, Appli
53	203	91.4	770	7	US-11-104-300-1	Sequence 1, Appli
54	202	91.0	40	1	US-09-731-899-5	Sequence 5, Appli
55	202	91.0	40	7	US-11-269-857-3	Sequence 3, Appli
56	202	91.0	42	6	US-10-515-919A-4	Sequence 4, Appli
57	202	91.0	42	6	US-10-515-919A-6	Sequence 6, Appli
58	202	91.0	42	6	US-10-515-919A-9	Sequence 9, Appli
59	202	91.0	42	6	US-10-515-919A-11	Sequence 11, Appli
60	201	90.5	42	6	US-10-515-919A-2	Sequence 2, Appli
61	201	90.5	42	6	US-10-515-919A-7	Sequence 7, Appli
62	199	89.6	38	6	US-10-966-645-39	Sequence 39, Appli
63	198	89.2	42	6	US-10-515-919A-22	Sequence 22, Appli
64	198	89.2	42	6	US-10-515-919A-23	Sequence 23, Appli
65	196	88.3	38	6	US-10-966-645-44	Sequence 44, Appli
66	155	69.8	32	1	US-09-731-899-6	Sequence 6, Appli
67	152	68.5	28	7	US-09-731-899-7	Sequence 7, Appli
68	125	56.3	26	1	US-09-731-899-9	Sequence 9, Appli
69	116	52.3	21	6	US-10-966-645-42	Sequence 42, Appli
70	106	47.7	19	6	US-10-966-645-43	Sequence 43, Appli
71	103	46.4	19	6	US-10-966-645-45	Sequence 45, Appli
72	84	37.8	19	6	US-10-890-071-75	Sequence 75, Appli
73	66	29.7	13	6	US-10-890-071-72	Sequence 72, Appli
74	62	27.9	11	6	US-10-966-645-40	Sequence 40, Appli
75	61	27.5	10	6	US-10-890-071-13	Sequence 13, Appli
76	61	27.5	10	6	US-10-890-071-14	Sequence 14, Appli
77	59	26.6	10	6	US-10-890-071-12	Sequence 12, Appli
78	59	26.6	11	6	US-10-966-645-35	Sequence 35, Appli
79	58	26.1	11	6	US-10-890-071-15	Sequence 15, Appli
80	58	26.1	624	6	US-10-449-302-33879	Sequence 33879, A
81	57	25.7	10	6	US-10-890-071-9	Sequence 9, Appli
82	56.5	25.5	1046	6	US-10-449-302-51230	Sequence 51230, A
83	56	25.2	10	6	US-10-890-071-10	Sequence 10, Appli
84	56	25.2	10	6	US-10-890-071-11	Sequence 11, Appli
85	56	25.2	10	6	US-10-890-071-16	Sequence 16, Appli
86	56	25.2	10	6	US-10-890-071-17	Sequence 17, Appli
87	56	25.2	10	6	US-10-890-071-18	Sequence 18, Appli
88	55.5	25.0	356	7	US-11-056-3558-51189	Sequence 51189, A
89	55.5	25.0	480	7	US-11-056-3558-51188	Sequence 51188, A
90	55.5	25.0	504	7	US-11-056-3558-51187	Sequence 51187, A
91	55.5	25.0	618	6	US-10-449-302-47542	Sequence 47542, A
92	55	24.8	10	6	US-10-890-071-19	Sequence 19, Appli
93	55	24.8	10	6	US-10-890-071-21	Sequence 21, Appli
94	55	24.8	429	7	US-11-056-3558-53789	Sequence 53789, A
95	55	24.8	556	7	US-11-056-3558-53788	Sequence 53788, A
96	55	24.8	642	7	US-11-056-3558-53787	Sequence 53787, A
97	54.5	24.5	826	7	US-11-056-3558-87461	Sequence 87461, A
98	54.5	24.5	828	7	US-11-056-3558-87460	Sequence 87460, A

99 54.5 24.5 1083 7 US-11-056-355B-87459 Sequence 87459, A
100 54 24.3 10 6 US-10-890-071-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-731-899-4
; Sequence 4, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-4

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 2

US-11-348-091-1
; Sequence 1, Application US/11348091
; Publication No. US20060211679A1
; GENERAL INFORMATION:
; APPLICANT: Han, Qi
; TITLE OF INVENTION: Substituted Lactams as Inhibitors of Abeta Protein Production
; FILE REFERENCE: BMS-PH-7164.1(C)
; CURRENT APPLICATION NUMBER: US/11/348,091
; CURRENT FILING DATE: 2006-02-06
; PRIOR APPLICATION NUMBER: US 10/685,031
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 09/832,455
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/196,549
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-348-091-1

Query Match 100.0%; Score 222; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 3

US-10-544-093-16
; Sequence 16, Application US/10544093

; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Padre-A-beta fragment fusion protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(56)
; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16

Query Match 100.0%; Score 222; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
Db 14 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 56

RESULT 4

US-10-544-093-19
; Sequence 19, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
US-10-544-093-19

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (46)-(46)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-19

Query Match 100.0%; Score 222; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
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DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 5
US-10-544-093-12

Sequence 12, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 152703-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12

Query Match 100.0%; Score 222; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 6
US-10-544-093-14

Sequence 14, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 152703-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856

PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 7
US-10-544-093-27

Sequence 27, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 152703-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27

Query Match 100.0%; Score 222; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 8
US-09-731-899-1

Sequence 1, Application US/09731899
Publication No. US20060088548A1

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGSVIAT 43

```

; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-1

Query Match          100.0%; Score 222; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43
Db 5 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 47

RESULT 9
US-10-544-093-20
; Sequence 20, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seibert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-20

Query Match          100.0%; Score 222; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43

RESULT 10
US-10-544-093-13
; Sequence 13, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seibert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13

Query Match          100.0%; Score 222; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43

RESULT 11
US-10-544-093-15
; Sequence 15, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seibert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-15

Query Match          100.0%; Score 222; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seibert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13

Query Match          100.0%; Score 222; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGVVIAT 43

RESULT 11
US-10-544-093-15
; Sequence 15, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seibert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-15

Query Match          100.0%; Score 222; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43
Db 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43

RESULT 12
US-10-544-093-22
Sequence 22, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Ted
APPLICANT: Yednock, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: US/10/544,093
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-22

Query Match 100.0%; Score 222; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43
Db 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43

RESULT 13
US-10-544-093-24
Sequence 24, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Ted
APPLICANT: Yednock, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: US/10/544,093
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2

SEQ ID NO 24
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-24

Query Match 100.0%; Score 222; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43
Db 1 DAERFHDGSEVHHOKLVFFAEDVGSNKGAIIIGLMVGSVIAT 43

RESULT 14
US-10-544-093-17
Sequence 17, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Ted
APPLICANT: Yednock, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT FILING DATE: 2005-08-01
PRIORITY APPLICATION NUMBER: US/10/544,093
PRIORITY FILING DATE: 2004-01-31
PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
PRIORITY FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: A-beta-A-beta-A-beta-Padre fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (87)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (132)..(132)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-17

Query Match 100.0%; Score 222; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 15

US-10-544-093-21
Sequence 21, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vaequez, Ted
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21

LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE: Fusion protein
FEATURE: MISC FEATURE
LOCATION: (141)-(156)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE: MISC FEATURE
NAME/KEY: (57)-(99)
LOCATION: (57)-(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE: MISC FEATURE
NAME/KEY: (100)-(142)
LOCATION: (100)-(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-21
Query Match 100.0%; Score 222; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 56

RESULT 16

US-10-544-093-23
Sequence 23, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vaequez, Ted
APPLICANT: Yednock, Ted
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE: Fusion protein
FEATURE: MISC FEATURE
LOCATION: (3)-(13)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
NAME/KEY: MISC FEATURE

FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23

LENGTH: 142

TYPE: PRT
ORGANISM: Artificial
FEATURE: Fusion protein
FEATURE: MISC FEATURE
LOCATION: (1)-(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE: MISC FEATURE
NAME/KEY: (44)-(86)
LOCATION: (44)-(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE: MISC FEATURE
NAME/KEY: (87)-(129)
LOCATION: (87)-(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-23
Query Match 100.0%; Score 222; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 17

US-10-544-093-18
Sequence 18, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vaequez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE: Fusion protein
FEATURE: MISC FEATURE
LOCATION: (3)-(13)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
NAME/KEY: MISC FEATURE

Query Match 100.0%; Score 222; DB 6; Length 203;

RESULT 20
US-10-515-919A-1
; Sequence 1, Application US/10515919A

```

; Publication No. US20060160146A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
; FILE REFERENCE: Q84952
; CURRENT APPLICATION NUMBER: US/10/515, 919A
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: PCT/JP03/06319
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: JP 2002-159472
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-515-919A-1

Query Match          100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1,9e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
Db
597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 639

RESULT 21
US-10-511-269-7
; Sequence 7, Application US/10511269
; Publication No. US20060205666A1
; GENERAL INFORMATION:
; APPLICANT: MORI, HIROSHI
; TITLE OF INVENTION: GAMMA-SECRETASE INHIBITORS
; FILE REFERENCE: 260276USOPCT
; CURRENT APPLICATION NUMBER: US/10/511,269
; CURRENT FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: PCT/JP03/050117
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: JP2002-121983
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 7
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-269-7

Query Match          100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1,9e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
Db
597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 639

RESULT 22
US-10-546-547-2
; Sequence 2, Application US/10546547
; Publication No. US20060188951A1
; GENERAL INFORMATION:
; APPLICANT: Mook, In Hee
; APPLICANT: Hur, Ji Yeun
; TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
; TITLE OF INVENTION: Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Sam
; FILE REFERENCE: DE-1646
; CURRENT APPLICATION NUMBER: US/10/546, 547
; CURRENT FILING DATE: 2005-08-23
; PRIOR APPLICATION NUMBER: PCT/KR2004/000371
; PRIOR FILING DATE: 2004-02-24
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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-546-547-2

Query Match          100.0%; Score 222; DB 6; Length 751;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
Db
653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 695

RESULT 23
US-10-511-269-9
; Sequence 9, Application US/10511269
; Publication No. US20060205666A1
; GENERAL INFORMATION:
; APPLICANT: MORI, HIROSHI
; TITLE OF INVENTION: GAMMA-SECRETASE INHIBITORS
; FILE REFERENCE: 260276USOPCT
; CURRENT APPLICATION NUMBER: US/10/511,269
; CURRENT FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: PCT/JP03/050117
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: JP2002-121983
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-269-9

Query Match          100.0%; Score 222; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 2,1e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 43
|||||
Db
672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIAT 714

RESULT 24
US-10-890-071-42
; Sequence 42, Application US/10890071
; Publication No. US20060121038A9
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152701-004760US
; CURRENT APPLICATION NUMBER: US/10/890, 071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580, 018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322, 289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-10-890-071-42
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Query Match 97.7%; Score 217; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 25

US-10-544-093-1
 ; Sequence 1, Application US/10544093
 ; Publication No. US20060188512A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yednock, Ted
 ; APPLICANT: Vasquez, Nicki
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Seubert, Peter A.
 ; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
 ; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
 ; FILE REFERENCE: 152701-009820US
 ; CURRENT APPLICATION NUMBER: US/10/544, 093
 ; CURRENT FILING DATE: 2005-08-01
 ; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
 ; PRIOR FILING DATE: 2004-01-31
 ; PRIOR APPLICATION NUMBER: US 60/444,150
 ; PRIOR FILING DATE: 2003-02-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-544-093-1

Query Match 97.7%; Score 217; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 26

US-10-546-547-3
 ; Sequence 3, Application US/10546547
 ; Publication No. US20060188951A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mock, In Hee
 ; APPLICANT: Hur, Ji Yeun
 ; TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
 ; TITLE OF INVENTION: Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Sat
 ; FILE REFERENCE: DE-1646
 ; CURRENT APPLICATION NUMBER: US/10/546,547
 ; CURRENT FILING DATE: 2005-08-23
 ; PRIOR APPLICATION NUMBER: PCT/KR2004/000371
 ; PRIOR FILING DATE: 2004-02-24
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: 1-42 amino acid of amyloid a4 precursor protein (App)
 US-10-546-547-3

Query Match 97.7%; Score 217; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 27

US-10-966-645-36
 ; Sequence 36, Application US/10966645
 ; Publication No. US20060189523A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHILLING, STEPHAN
 ; APPLICANT: HOFFMANN, TORSTEN
 ; APPLICANT: NIESTROJ, ANDRE JOHANNES
 ; APPLICANT: DEMUTH, HANS-ULRICH
 ; APPLICANT: HEISER, ULRICH
 ; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
 ; FILE REFERENCE: 20488/59
 ; CURRENT APPLICATION NUMBER: US/10/966,645
 ; CURRENT FILING DATE: 2004-10-15
 ; PRIOR APPLICATION NUMBER: 60/512,038
 ; PRIOR FILING DATE: 2003-10-15
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 36
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-966-645-36

Query Match 97.7%; Score 217; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 28

US-11-104-300-2
 ; Sequence 2, Application US/11104300
 ; Publication No. US20060099211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monthe, Carmen
 ; APPLICANT: Szabo, Paul
 ; APPLICANT: Weksler, Mark
 ; APPLICANT: Cornell Research Foundation, Inc.
 ; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treating
 ; TITLE OF INVENTION: Alzheimer's Disease
 ; FILE REFERENCE: 1676.027US1
 ; CURRENT APPLICATION NUMBER: US/11/104,300
 ; CURRENT FILING DATE: 2005-04-12
 ; PRIOR APPLICATION NUMBER: US 60/561,423
 ; PRIOR FILING DATE: 2004-04-12
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-104-300-2

Query Match 97.7%; Score 217; DB 7; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 29

US-11-297-316-1

```

; Sequence 1, Application US/11297316
; Publication No. US20060141602A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; TITLE OF INVENTION: particles
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-1

```

```

Query Match          97.7%; Score 217; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

```

```

RESULT 30
US-11-287-157A-49
; Sequence 49, Application US/11287157A
; Publication No. US20060154863A1
; GENERAL INFORMATION:
; APPLICANT: SKUBATCH, HANNA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
; FILE REFERENCE: 32051-701.201
; CURRENT APPLICATION NUMBER: US/11/287,157A
; CURRENT FILING DATE: 2005-11-25
; PRIOR APPLICATION NUMBER: 60/658,859
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/652,287
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/630,880
; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-287-157A-49

```

```

Query Match          97.7%; Score 217; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

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Search completed: September 28, 2006, 07:10:56
 Job time : 17.7758 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 106.906 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-5
Perfect score: 202
Sequence: 1 XFRHDSGEVHHQKLVFPAEDVGSNKGAIIIGLAVGVVIA 40

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A Geneseq_8:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*
10: geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202	100.0	40	4	AA884429 Partial s
2	202	100.0	40	8	ADU24435 Novel glu
3	202	100.0	40	8	ADU46709 Amyloid b
4	202	100.0	40	9	ADZ71361 Human bet
5	202	100.0	40	9	AEA35394 Novel OC
6	202	100.0	40	9	AE892567 Glutamin
7	202	100.0	42	2	AA820330 Sequence
8	202	100.0	42	2	AA603566 Beta-amy1
9	202	100.0	42	2	AA695248 Beta/A4-a
10	202	100.0	42	2	AA695248 Beta/A4-a
11	202	100.0	42	2	AA695248 Beta/A4-a
12	202	100.0	42	2	AA695248 Beta/A4-a
13	202	100.0	42	2	AA695248 Beta/A4-a
14	202	100.0	42	2	AA695248 Beta/A4-a
15	202	100.0	42	2	AA695248 Beta/A4-a
16	202	100.0	42	2	AA695248 Beta/A4-a
17	202	100.0	42	2	AA695248 Beta/A4-a
18	202	100.0	42	2	AA695248 Beta/A4-a
19	202	100.0	42	2	AA695248 Beta/A4-a
20	202	100.0	42	2	AA695248 Beta/A4-a
21	202	100.0	42	2	AA695248 Beta/A4-a
22	202	100.0	42	2	AA695248 Beta/A4-a
23	202	100.0	42	2	AA695248 Beta/A4-a

24	202	100.0	42	4	AA86134 Human Alz
25	202	100.0	42	4	AA835589 Beta/A4-a
26	202	100.0	42	4	AA849098 Human amy
27	202	100.0	42	4	AA884427 Partial s
28	202	100.0	42	4	AA848497 Human amy
29	202	100.0	42	4	AA891779 Amyloid b
30	202	100.0	42	4	AA891812 Amyloid b
31	202	100.0	42	4	AA882622 Amyloid-b
32	202	100.0	42	4	AA849395 Human amy
33	202	100.0	42	4	AA848830 Human amy
34	202	100.0	42	4	AA805484 Human pep
35	202	100.0	42	5	AA881321 Amyloid p
36	202	100.0	42	5	AAU80961 Human amy
37	202	100.0	42	5	AAU98727 Human amy
38	202	100.0	42	5	ABG94281 Amyloid b
39	202	100.0	42	5	AAE21438 Human bet
40	202	100.0	42	5	AB876029 Beta amy1
41	202	100.0	42	5	AAE25335 Modified
42	202	100.0	42	5	AAO15848 Beta-amy1
43	202	100.0	42	5	AAU76483 Amino aci
44	202	100.0	42	5	AAE26080 Beta amy1
45	202	100.0	42	5	AA668314 Human bet
46	202	100.0	42	5	AAU96896 Human Amy
47	202	100.0	42	5	AAU93988 Human bet
48	202	100.0	42	5	AAE26300 Human bet
49	202	100.0	42	5	ABG80593 Human amy
50	202	100.0	42	5	AA651864 Neuronal
51	202	100.0	42	5	AAU75433 Amyloid p
52	202	100.0	42	5	AB883306 Amyloid-b
53	202	100.0	42	5	AB877990 Beta-amy1
54	202	100.0	42	6	AAE35671 Human bet
55	202	100.0	42	6	ABU08711 Amyloid b
56	202	100.0	42	6	AAU016344 A-beta pr
57	202	100.0	42	6	ABU08506 Human amy
58	202	100.0	42	6	AAE33793 Beta-amy1
59	202	100.0	42	6	ABP99423 Beta-amy1
60	202	100.0	42	6	AB882633 Abeta f1b
61	202	100.0	42	6	ABP96144 Human Abe
62	202	100.0	42	6	ABG72233 Human bet
63	202	100.0	42	6	AAE35428 Abeta pro
64	202	100.0	42	6	AAE33218 Beta amy1
65	202	100.0	42	6	ABP97882 Amino aci
66	202	100.0	42	6	ABU63707 Rat amylo
67	202	100.0	42	6	AA889912 Abeta42 a
68	202	100.0	42	7	ADA33767 Human bet
69	202	100.0	42	7	ADB37652 Human bet
70	202	100.0	42	7	ADB85562 Beta-amy1
71	202	100.0	42	7	ADB75176 Amyloid b
72	202	100.0	42	7	AAE38649 Human amy
73	202	100.0	42	7	ADC66002 Human A(b
74	202	100.0	42	7	ADC35181 Beta-amy1
75	202	100.0	42	7	ADD20743 Human bet
76	202	100.0	42	7	AD610848 Chimeric
77	202	100.0	42	7	AD660932 Human bet
78	202	100.0	42	7	AD655649 Human A b
79	202	100.0	42	7	ADK82703 Beta-amy1
80	202	100.0	42	7	ADK39753 B-cell pe
81	202	100.0	42	7	ADP53271 Amyloid A
82	202	100.0	42	8	ADG63948 Recombina
83	202	100.0	42	8	AD140716 Human amy
84	202	100.0	42	8	ADK52267 Human amy
85	202	100.0	42	8	ADN00694 A42, SEQ
86	202	100.0	42	8	ADN97740 Native Am
87	202	100.0	42	8	ADN41875 Amino aci
88	202	100.0	42	8	ADP61369 Beta-amy1
89	202	100.0	42	8	ADP73482 Alzheimer
90	202	100.0	42	8	ADP64925 Beta-amy1
91	202	100.0	42	8	ADQ74960 Human bet
92	202	100.0	42	8	ADQ26240 Human amy
93	202	100.0	42	8	ADQ37252 Vaccine a
94	202	100.0	42	8	ADR16409 Human Abe
95	202	100.0	42	8	ADR04018 Human amy
96	202	100.0	42	8	ADR12775 Human bet

97	202	100.0	42	8	ADRA3293	Ad43293	Abeta42	B
98	202	100.0	42	8	ADR30645	Ad30645	GPBP	cataca
99	202	100.0	42	8	ADR90380	Ad90380	Beta-amy1	
100	202	100.0	42	8	ADT77110	Adt77110	Human amy	

ALIGNMENTS

RESULT 1
 AAB84429
 ID AAB84429 standard; peptide; 40 AA.
 XX
 AC AAB84429;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 XX
 KW Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KM vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note="pyroglutamate"
 FT
 PN MO200142306-A2.
 PN
 PD 14-JUN-2001.
 PF
 XX 08-DEC-2000; 2000MO-US033203.
 XX
 XX 08-DEC-1999; 99US-0169687P.
 XX
 PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 XX
 PL Chain B;
 XX
 DR WPI; 2001-381648/40.
 XX
 PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 PS
 PS Claim 3; Page 42; 47pp; English.
 XX
 XX The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal
 XX
 SQ Sequence 40 AA;
 XX
 XX Query Match 100.0%; Score 202; DB 4; Length 40;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX
 XX 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40

Db	2	FRHDSGEVHHQKLVFAEDVGSNGKAIITGLWVGGVIA	40
RESULT 2			
ADU24435			
ID	ADU24435	standard; protein; 40 AA.	
XX	AC		
XX	ADU24435;		
DT	27-JAN-2005	(first entry)	
XX			
DE	Novel glutaminyl cyclase (QC) inhibitor-related protein #3.		
XX			
KW	Alzheimer's disease; Down's syndrome; Huntington's disease;		
KW	glutaminyl cyclase inhibitor; QC inhibitor; nootropic; neuroprotective;		
KW	antiparkinsonian; neuroleptic; antipyretic; antidepressant; hypotensive;		
KW	eating-disorders-gen; anticonvulsant; antialcoholic; antidiabetic;		
KW	hypnotic; CNS-gen; endocrine-gen; tranquiliser; antiulcer; cyrostatic;		
KW	antiinflammatory; antiporiatic; antirheumatic; antiarthritic;		
KW	antiarteriosclerotic; pyrogutamic acid; neuronal disease;		
KW	parkinson's disease; Huntington's chorea; pathogenic psychotic condition;;		
KW	schizophrenia; impaired food intake; sleep-wakefulness;		
KW	homeostatic regulation; energy metabolism; autonomic function;		
KW	hormonal balance; body fluid regulation; hypertension; fever;		
KW	sleep dysregulation; anorexia; anxiety related disorder; depression;		
KW	seizure; epilepsy; drug withdrawal; alcoholism;		
KW	neurodegenerative disorder; cognitive dysfunction; dementia; ulcer;		
KW	gastric cancer; neoplasia; inflammatory host response; cancer; melanoma;		
KW	malignant metastasis; psoriasis; rheumatoid arthritis; atherosclerosis;		
KW	leukocyte adhesion.		
XX			
OS	unidentified.		
XX			
XX	US2004224875-A1.		
PD			
XX	11-NOV-2004.		
XX			
XX	05-MAY-2004; 2004US-00838993.		
PF			
PR	05-MAY-2003; 2003US-0468014P.		
XX			
XX	(SCHI/) SCHILLING S.		
PA	(NIES/) NESTROJ A. J.		
PA	(HEIS/) HEISER U.		
PA	(BUCH/) BUCHHOLZ M.		
PA	(DEMU/) DEMUTH H.		
XX			
PI	Schilling S, Nestroj AJ, Heiser U, Buchholz M, Demuth H;		
DR	WPI; 2004-813067/80.		
XX			
PT	Use of glutaminyl cyclase inhibitor for the treatment of e.g. Alzheimer's		
PPT	disease, Down syndrome, pathogenic psychotic conditions, schizophrenia		
PT	and Huntington's disease.		
XX			
PS	Disclosure; Page 5; 34p; English.		
XX			
CC	This invention relates to a novel treatment of Alzheimer's disease,		
CC	Down's syndrome or Huntington's disease which involves administering a		
CC	glutaminyl cyclase (QC) inhibitor. The invention may be useful for the		
CC	development of compounds with a nootropic, neuroprotective,		
CC	antiparkinsonian, neuroleptic, antipyretic, antidepressant, hypotensive,		
CC	eating-disorders-gen, anticonvulsant, antialcoholic, antidiabetic,		
CC	hypnotic, CNS-gen, endocrine-gen, tranquiliser, antiulcer, cyrostatic,		
CC	antiinflammatory, antiporiatic, antirheumatic, antiarthritic or		
CC	antiarteriosclerotic activity acting as glutaminyl cyclase inhibitors.		
CC	Glutaminyl cyclase catalyzes both the intramolecular cyclisation of N-		
CC	terminal glutamate residues into pyrogutamic acid with liberation of		
CC	ammonia and the intramolecular cyclisation of N-terminal glutamate		
CC	residues into pyrogutamic acid with liberation of water, the glutaminyl		
CC	cyclase inhibitors are useful in the treatment of various neuronal		
CC	diseases. The composition containing a QC inhibitor is useful for the		

CC treatment of neuronal disorders such as Alzheimer's disease, Down
CC syndrome, Parkinson's disease, Chorea Huntington, pathogenic psychotic
CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,
CC impaired homeostatic regulation of energy metabolism, impaired autonomic
CC function, impaired hormonal balance, impaired regulation of body fluids,
CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
CC disorders (including depression, seizures including epilepsy, drug
CC withdrawal and alcoholism), and neurodegenerative disorders (such as
CC cognitive dysfunction and dementia). The compositions may also be useful
CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host
CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid
CC arthritis, atherosclerosis and leukocyte adhesion and migration processes
CC in the endothelium. The present sequence is that of a protein which is
CC related to the treatment method of the invention.

CC Sequence 40 AA:

Query Match 100.0%; Score 202; DB 8; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.5e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLWGVVIA 40
Db 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLWGVVIA 40

RESULT 3

ADU46709 standard; peptide; 40 AA.

ADU46709;

10-FEB-2005 (first entry)

Amyloid beta peptide (3-42), substrate of glutaminyl cyclase.

KW Amyloid-beta peptide (3-42); glutaminyl cyclase; neurotropic;
KM neuroprotective; anticonvulsant; anticancer; cytosolic; neuroleptic;
KM antiinfectivity; antiparasitic; antirheumatic; antichrithic;
KM antitartaric; Alzheimer's disease; human.

OS Homo sapiens.

PN WO2004098625-A2.

PD 18-NOV-2004.

PF 05-MAY-2004; 2004WO-EP004778.

PR 05-MAY-2003; 2003US-0468014P.

PR 05-MAY-2003; 2003US-0468043P.

PR 15-OCT-2003; 2003US-0512038P.

PA (PROB-) PROBIODRUG AG.

PI Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U;

DR WPI; 2004-805062/79.

PT Use of effectors of glutaminyl cyclase (QC) for treating diseases and/or

PT for modulating physiological processes based on the action of pglu-

PT containing peptides.

PS Disclosure; Page 12; 106pp; English.

XX The present sequence is that of amyloid beta peptide (3-42).
CC Pyroglutamate (pglu)-containing isoforms of amyloid beta peptides
CC represent the prominent forms of N-truncated amyloid beta peptides in
CC senile plaques. The pglu modification exacerbates the toxic properties of
CC amyloid beta peptides. The invention shows that glutaminyl cyclase (QC,
CC EC 2.3.2.5) is involved in the cyclisation of Glu to pglu, making this
CC enzyme a target in drug development. The invention relates to the
CC identification, screening and use of effectors of QC for the preparation

CC of a medicament for: (a) the treatment of diseases that can be treated by
CC modulation of QC activity in vivo; and/or (b) the modulation of
CC physiological processes based on the action of pglu-containing peptides
CC caused by modulation of QC activity. The QC effectors are used to alter
CC the conversion of N-terminal Glu or Gln residues to pglu residues in a QC
CC substrate such as amyloid beta-40/42. They can be used to treat
CC Alzheimer's disease, Down Syndrome, Huntington's disease, Kennedy's
CC disease, ulcer disease and gastric cancer with or without Helicobacter
CC pylori infections, pathogenic psychotic conditions, schizophrenia,
CC infertility, neoplasia, inflammatory host responses, cancer, malign
CC metastasis, melanoma, psoriasis, rheumatoid arthritis, atherosclerosis,
CC impaired humoral and cell-mediated immune responses, leukocyte adhesion
CC and migration processes in the endothelium, impaired food intake, sleep-
CC wakefulness, impaired homeostatic regulation of energy metabolism,
CC impaired autonomic function, impaired hormonal balance and impaired
CC regulation of body fluids. The effectors of QC are also useful for:
CC regulating and/or controlling male fertility; stimulating
CC gastrointestinal tract cell proliferation, preferably proliferation of
CC gastric mucosal cells, epithelial cells, acute acid secretion and for
CC differentiating acid-producing parietal cells and histamine-secreting
CC enterochromaffin-like cells (all claimed). Amyloid beta peptides were
CC also shown to be substrates of dipeptidyl peptidase IV (DP IV) and DP IV-
CC like enzymes, and preferred effector compositions additionally comprise
CC inhibitors of these enzymes.

CC Sequence 40 AA:

Query Match 100.0%; Score 202; DB 8; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.5e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLWGVVIA 40
Db 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLWGVVIA 40

RESULT 4

ADZ71361 standard; peptide; 40 AA.

ADZ71361;

14-JUL-2005 (first entry)

Human beta-amyloid peptide #3.

KW Zollinger-ellison syndrome; gastrointestinal disease; neoplasia;

KM colorectal tumor; gastrointestinal tumor; Helicobacter pylori infection;

KM antibacterial; infection; beta-amyloid.

OS Homo sapiens.

PN WO2005039548-A2.

PD 06-MAY-2005.

PF 15-OCT-2004; 2004WO-EP011630.

PR 15-OCT-2003; 2003US-0512038P.

PA (PROB-) PROBIODRUG AG.

PI Schilling S, Hoffmann T, Niestroj AJ, Demuth H, Heiser U;

DR WPI; 2005-346574/35.

PT Use of glutaminyl cyclase effectors in the manufacture of a medicament
PT for modulating conversion of glutamic acid/glutamine residue to
PT pyroglutamic acid residue at the N-terminus of glutaminyl cyclase

PS Disclosure; Page 13; 105pp; English.

XX

CC The invention relates to the use of a glutaminyl cyclase effector (B1)
CC for modulating conversion of glutamic acid/glutamine residue to
CC pyroglutamic acid residue at the N-terminus of a glutaminyl cyclase (QC)
CC substrate. The glutaminyl cyclase effector is useful for treating a
CC condition mediated by modulation of QC enzyme activity e.g. Familial
CC British Dementia (FBD) and Familial Danish Dementia (FDD), ulcer disease
CC and duodenal cancer with or with out *Helicobacter pylori* infections,
CC colorectal cancer, Zollinger-Ellison syndrome, gastric cancer, Alzheimer's
CC disease, Down's syndrome, pathogenic psychotic conditions, schizophrenia,
CC infertility, neoplasia, inflammatory host responses, cancer, malign
CC metastasis, psoriasis, rheumatoid arthritis, atherosclerosis, impaired
CC humoral and cell-mediated immunity responses, leukocyte adhesion and
CC migration processes in the endothelium, impaired food intake, sleep
CC wakefulness, impaired homeostatic regulation of energy metabolism,
CC impaired autonomic function, impaired hormonal balance and impaired
CC regulation of body fluids, for the preparation of contraceptive
CC medicaments for males. The amino acid sequence of the human beta-amyloid
CC peptide.

SQ Sequence 40 AA;

Query Match 100.0%; Score 202; DB 9; Length 40;

```
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 PRHDSGYEVHHQKLVFAEDVGSNKGATITGLMWGSVYA 40
|||
Db 2 PRHDSGYEVHHQKLVFAEDVGSNKGATITGLMWGSVYA 40

RESULT 5
AEA35394

AC AEA35394;

DT 11-AUG-2005 (first entry)

DE Novel QC inhibitor composition-related Abeta(3-42) polypeptide.

KM pharmacologic; nootropic; neuroprotective; antiparkinsonian;
KM neuroleptic; hypotensive; antipruritic; tranquilizer; antidepressant;
KM antialcoholic; anticonvulsant; anabolic; eating-Disorders-Gen.; hypnotic;
KM amyloid; neurological disease; Alzheimer disease; Downs Syndrome;
KM Parkinsons disease; Huntingtons chorea; psychotic disorders;
KM schizophrenia; sleep disorder; hypertension; anorexia nervosa;
KM anxiety disorder; major depressive disorder; epilepsy; alcoholism;
KM neurodegenerative disease; cognitive disorder; dementia.

OS Unidentified.

PN WO2005049027-A2

PD 02-JUN-2005

PF 29-OCT-2004; 2004WO-EP012301.

PR 03-NOV-2003; 2003US-0516717P.

PA (PROB-) PROBIODRUG AG.

PI Schulz I, Schilling S, Niestroj AJ, Demuth H, Rossner S,

DR WPI; 2005-395979/40.

PT Composition used for treating neuronal diseases e.g. Alzheimer's disease.
PT Down Syndrome, Parkinson disease, Chorea Huntington comprises glutaminyl
PT cyclase inhibitor.

PS Disclosure; Page 15; 123pp; English.

CC This invention relates to a novel composition which comprises at least
CC one glutaminy] cyclase (GC) inhibitor and optionally at least one of

CC prolyl endopeptidase (PEP) inhibitors, inhibitors of dipeptidyl
CC aminopeptidases (DP), neurotrophin x (NPx) receptor ligands, NPY agonists
CC or antagonists, acetylcholinesterase (AChE) inhibitors, protein
CC isospartate carboxymethyl transferase (PMT) enhancers, inhibitors of
CC beta or gamma secretases and inhibitors of neutral endopeptidase. The
CC invention may be useful for the development of compounds with a
CC neurotropic, neuroprotective, antiparkinsonian, neuroleptic, hypotensive,
CC antipsychotic, tranquilizer, antidepressant, antialcoholic, anticonvulsant,
CC anabolic, eating-disorders-gen. or hypnotic activity acting as amyloid
CC beta-peptide formation inhibitors. The invention may be used for the
CC treatment of neuronal diseases, particularly Alzheimers disease, Downs
CC Syndrome, Parkinsons disease, Huntingtons chorea, pathogenic psychotic
CC conditions, Schizophrenia, impaired food intake, sleep-wakefulness,
CC impaired homeostatic regulation of energy metabolism, impaired autonomic
CC function, impaired hormonal balance, impaired regulation, body fluids,
CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
CC disorders including depression, seizures including epilepsy, drug
CC withdrawal and alcoholism, neurodegenerative disorders including
CC cognitive dysfunction and dementia. The OC inhibitors prevent the
CC aggregation of plaque-forming amyloid-beta-peptides 3-40/42 or amyloid-
CC beta-peptides 11-40/42, reducing the onset and progression of the
CC diseases. The present sequence is that of an amyloid beta polypeptide
CC which is related to the novel compositions of the invention.

SQ Sequence 40 AA:

Query Match	100.0%; Score 202; DB 9; Length 40;
-------------	-------------------------------------

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 40
|||
Db 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 40

RESULT 6
AEB92567

XX
AC AEB92567;

DT	20-OCT-2005 (first entry)
XX	
DE	Glutaminyl cyclase inhibitor peptide #3

KM Pharmaceutical; enzyme inhibition; neurological disease;
KM Alzheimer disease; Down syndrome; Parkinson disease;
KM Huntingtons chorea; psychotic disorder; schizophrenia; sleep disorder;
KM metabolic disorder; hypertension; fever; anorexia nervosa;
KM anxiety disorder; depression; epilepsy; drug dependence; alcoholism;
KM neurodegenerative disease; cognitive disorder; dementia; neuroprotective;
KM nootropic; antiparkinsonian; anticonvulsant; neuroleptic; hypnotic;
KM endocrine-gen.; hypotensive; antipyretic; anabolic;
KM eating-disorder-gen.; tranquilizer; antidepressant; antidiabetic;
KM antialcoholic; antifertility; glutamyl cyclase inhibitor;
KM glutamyl-peptide cyclotransferase.

OS Synthetic.

PN W02005075436-A2.

PD 18-AUG-2005

PF 04-FEB-2005; 2005WO-EP001153.

PR 05-FEB-2004; 2004US-0542133P;
PR 05-MAY-2004; 2004US-00838993;
PR 08-DEC-2004; 2004US-0634364P;

PA (PROB-) PROBIODRUG AG.

PI Schilling S, Buchholz M, Niestroj AJ, Demuth H, Helser U;
XX

DR WPI: 2005-591611/60.

XX New imidazole derivatives are [glutaminyl] cyclase inhibitors useful to

PT treat neuronal disorders e.g. Alzheimer's disease, Down syndrome,

PT Parkinson disease, Chorea Huntington, pathogenic psychotic conditions and

PT schizophrenia.

XX

PS Disclosure: Page 20, 122pp; English.

XX

CC The invention relates to imidazole derivatives and their salts,

CC stereoisomers and polymorphs. The invention also relates to a composition

CC comprising an imidazole optionally in combination with a carrier and/or

CC excipient. The imidazole derivatives are useful in the manufacture of a

CC medicament for the treatment of neurological diseases especially

CC Alzheimer's disease, Down syndrome, Parkinson's disease, Huntington's

CC chorea, psychotic disorders, schizophrenia, impaired food intake, sleep

CC disorders, impaired homeostatic regulation of energy metabolism,

CC hypertension, fever, anorexia nervosa, anxiety disorders, depression,

CC epilepsy, drug dependence, alcoholism and neurodegenerative diseases

CC including cognitive disorders and dementia. The imidazole derivatives are

CC also useful for stimulating the proliferation of myeloid progenitor cells

CC or to suppress male fertility. This sequence represents a glutaminyl

CC cyclase inhibitor peptide used in the scope of the invention.

XX

SQ Sequence 40 AA;

Query Match 100.0%; Score 202; DB 9; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.5e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 2 FRHDSGYEVHNOKLVFPAEDVGSNKGAIIGLMVGVYA 40

|||||

Db 2 FRHDSGYEVHNOKLVFPAEDVGSNKGAIIGLMVGVYA 40

|||||

RESULT 7

AAR20330

ID AAR20330 standard; peptide; 42 AA.

XX

AC AAR20330;

XX

DT 25-MAR-2003 (revised)

DT 14-APR-1992 (first entry)

XX

DE Sequence of A99 (beta-amyloid core domain).

XX

KM Transgenic mice; Alzheimer's disease; diagnosis; beta-amyloid precursor;

XX plaque core protein.

XX

OS Homo sapiens.

XX

PN WO9119810-A.

XX

PD 26-DEC-1991.

XX

PF 15-JUN-1990; 90US-00538857.

XX

PR 15-JUN-1990; 90US-00538857.

PR 17-JUN-1991; 91US-00716725.

PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.

PI Cordell B;

XX

DR WPI: 1992-024426/03.

XX

PT Transgenic mice as models for studying Alzheimer's disease proteins -

PT contg. cells with promoter and beta-amyloid precursor protein

XX deoxyribonucleic acid, useful for testing anti-alzheimer's drugs.

PS Disclosure: Fig 3; 98pp; English.

XX

CC The inventors specifically claim transgenic mice contg. DNA encoding A42

CC	(beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid catboxy tail) (AAI20329), A695 (beta-amyloid precursor protein), A751 (precursor plus inhibitor) or A41 (protease inhibitor) (AAR20328). Human fibroblast CC CC cDNA clone lambdaBAPcP16814 was deposited at ATCC on July 1, 1987 and has CC accession No. 40347. The promoter is pref. the NSB promoter with the A751 CC or the A695 sequence. (updated on 25-MAR-2003 to correct PR field.) CC CC (updated on 25-MAR-2003 to correct PA field.) XX SQ Sequence 42 AA;
OY	Query Match 100.0%; Score 202; DB 2; Length 42; Best Local Similarity 100.0%; Pred. No. 1.6e-22; Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGCVIA 40 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGCVIA 42
RESULT 8	AAR60366 ID AAR60366 standard; peptide; 42 AA.
XX AC AAR60366;	
XX DT 25-MAR-2003 (revised)	
XX DT 15-MAR-1995 (first entry)	
XX DE Beta-amyloid (1-42).	
XX KM Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;	
XX KW anti-beta-amyloid antibody; diagnosis.	
XX OS Homo sapiens.	
XX PN WO9417197-A1.	
XX PD 04-AUG-1994.	
XX PF 24-JAN-1994; 94WO-JP000089.	
XX PR 25-JAN-1993; 93JP-00010132.	
PR 05-FEB-1993; 93JP-00019035.	
PR 16-NOV-1993; 93JP-00286985.	
PR 28-DEC-1993; 93JP-00334773.	
XX PA (TAKE) TAKEDA CHEM IND LTD.	
PI Suzuki N, Odaka A, Kitada C;	
XX DR WPI; 1994-264110/32.	
PT Antibodies recognising specific parts of beta-amyloid - can be used for PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease.	
XX PS Disclosure; Page 83; 116pp; Japanese.	
CC Antibodies which recognise specific subfragments of the beta-amyloid CC protein are claimed. Specifically, the antibodies (which are pref. CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from CC the C-terminal portion. The antibodies are useful for assaying beta- amyloid and its derivatives for diagnosis of Alzheimer's disease. (Updated on 25-MAR-2003 to correct PN field.) CC CC (Updated on 25-MAR-2003 to correct PA field.) XX SQ Sequence 42 AA;	
Query Match 100.0%; Score 202; DB 2; Length 42; Best Local Similarity 100.0%; Pred. No. 1.6e-22; Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGCVIA 40	

Db 4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 9

AAAR95248 standard; peptide; 42 AA.

AAAR95248;

20-JAN-1997 (first entry)

Beta/A4-amyloid peptide.

Beta/A4-amyloid peptide; tissue plasminogen activator;

Alzheimer's disease; stimulation; investigation; pathogenesis;

hereditary cerebral haemorrhage with amyloidosis-Dutch type; control;

cerebral amyloid angiopathy; cerebral; haemorrhage; hemorrhage.

Homo sapiens.

MO9615799-A1.

30-MAY-1996.

22-NOV-1995; 95MO-US015007.

22-NOV-1994; 94US-00347144.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Anderson S;

WPI; 1996-268332/27.

Use of agents which bind beta-amyloid peptide - for diagnosis, prevention

and treatment of vascular damage caused by amyloid deposits, partic. in

haemorrhaging and Alzheimer's disease.

Example 1; Fig 1; 52pp; English.

To investigate the effects of beta-amyloid peptide (BAP) on tissue

plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide

contained 42 amino acids and corresp. to the full length BAP (AAAR95248).

The other 2 peptides (AAAR95249 and 50) contained the 28 N-terminal

residues of the BAP found in Alzheimer's disease and hereditary cerebral

haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an

assay to determine the effect of the peptides on t-PA activation, each

peptide (AAAR95248, 49 and 50) gave 1st order rate constant of activation

(k_{app}) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and

7.8 for null and fibrinogen controls. The results demonstrate that the

BAP are able to stimulate t-PA activity in vitro, which is significant in

that it provides a means for investigating and controlling the

pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid

angiopathy related cerebral haemorrhage

Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGGVIA 40

4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 10

AAAR94591 standard; peptide; 42 AA.

AAAR94591;

25-MAR-2003 (revised)

21-AUG-1996 (first entry)

Alzheimer amyloid beta-protein active site sequence.

Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;

serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;

complex formation; alpha(1)-antichymotrypsin; Down's disease; ageing.

Synthetic.

US5506097-A.

09-APR-1996.

10-JAN-1994; 94US-00179574.

24-AUG-1990; 90US-00572671.

13-JAN-1992; 92US-00819361.

13-JAN-1993; 93MO-US000325.

(HARD) HARVARD COLLEGE.

Kayyali U, Potter H;

WPI; 1996-200270/20.

Inhibiting enzymatic activity of Alzheimer amyloid beta-protein - using p

-amidinophenylmethanesulphonyl fluoride or ebelactone A, for treatment,

study and diagnosis of Alzheimer's disease, etc.

Disclosure; Fig 1; 17pp; English.

This is the sequence of a fragment of the beta-amyloid protein associated

with Alzheimer's disease. The protein contains esterase (cholinesterase

and lipase) activities based on active site similarities with serine

proteases (see AAR94592-96). The esterase activity of the beta-amyloid

protein is inhibited by the cpds. of the invention i.e. ebelactone A or

para-amidinophenylmethanesulphonyl fluoride. Inhibition of these

activities prevent complex formation between the beta-amyloid protein and

CC Alpha(1)-antichymotrypsin, thus can be used to treat, study or diagnose

Alzheimer's or Down's diseases or normal ageing. (Updated on 25-MAR-2003

to correct pf field.)

Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGGVIA 40

4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 11

AAAM12828 standard; peptide; 42 AA.

AAAM12828;

08-DEC-1997 (first entry)

Beta A4 peptide.

Beta A4 peptide; Alzheimer's disease; peptide aggregation; brain;

therapy; inhibitor.

Homo sapiens.

MO9707403-A1.

27-FEB-1997.

XX 23-JUL-1996; 96WO-US012034.
 XX
 XX 16-AUG-1995; 95US-00515606.
 XX
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 XX Goyal S, Paul J, Riedel NG, Sahasrabudhe SR;
 XX WPI, 1997-165447/15.
 XX
 XX Determn. of the degree of betaA4 peptide aggregation using binding agent
 PT - used to screen cpds. for possible use in Alzheimer's disease treatment.
 XX
 XX
 XX Disclosure; Page 10; 18pp; English.
 XX
 XX This sequence represents the beta A4 peptide. The degree of aggregation
 CC of this peptide is determined using the method of the invention. The beta
 CC A4 peptide is present in the brain of Alzheimer's disease patients, but
 CC not in the brain of non-Alzheimer's disease individuals. The peptide
 CC clumps or aggregates in the brain of Alzheimer's disease patients, where
 CC it may be responsible for the destruction of normal brain cells. Once the
 CC clumps or aggregates form, the formulation is almost irreversible. The
 CC method of the invention comprises reacting this sequence with a binding
 CC reagent capable of binding to it only in its non-aggregated state, to
 CC form an amount of a beta A4 peptide-bound reagent and an amount of
 CC protein free reagent. The amount of the beta A4 peptide, binding reagent
 CC complex is then measured. Compounds which inhibit aggregation of beta A4
 CC peptide are potentially useful for treatment of Alzheimer's disease
 XX
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
 |||||
 Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 12
 AAM64507
 ID AAM64507 standard; peptide; 42 AA.
 XX
 XX AAM64507;
 AC
 XX 20-OCT-1998 (first entry)
 DT
 XX
 XX Neurotoxic beta-amyloid peptide decoy peptide #20.
 DE
 XX Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
 KW aggregate; Alzheimers disease; decoy; treatment.
 XX
 XX Synthetic.
 OS
 XX WO9830229-A1.
 PN
 XX 16-JUL-1998.
 PD
 XX
 XX 09-JAN-1998; 96WO-US000653.
 PF
 XX 10-JAN-1997; 97US-0035847P.
 PR 29-OCT-1997; 97US-00960188.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 XX Ingram VM, Blanchard BJ;
 PI WPI, 1998-398795/34.
 DR
 XX
 XX Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor, useful

PT for, e.g. treating Alzheimer's disease.
 XX
 XX Example 8; Page 46; 68pp; English.
 PS
 XX AAM64488-M64517 are decoy peptides that bind to a neurotoxic beta-amyloid
 CC peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates
 CC that increase calcium influx into neuronal cells. Such peptides can be
 CC used in the treatment of diseases associated with neurotoxic aggregates
 CC of beta-AP specifically Alzheimer's disease. The peptides are
 CC administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and
 CC orally, or from slow-release implants
 XX
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
 |||||
 Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 13
 AAM42989
 ID AAM42989 standard; peptide; 42 AA.
 XX
 XX AAM42989;
 AC
 XX 01-MAY-1998 (first entry)
 DT
 XX
 XX Full length beta-amyloid peptide (BAP).
 DE
 XX
 XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage.
 XX
 XX Homo sapiens.
 OS
 XX US5703209-A.
 PN
 XX 30-DEC-1997.
 PD
 XX
 XX 05-JUN-1995; 95US-00464248.
 PF
 XX 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX Jacobson JS, Vitrek MP;
 PI WPI, 1998-076482/07.
 DR
 XX
 XX Amyloid precursor protein fusion polypeptides - comprising APP fragment
 PT and marker, useful for research and drug screening.
 XX
 XX Disclosure; Col 7; 84pp; English.
 PS
 XX The present sequence represents a beta-amyloid peptide (BAP). Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
 CC 770. These isoforms are derived by alternative splicing. APP-APP 751 is a
 CC deletion construct of APP-751, which has a deletion of 276 amino acids to
 CC within 15 amino acids of the BAP domain. APP can be used as a substrate
 CC for studying abnormal proteolytic cleavage which results in the release

CC of BAP, and also to screen for drugs that will inhibit such cleavage
 XX
 SO Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 40
 DB 4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 42

RESULT 14
 AAM47230
 ID AAM47230 standard; peptide; 42 AA.

XX AAM47230;

DT 22-MAY-1998 (first entry)

DE Beta-amyloid peptide residues 1-42.

XX Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;
 KW Alzheimer's disease.

XX Homo sapiens.

OS US5721106-A.

PN 24-FEB-1998.

PD 12-SEP-1994; 94US-00304585.

PR 13-AUG-1991; 91US-00744767.

XX (MINU) UNIV MINNESOTA.

PA (HARD) HARVARD COLLEGE.

PI Mantyh PW, Maggio JE;

XX WPI; 1998-168404/15.

DR New in vitro screening assay for Alzheimer's disease drugs - comprises
 XX assessing binding of labelled beta-amyloid peptide to silk sample.

PT Claim 8; Col 29-30; 36pp; English.

XX The present sequence was used in the development of a novel in vitro
 CC screening assay for agents capable of affecting the deposition of beta-
 CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk
 CC sample with labelled BAP, optionally in the presence of a test agent,
 CC detecting the amount of label bound to the silk and assessing the effect
 CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
 CC to silk are potentially useful for treating amyloidosis diseases,
 CC especially Alzheimer's disease

XX Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 40
 DB 4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 42

RESULT 15
 AAY49691
 ID AAY49691 standard; peptide; 42 AA.
 XX
 AC AAY49691;

XX 13-JAN-2000 (first entry)
 DT
 XX Human beta amyloid precursor protein peptide.

DE Human; beta amyloid precursor protein; APP; beta secretase inhibition;
 KW alpha secretase; neurological disorder; Alzheimer's disease;
 KM Down syndrome; mutation.

XX Homo sapiens.

OS WO9951752-A1.

PN 14-OCT-1999.

PD 31-MAR-1999; 99WO-JP001701.

PR 31-MAR-1998; 98JP-00101821.

XX (CHUS) CHUGAI SEIYAKU KK.

PA Ozawa K, Ikeda S, Tabira T;

PI WPI; 1999-620208/53.

DR A cell line which produces beta amyloid precursor protein, used in the
 XX investigation of neurological disorders such as Alzheimer's disease.

PT Disclosure; Page 41; 70pp; Japanese.

XX The present invention describes a cell line which produces beta amyloid
 CC precursor protein (APP) and expresses alpha secretase activity but
 CC expresses beta secretase activity only under an external stimulus. Also
 CC described is a cloning method for DNA encoding beta secretase,
 CC comprising: (1) inserting a DNA library into the cell line, expressing
 CC the inserted DNA, and selecting cells expressing beta secretase then
 CC isolating the beta secretase DNA from them; or (2) isolating nucleic acid
 CC from the cell line with or without external stimulation and performing
 CC subtractive cloning to identify DNA expressed only under stimulation.
 CC Products from the present invention may be used in the investigation of
 CC neurological disorders such as Alzheimer's disease and Down syndrome and
 CC in particular the association of mutations of the beta APP with them. The
 CC present sequence represents a human beta APP peptide

XX Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 40
 DB 4 FRHDSGYEVHHOKLVFFAEDVGSNKGATIGLMVGCVIA 42

RESULT 16
 AAM99585
 ID AAM99585 standard; peptide; 42 AA.

XX AAM99585;

DT 22-JUN-1999 (first entry)

DE Mutant aggregating amyloid-beta peptide.

XX Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KW diagnosis; Alzheimer's disease.

XX Homo sapiens.

OS Synthetic.

PN WO9908695-A1.

XX

PD 25-FEB-1999.
XX 13-AUG-1998; 98MO-US016809.
XX 14-AUG-1997; 97US-0055660P.
XX (REGC) UNIV CALIFORNIA.
XX Glabe C, Garzon-Rodriguez W;
XX WPI; 1999-190112/16.
DR New fluorescent labeled amyloid A-beta peptides.
XX
XX Example 1; Page 21; 50pp; English.
PS
XX This sequence corresponds to a mutant aggregating amyloid-beta peptide
CC which can be covalently labelled with a fluorescent group. The detection
CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
CC or detect a predisposition to Alzheimer's disease. The screening assays
CC can be used to identify compounds for the treatment or amelioration of
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
CC amyloid-beta peptide are also useful for exploring other aspects of
CC amyloid structure.
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2. FRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGAVIA 40
DB 4 FRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGAVIA 42

RESULT 17
AAW81474
ID AAW81474 standard; peptide; 42 AA.
XX AAW81474;
XX
XX 28-JAN-1999 (first entry)
XX
XX Synthetic amyloid beta (Abeta) peptide 9 (residues 1-42).
DE Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
XX Synthetic.
XX
XX US5840838-A.
XX
XX 24-NOV-1998.
XX
XX 29-FEB-1996; 96US-00609090.
XX
XX 29-FEB-1996; 96US-00609090.
XX
XX (KENT) UNIV KENTUCKY RES FOUND.
XX
XX Aksenov M, Carney JM, Hensley K, Butterfield DA;
XX WPI; 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic solvent
XX treatment, useful for studying neurotoxicity.
XX
XX Claim 5; Col 11-12; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic Abeta
CC peptide that comprises dissolving the peptide in a deoxygenated solvent

CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution
CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by "evaporative
CC deposition" in 5-10 minutes. Synthetic amyloid beta peptides are useful
CC as research tools for studying neurotoxicity resulting from Abeta peptide
CC -enhanced free-radical production. The treatment increases the activity
CC of the synthetic Abeta peptides in tests to determine free-radical
CC generating capacity and glutamine synthetase inactivation
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2. FRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGAVIA 40
DB 4 FRHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGAVIA 42

RESULT 18

AAV08607
ID AAV08607 standard; protein; 42 AA.
XX
XX AAV08607;
XX
XX 05-AUG-1999 (first entry)
XX
XX

DE Human beta-amyloid precursor core protein A42.

KW APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
KW Alzheimer's disease; model; therapeutic compound; brain; mechanism;
KW nerve tissue specific promoter; synthesis; inhibitor; deposition;
KW plaque formation; treatment; A42.
XX

OS Homo sapiens.

PN US5912410-A.

PD 15-JUN-1999.

PF 13-APR-1995; 95US-00422333.

PR 15-JUN-1990; 90US-00538857.

PR 17-JUN-1991; 91US-00716725.

PR 21-OCT-1994; 94US-00327381.

PA (SCIO-) SCIOS INC.

PI Cordell B;

DR WPI; 1999-357231/30.

PT Transgenic mice useful for studying compounds potentially useful in the

XX treatment of Alzheimer's disease.
XX Disclosure; Fig 3; 72pp; English.

CC This invention describes novel transgenic mice expressing proteins
CC related to the pathology of Alzheimer's disease and which provide models
CC for studying potentially therapeutic compounds. The transgenic mice
CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)
CC and a nerve tissue specific promoter operably linked to the beta-APP
CC allowing its expression to form beta-amyloid protein deposits in the
CC animal's brain. The transgenic mouse is useful for elucidating the
CC molecular mechanisms involved in the synthesis of and, more importantly,
CC inhibiting the synthesis and deposition of beta-amyloid proteins (most
CC importantly in the brain where plaque formation is associated with
CC Alzheimer's disease) by inhibiting production and/or increasing cleavage
CC after production. The transgenic animals provide useful models for
CC studying the in vivo relationships of the proteins to each other and to
CC other compounds being tested for their usefulness in treating Alzheimer's

CC disease
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19
AAM29093
ID AAM29093 standard; peptide; 42 AA.

XX AAM29093;

DT 20-JUL-1999 (first entry)

XX A-beta-binding peptide 1-42.

XX Cyclosporin; A-beta peptide; conjugate; neurological disease; Alzheimer;
KM multiple sclerosis; amyotrophic lateral sclerosis; ALS;
KW non-immunosuppressive; amyloid plaque formation.

XX Homo sapiens.

PN WO9910374-A1.

PD 04-MAR-1999.

PF 25-AUG-1998; 98WO-US017544.

XX 26-AUG-1997; 97US-0057751P.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

PI Rich DH, Solomon ME;

DR WPI; 1999-276928/23.

PT New A-beta-binding peptide conjugates and Cys analogs - useful in treatment
of neurological diseases e.g. Alzheimer's disease, Multiple Sclerosis
etc.

PS Claim 5; Page 98; 129pp; English.

CC New conjugates are disclosed which are of formula A-Z, in which: A is (1)
CC a cyclosporin A analogue described in AAM29087 or (2) an FK506 binding
CC peptide inhibitor; and Z is a polypeptide comprising 5 or more contiguous
CC residues of A-beta peptide. The compounds are novel chemical inducers of
CC dimerization which are non-immunosuppressive and which are inhibitors of
CC A-beta peptide aggregation and deposition in amyloid plaques. The adverse
CC consequences of amyloid plaque formation can be prevented or ameliorated
CC by sequestering the A-beta peptide in monomeric form with a conjugate
CC which links the A-beta to cyclophilin or FKBP, therefore providing a
CC mechanism to minimize the amount of free A-beta available for fibril
CC formation and deposition. The compounds can be used for the treatment of
CC Alzheimer's disease, multiple sclerosis and amyotrophic lateral sclerosis
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 20
AAY25137
ID AAY25137 standard; peptide; 42 AA.

XX AAY25137;

DT 26-AUG-1999 (first entry)

XX Human amyloid beta-A4 peptide 5.

KM Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
KW therapeutic drug; brain; Alzheimer's disease.

XX Homo sapiens.

OS US5919631-A.

PN 06-JUL-1999.

PD 17-JUL-1996; 96US-00682245.

PF 17-JUL-1996; 96US-00682245.

PR 17-JUL-1996; 96US-00682245.

XX (HMRI) HOECHST MARION ROUSSEL INC.

PA Sahasrabudhe SR, Paul JW, Goyal S, Riedel NG;

PI WPI; 1999-403957/34.

DR Determination of degree of aggregation of a peptide, useful for
identifying therapeutic drugs for treating Alzheimer's disease.

XX Claim 1; Col 7-8; 8pp; English.
XX This invention describes a novel method for the determination of the
XX degree of aggregation of an amyloid beta A4 peptide (I) in solution.
XX Determination comprises: (a) incubating a sample of unaggregated (I) with
XX Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
XX (I); (b) measuring the amount of (II) bound to (I) to obtain a value (I);
XX (c) repeating steps (a) and (b) with a second sample at a different time
XX to obtain a second value (II); and (d) determining the difference between
XX (I) and (II) which is inversely related to the degree of aggregation of
XX (I). This method may be applied to a screen for compounds that inhibit
XX aggregation of (I). These inhibitors may be used as therapeutic drugs to
XX inhibit the formation of these aggregates in the brains of patients
XX suffering from Alzheimer's disease
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 21

AAM92726
ID AAM92726 standard; peptide; 42 AA.

XX AAM92726;

AC 20-MAR-2003 (revised)

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #72.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX

OS Homo sapiens.
 XX US5876948-A.
 XX PD 02-MAR-1999.
 XX 29-JUL-1991; 91US-00737371.
 XX PF 27-JUL-1990; 90US-00559173.
 XX PR (CHIL-) CHILDRENS MEDICAL CENT.
 XX PA Yankner BA;
 XX P1 WPI; 1999-189630/16.
 XX DR Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
 PS Disclosure; Col 41-42; 28pp; English.
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAM2655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
 Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 22
 AAY33407
 ID AAY33407 standard; peptide: 42 AA.
 XX AAY33407;
 AC
 XX 03-DEC-1999 (first entry)
 DT
 XX Human amyloidogenic A-beta peptide 1.
 DE
 XX Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
 KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
 KW Down's Syndrome.
 XX Homo sapiens.
 OS
 XX WO9941279-A2.
 PN
 XX 19-AUG-1999.
 PD
 XX 12-FEB-1999; 99WO-US003231.
 PF
 XX 13-FEB-1998; 98US-0074658P.
 PR
 XX (ARCH-) ARCH DEV CORP.
 PA
 XX Lynn DG, Meredith SC, Burkoth TS;
 PI WPI; 1999-561326/47.
 XX

PT Inhibiting amyloid plaque formation in humans suffering from amyloidosis,
 PT Alzheimer's disease or Down's Syndrome.
 XX Claim 21; Page 140; 141pp; English.
 XX This invention describes a novel method for inhibiting amyloid
 CC fibrillogenesis which comprises contacting tissue with a composition
 CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
 CC at an end terminal or a side chain, by conjugation to polyethylene
 CC glycol, by conjugation to a second compound and a pharmaceutically
 CC acceptable buffer, solvent or diluent. The methods are used to inhibit
 CC amyloid plaque formation in humans suffering from amyloidosis,
 CC Alzheimer's disease or Down's Syndrome. This sequence represents a
 CC fragment of the beta-amyloid peptide described in the method of the
 CC invention
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
 Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 23
 AAY96956
 ID AAY96956 standard; peptide: 42 AA.
 XX AAY96956;
 AC
 XX 31-OCT-2000 (first entry)
 DT
 XX Beta-amyloid 1-42 peptide.
 DE
 XX prUBEX3; polyhistidine; tag; rubredoxin; antigen; vaccine; carrier;
 KW immunogenic; flag tag; beta-amyloid; fusion.
 KW Homo sapiens.
 XX
 OS
 XX WO200039310-A1.
 PN
 XX 06-JUL-2000.
 PD
 XX 29-DEC-1999; 99WO-US031176.
 PF
 XX 29-DEC-1998; 98US-00114034.
 PR
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA
 XX Przybyla A, Menon N;
 PI WPI; 2000-452403/39.
 DR
 XX Nucleic acids encoding fusion peptides comprising rubredoxin, useful as
 PT vaccines.
 PT
 XX Example 2; Page 63; 67pp; English.
 XX Fusion proteins comprising rubredoxin and fused antigens and/or haptens
 CC may be used as vaccines to initiate immune responses. In this case, the
 CC rubredoxin acts as a carrier. The fusion protein is capable of binding
 CC iron (Fe-2+) when properly folded, giving it a red color that makes it
 CC easy to identify following or during purification. The C-terminal fused
 CC protein may be insoluble or known to form inclusion bodies in a host
 CC cell. The rubredoxin serves as the carrier molecule to yield immunogenic
 CC fusion products. As rubredoxin is itself only negligibly antigenic, there
 CC is no need to include a cleavage site in the fusion product to allow
 CC cleavage of the N-terminal and C-terminal constituents
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 3; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 40
 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

Db

RESULT 24
 AAB86134
 ID AAB86134 standard; protein; 42 AA.
 AC AAB86134;
 XX
 XX
 DT 31-JUL-2001 (first entry)
 XX
 XX Human Alzheimer-beta-peptide (1-42).
 DE
 XX Beta-peptide; subunit-containing molecular associate; gene therapy;
 KW neurodegenerative disorder; amyloidogenic disorder; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; type II diabetes mellitus;
 KW transmissible spongiform encephalopathy; muscular dystrophy;
 KW virus-like protein shell.
 XX
 OS Homo sapiens.
 XX
 XX MO200132694-A2.
 XX
 XX 10-MAY-2001.
 XX
 XX 03-NOV-2000; 2000MO-EP010877.
 XX
 XX 03-NOV-1999; 99DE-01052955.
 PR
 XX (ACGT-) ACGT PROGENOMICS AG.
 PA
 XX
 PI Boehm G, Schmidt U;
 XX
 XX WPI; 2001-316418/33.
 DR
 XX
 PT Characterizing molecular associates of subunits, useful e.g. for
 PT diagnosis of neurodegenerative diseases, by fluorescence-activated cell
 PT sorting of associates containing labeled subunits.
 PT
 XX
 PS Disclosure; Page 45; 45pp; German.
 XX

This invention describes a novel method for characterizing subunit (SU)-
 containing molecular associates (A) by: (i) labeling non-associated SU
 with a fluorescent dye (I); (ii) contacting labeled SU, with each other
 or with unlabeled SU or with (A), so that labeled (A) are formed by
 attachment of labeled SU; (iii) characterizing the labeled (A) by
 fluorescence-activated cell sorting (FACS); and (iv) optionally
 separating (A) by known methods. The method is used to characterize (and
 optionally separate) (A): (i) associated with a wide range of
 neurodegenerative or other amyloidogenic disorders, e.g. Alzheimer's,
 Huntington's or Parkinson's diseases, transmissible spongiform
 encephalopathies, type II diabetes mellitus and muscular dystrophy, for
 diagnosis and prediction of such diseases; or (ii) produced during
 recombinant protein production (inclusion bodies). It may also be used to
 detect homologous subunits and for measuring kinetics of
 aggregate/associate formation. A particular application is determining
 the packaging efficiency of virus-like protein shells for therapeutic
 proteins and nucleic acid, for use as gene therapy vectors. Separated (A)
 are useful experimentally, e.g. in cell cultures or animal models. The
 method has high specificity and sensitivity for detection/quantification
 of disease-related associates, and can provide an unequivocal diagnosis,
 at an early stage to allow treatment to start before symptoms are
 evident. Fluorescence-activated cell sorting (FACS) is a standardizable
 and generally applicable method, suitable for automation and high
 throughput screening. This sequence represents the human Alzheimer's
 disease associated beta-peptide (1-42) which is used to illustrate the

CC method of the invention
 XX
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 40
 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

Db

RESULT 25
 AAB35589
 ID AAB35589 standard; peptide; 42 AA.
 XX
 XX AAB35589;
 AC
 XX
 DT 15-FEB-2001 (first entry)
 XX
 XX Beta/A4-amyloid peptide.
 DE
 XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KW acute cardiovascular disease; therapy.
 KW
 KW
 XX
 OS Undifferentiated.
 XX
 XX US6136548-A.
 XX
 XX 24-OCT-2000.
 XX
 XX 02-SEP-1999; 99US-00388890.
 XX
 XX 22-NOV-1994; 94US-00347144.
 PR 22-NOV-1995; 95MO-US015007.
 PR 26-JUL-1996; 96US-00686959.
 XX
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA
 XX
 PI Anderson S;
 XX
 XX WPI; 2001-030939/04.
 DR
 XX
 PT Identifying mutant tissue-type plasminogen activator (t-PA) for improving
 PT thrombolytic therapy or treating vascular hemorrhaging, by determining
 PT whether t-PA binds to fibrin but not to a beta amyloid peptide.
 PT
 XX
 PS Disclosure; Col 10; 23pp; English.
 XX

The present invention describes a method for identifying mutant
 derivatives of tissue-type plasminogen activator, which involves
 determining whether or not they bind to beta-amyloid peptides and fibrin.
 CC Mutants will only bind to the latter. These mutants are useful in
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
 CC and in the treatment of acute cardiovascular disease, which may be caused
 CC by myocardial infarction, stroke, ischemia and pulmonary embolism
 XX

Sequence 42 AA;
 SQ

Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 40
 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

Db

RESULT 26
 AAB49098
 ID AAB49098 standard; peptide; 42 AA.
 XX

AC AAB49098;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Human amyloid beta peptide A-beta 42, SEQ ID NO:1.
 XX
 XX Amyloid disease; amyloid fibril deposition; amyloid plaque; immunogenic;
 KW antibody; vaccine; Alzheimer's disease; type 2 diabetes;
 KW reactive system amyloidosis; systemic senile amyloidosis;
 KW familial amyloid cardiomyopathy; transmissible spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; Kuru;
 KW haemodialysis-associated beta-2-microglobulin deposition;
 KW amyloid beta peptide; A-beta 42.
 XX
 OS Homo sapiens.
 XX
 FN WO200072876-A2.
 XX
 PD 07-DEC-2000.
 XX
 PE 01-JUN-2000; 2000WO-US015239.
 XX
 PR 01-JUN-1999; 99US-0137010P.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB;
 XX
 DR WPI; 2001-070921/08.
 XX
 PT Pharmaceutical composition comprising immunogen against amyloid component
 PT such as fibril peptide or protein, or antibody against amyloid component
 PT useful for treating amyloid diseases or amyloidoses.
 PS
 XX Disclosure: Page 24; 140pp; English.
 CC The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril deposits
 CC (amyloid plaques) in a patient. The pharmaceutical composition comprises
 CC an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining the
 CC prognosis of a patient undergoing treatment for an amyloid disorder which
 CC involves measuring a patient serum amount of immunoreactivity against a
 CC selected amyloid component. A patient serum immunoreactivity of at least
 CC four times a base line serum immunoreactivity control level indicates a
 CC prognosis of improved status with respect to the disorder. The
 CC pharmaceutical compositions of the invention are useful for treating a
 CC wide variety of disorders characterised by amyloid fibril deposition in a
 CC patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits, type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeldt-Jakob disease, Kuru) characterised by a
 CC prion protein deposits; and beta-2-microglobulin deposits which form as a
 CC result of long term haemodialysis treatment. The present sequence
 CC represents human amyloid beta peptide A-beta 42
 XX
 SQ Sequence 42 AA:
 Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLMVGSVIA 40
 DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLMVGSVIA 42

RESULT 27
 AAB4427
 ID AAB84427 standard; peptide; 42 AA.
 XX
 AC AAB84427;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 KW Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 FN Key Location/Qualifiers
 FT Misc-difference 1/note="L-Asp, D-Asp or L-iso-Asp"
 FT
 PN WO200142306-A2.
 XX
 PD 14-JUN-2001.
 XX
 PE 08-DEC-2000; 2000WO-US033203.
 XX
 PR 08-DEC-1999; 99US-0169687P.
 XX
 PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain B;
 XX
 DR WPI; 2001-381648/40.
 XX
 PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 PS
 XX Claim 3; Page 42; 47pp; English.
 CC The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal
 XX
 SQ Sequence 42 AA:
 Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLMVGSVIA 40
 DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAITIGLMVGSVIA 42
 RESULT 28
 AAB48497
 ID AAB84897 standard; protein; 42 AA.
 XX
 AC AAB48497;

XX 02-MAR-2001 (first entry)
 DT Human amyloid protein.
 DE
 XX Noctropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease; human; amyloid protein.
 XX Homo sapiens.
 OS
 XX WO200068263-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 04-MAY-2000; 2000WO-CA000515.
 PF
 XX 05-MAY-1999; 99US-0132592P.
 PR
 XX (NEUR-) NEUROCHEM INC.
 PA
 XX Chalfour R, Gervais F, Gupta A;
 PI
 XX WPI; 2001-031852/04.
 DR
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 PS
 XX Disclosure; Fig 1; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein (the present sequence)
 CC
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIA 40
 DB 4 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIA 42
 RESULT 29
 AAB91779
 ID AAB91779 standard; peptide; 42 AA.
 AC
 XX AAB91779;
 AC
 XX 22-JUN-2001 (first entry)
 DT
 XX Amyloid beta-protein fragment peptide SEQ ID NO:955.
 DE
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX WO200069900-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 17-MAY-2000; 2000WO-US013576.
 PF
 XX

PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 PI
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.
 DR
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 PT
 XX Disclosure; Page 506; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 202; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIA 40
 DB 4 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIA 42
 RESULT 30
 AAB91812
 ID AAB91812 standard; peptide; 42 AA.
 AC
 XX AAB91812;
 AC
 XX 22-JUN-2001 (first entry)
 DT
 XX Amyloid beta-protein fragment peptide SEQ ID NO:988.
 DE
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX WO200069900-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 17-MAY-2000; 2000WO-US013576.
 PF
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI: 2001-112059/12.
 XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX

PS Disclosure: Page 517-518; 733pp; English.
 XX

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SO Sequence 42 AA;

Query Match 100.0%; Score 202; DB 4; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVIA 40
 |||||||
 Db 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVIA 42

Search completed: September 28, 2006, 06:10:48
 Job time : 106.906 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 16.5022 Seconds
(without alignments)
233.221 Million cell updates/sec

Title: US-09-731-899-5

Perfect score: 202
Sequence: 1 XFRHDSGYEVHHQKLVFAEDVGSNKGAIIGMGVAVIA 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202	100.0	42	2	beta-amyloid prote
2	202	100.0	57	2	Alzheimer's diseas
3	202	100.0	57	2	Alzheimer's diseas
4	202	100.0	57	2	Alzheimer's diseas
5	202	100.0	57	2	Alzheimer's diseas
6	202	100.0	57	2	Alzheimer's diseas
7	202	100.0	57	2	Alzheimer's diseas
8	202	100.0	82	2	Alzheimer's diseas
9	202	100.0	695	1	Alzheimer's diseas
10	202	100.0	770	1	Alzheimer's diseas
11	186	92.1	747	2	Alzheimer's diseas
12	183	90.6	695	2	Alzheimer's diseas
13	183	90.6	695	2	Alzheimer's diseas
14	118	58.4	33	2	Alzheimer's diseas
15	63	31.2	755	2	Alzheimer's diseas
16	62	30.7	755	1	Alzheimer's diseas
17	61	30.2	755	1	Alzheimer's diseas
18	57	28.0	503	2	Alzheimer's diseas
19	56.5	28.0	378	2	Alzheimer's diseas
20	55	27.2	291	2	Alzheimer's diseas
21	55	27.2	317	2	Alzheimer's diseas
22	55	27.2	488	2	Alzheimer's diseas
23	54.5	27.0	832	2	Alzheimer's diseas
24	54.5	27.0	832	2	Alzheimer's diseas
25	54	26.7	763	2	Alzheimer's diseas
26	53.5	26.5	708	2	Alzheimer's diseas
27	53	26.2	390	2	Alzheimer's diseas
28	53	26.2	422	2	Alzheimer's diseas
29	52	25.7	272	2	Alzheimer's diseas

30	52	25.7	339	2	Alzheimer's diseas
31	52	25.7	417	2	Alzheimer's diseas
32	52	25.7	527	2	Alzheimer's diseas
33	52	25.7	601	2	Alzheimer's diseas
34	52	25.7	611	2	Alzheimer's diseas
35	52	25.7	678	2	Alzheimer's diseas
36	52	25.7	738	2	Alzheimer's diseas
37	51.5	25.5	314	2	Alzheimer's diseas
38	51.5	25.5	1364	2	Alzheimer's diseas
39	51	25.2	103	2	Alzheimer's diseas
40	51	25.2	257	2	Alzheimer's diseas
41	51	25.2	494	2	Alzheimer's diseas
42	51	25.2	769	1	Alzheimer's diseas
43	50.5	25.0	165	2	Alzheimer's diseas
44	50.5	25.0	245	2	Alzheimer's diseas
45	50.5	25.0	245	2	Alzheimer's diseas
46	50.5	25.0	292	2	Alzheimer's diseas
47	50.5	25.0	621	2	Alzheimer's diseas
48	50.5	25.0	621	2	Alzheimer's diseas
49	50.5	25.0	642	2	Alzheimer's diseas
50	50.5	25.0	833	2	Alzheimer's diseas
51	50.5	25.0	1014	2	Alzheimer's diseas
52	50.5	25.0	1345	2	Alzheimer's diseas
53	50	24.8	234	2	Alzheimer's diseas
54	50	24.8	285	1	Alzheimer's diseas
55	50	24.8	296	2	Alzheimer's diseas
56	50	24.8	390	2	Alzheimer's diseas
57	50	24.8	441	2	Alzheimer's diseas
58	50	24.8	487	2	Alzheimer's diseas
59	50	24.8	946	1	Alzheimer's diseas
60	50	24.8	971	2	Alzheimer's diseas
61	50	24.8	1286	2	Alzheimer's diseas
62	49.5	24.5	1292	2	Alzheimer's diseas
63	49.5	24.5	311	2	Alzheimer's diseas
64	49	24.3	246	2	Alzheimer's diseas
65	49	24.3	312	2	Alzheimer's diseas
66	49	24.3	322	2	Alzheimer's diseas
67	49	24.3	403	2	Alzheimer's diseas
68	49	24.3	469	2	Alzheimer's diseas
69	49	24.3	489	2	Alzheimer's diseas
70	49	24.3	533	2	Alzheimer's diseas
71	49	24.3	577	2	Alzheimer's diseas
72	49	24.3	649	2	Alzheimer's diseas
73	49	24.3	674	2	Alzheimer's diseas
74	49	24.3	704	2	Alzheimer's diseas
75	49	24.3	891	2	Alzheimer's diseas
76	48.5	24.0	144	2	Alzheimer's diseas
77	48.5	24.0	390	2	Alzheimer's diseas
78	48.5	24.0	459	2	Alzheimer's diseas
79	48.5	24.0	497	2	Alzheimer's diseas
80	48.5	24.0	510	2	Alzheimer's diseas
81	48.5	24.0	519	2	Alzheimer's diseas
82	48.5	24.0	519	2	Alzheimer's diseas
83	48.5	24.0	614	2	Alzheimer's diseas
84	48.5	24.0	678	2	Alzheimer's diseas
85	48.5	24.0	678	2	Alzheimer's diseas
86	48.5	24.0	678	2	Alzheimer's diseas
87	48	23.8	269	2	Alzheimer's diseas
88	48	23.8	327	2	Alzheimer's diseas
89	48	23.8	337	2	Alzheimer's diseas
90	48	23.8	362	2	Alzheimer's diseas
91	48	23.8	409	2	Alzheimer's diseas
92	48	23.8	415	2	Alzheimer's diseas
93	48	23.8	523	2	Alzheimer's diseas
94	48	23.8	639	2	Alzheimer's diseas
95	48	23.8	639	2	Alzheimer's diseas
96	48	23.8	644	2	Alzheimer's diseas
97	48	23.8	656	2	Alzheimer's diseas
98	48	23.8	701	2	Alzheimer's diseas
99	48	23.8	728	2	Alzheimer's diseas
100	48	23.8	976	2	Alzheimer's diseas
			1112	2	Alzheimer's diseas

signal transductio
conserved hypotet
conserved hypotet
nodulin-like prote
3-methyl-2-oxobuta
conserved hypotet
cation transporter
probable xanthine
sugar protein - Del
probable dimethyl
probable cobQ prot
leukocyte adhesio
ABC transporter at
a probable phospho
asparaginase fam1
Na+/H+ antiporter
probable sodium/hy
probable phosphol
hypothetical prote
legumen protein 7
hypothetical glyci
naphthoate synthas
polysugar degradin
probable Na+/H+-ex
hypothetical prote
hypothetical prote
multidrug resistan
conserved hypotet
probable ABC trans
P-glycoprotein hom
hypothetical prote
B2 glycoprotein pr
triose-phosphate 1
hypothetical prote
hypothetical prote
phosphoglycerate k
permease, multidu
glutamate synthase
phosphoprotein pho
nodulin-like prote
hdc protein - fru
kinase-like transm
storage protein 2
hypothetical prote
hypothetical prote
probable membrane-
aromatic amino aci
serine hydroxymeth
probable membrane
serine hydroxymeth
glycine hydroxymet
probable s/c prote
hypothetical prote
3-methyl-2-oxobuta
naphthoate synthas
genome polyprotein
probable zinc-bind
hypothetical prote
membrane glycoprot
hypothetical prote
linoleoyl-CoA deas
beta-N-acetylhexos
beta-n-acetylhexos
methionyl-tRNA syn
probable serine/th
probable membrane
hypothetical prote
probable receptor-
probable outer mem

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)
C1Species: Cavia porcellus (guinea pig)
C1Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C1Accession: PN0512
R1Shimoharashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A1Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A1Reference number: PN0512; MUID:93290653; PMID:7685598
A1Accession: PN0512
A1Molecule type: protein
A1Residues: 1-42 <JOH>
A1Cross-references: UNIPROT:Q7M088, UNIPARC:UPI0000031558
A1Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C1Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C1Species: Canis lupus familiaris (dog)
C1Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C1Accession: A60045
R1Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A1Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A1Reference number: A60045; MUID:92017079; PMID:1656157
A1Accession: A60045
A1Molecule type: mRNA
A1Residues: 1-57 <JOH>
A1Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
A1Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C1Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
DB 9 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 3

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C1Species: Sus scrofa domestica (domestic pig)
C1Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C1Accession: F60045
R1Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A1Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A1Reference number: A60045; MUID:92017079; PMID:1656157
A1Accession: F60045
A1Molecule type: mRNA
A1Residues: 1-57 <JOH>
A1Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIND:CAA39592.1; PID:
A1Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C1Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
DB 9 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 4

D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C1Species: Bos primigenius taurus (cattle)
C1Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C1Accession: D60045
R1Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A1Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A1Reference number: A60045; MUID:92017079; PMID:1656157
A1Accession: D60045
A1Molecule type: mRNA
A1Residues: 1-57 <JOH>
A1Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
A1Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C1Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
DB 9 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 5

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C1Species: Ovis sp. (sheep)
C1Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C1Accession: A60045
R1Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A1Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A1Reference number: A60045; MUID:92017079; PMID:1656157
A1Accession: A60045
A1Molecule type: mRNA
A1Residues: 1-57 <JOH>
A1Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
A1Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C1Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
DB 9 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 47

RESULT 6

G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C1Species: Cavia porcellus (guinea pig)
C1Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C1Accession: G60045
R1Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A1Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A1Reference number: A60045; MUID:92017079; PMID:1656157
A1Accession: G60045
A1Molecule type: mRNA
A1Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
Db 9 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 47

RESULT 7

B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:92165; PIDN:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 202; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
Db 9 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 47

RESULT 8

P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: P00438; MUID:93075180; PMID:1445331
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 202; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
Db 20 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 58

RESULT 9

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolani, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: UNIPARC:UPI00002A2F2; GB:M58727; NID:9342062; PIDN:AA36829.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 202; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
Db 600 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 638

RESULT 10

Q8H0U4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor xia inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; J10038; S06121; A38384; S29076; S38252; S3
R:Lemaitre, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded t
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: UNIPARC:UPI00002A2F2; EMBL:X13466
A:Note: alternative splice form APP(695)
A:Cross-references: UNIPARC:UPI00002A2F2; EMBL:X13466
R:Lemaitre, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: UNIPARC:UPI000016A5FC; EMBL:X13466; NID:935598; PIDN:CAA31830.1; P1
A:Note: alternative splice form APP(695)
R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:9178863; PIDN:AA51768.1; PID:
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Duyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE>
 A:Cross-references: UNIPARC:UPI0000148176
 A>Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R.Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: 139451; MUID:90236318; PMID:2110105
 A:Accession: 139452
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: UNIPARC:UPI000002DBIC; GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-530/'QWLMPVLPARWEAKVGR' <YOS2>
 A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:
 R.Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Accession: 139453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:
 A>Note: a mutation with 693-Gln is presented
 R.Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A:Reference number: 159562; MUID:92022553; PMID:1925564
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716/'F', 718-737 <MUR>
 A:Cross-references: UNIPARC:UPI000011F7BA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:
 A:Cross-references: UNIPARC:UPI000011F7BA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:
 R.Kamino, K.; Orr, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pulsat, S.M.; Anderson,
 Arakaki, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692/'G', 694-718 <KAM>
 A:Cross-references: UNIPARC:UPI000011F7BA; GB:S45135; NID:g257377; PIDN:AAB3645.1; PID:
 A:Experimental source: Familial Alzheimer disease family SB
 A>Note: sequence extracted from NCBI backbone (NCBI:P.115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g257379; PIDN:AAB3646.1; PID:
 A:Experimental source: Familial Alzheimer disease family LIT
 A>Note: sequence extracted from NCBI backbone (NCBI:P.115376)
 A>Note: this sequence has a silent mutation
 R.Kang, J.; Lemire, H.G.; Untereck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288/'V', 365-770 <KAN>
 A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:
 A>Note: alternative splice form APP(695)
 R.Robkles, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288/'V', 365-646/'F', 648-770 <ROB>
 A:Cross-references: UNIPARC:UPI000016A545; GB:M6765; NID:g178539; PIDN:AAA51722.1; PID:
 A>Note: the authors translated the codon GAG for residue 647 as Asp
 R.Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, V.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328; PMID:3810169
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756/'S', 758-770 <GOL>
 A:Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:g178706; PIDN:AAA5540.1; PID:
 A:Experimental source: brain
 R.Tanzi, R.E.; Guealle, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329; PMID:2949367
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: UNIPARC:UPI000016A46F; GB:M15533; NID:g177957; PIDN:AAA51564.1; PID:
 R.Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437; PMID:2900137
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 A:Cross-references: UNIPARC:UPI000035A80
 R.Tanzi, R.E.; McGeachy, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Guealle, J.F.; Neve
 Nature 331, 528-530, 1988
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640; PMID:2893290
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344/'I', 365-366 <TAN2>
 A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:
 A:Experimental source: promyelocytic leukemia cell line HL60
 A>Note: alternative splice form APP(751)
 R.Ponte, P.; Gonzalez-DeWitt, P.; Schilling, J.; Miller, J.; Heu, D.; Greenberg, B.; Da
 Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639; PMID:2893289
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344/'I', 365-770 <RO2>
 A:Cross-references: UNIPARC:UPI00002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA3
 A>Note: alternative splice form APP(751)
 R.Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641; PMID:2893291
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: UNIPARC:UPI00001455B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:
 A:Experimental source: glioblastoma cell line
 A>Note: alternative splice form APP(770)
 R.Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288/'V', 365-770 <VIN1>
 A:Cross-references: UNIPARC:UPI0000174094
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA

A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
A:Cross-references: UNIPARC:UPI0000174094
R:Zain, S.B.; Sallin, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:8812454; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

Query Match 100.0%; Score 202; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 7, 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 40
Db 675 FRHDSGYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 713

RESULT 11
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homolog of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein, animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 92.1%; Score 186; DB 2; Length 747;
Best Local Similarity 89.7%; Pred. No. 9, 5e-17;
Matches 35; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 40
Db 652 YRHDTAYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 690

RESULT 12
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinnexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:9191568; PIDN:
A:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van den Bergh, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA

A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: UNIPARC:UPI000002AF9; EMBL:X59379
R:Izumii, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:9220328; PIDN:BA01456.1; PID:
C:Genetics: 16C3
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein, animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 90.6%; Score 183; DB 2; Length 695;
Best Local Similarity 92.3%; Pred. No. 2, 2e-16;
Matches 36; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 40
Db 600 FRHDSGYEVHHQKLVFPADVGSNKGAIITGLMVGGVIA 638

RESULT 13
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hlilich, C.; Malthaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002AFB; EMBL:X07648; NID:955616; PIDN:
R:Schubert, D.; Schroeder, R.; Lacrobiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Cross-references: UNIPARC:UPI00001777FD
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behar, D.; Masters, C.L.; Malthaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Cross-references: UNIPARC:UPI00001777FE
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C:Superfamily: Alzheimer's disease amyloid beta protein, animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 90.6%; Score 183; DB 2; Length 695;
Best Local Similarity 92.3%; Pred. No. 2, 2e-16;
Matches 36; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

A>Note: catalyzes the first step in the biosynthesis of auxins from tryptophan
C:Superfamily: tryptophan 2-monooxygenase
C:Keywords: monooxygenase; oxidoreductase

Query Match 30.2%; Score 61; DB 1; Length 755;
Best Local Similarity 41.7%; Pred. No. 4.7;
Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

QY 5 DSGYEVHOKLVFAEDVGSNKGATIGLMVGGVIA 40
DB 223 DSG-----RIGFFEDVPRKVAIVTGAIGSLVVA 252

RESULT 18

57843
general amino acid permease GAP1 homolog F10_orf503 - Mycoplasma pneumoniae (strain ATCC
M16Ternate names: hypothetical protein F10_orf503
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S73843
R:Himmelfeich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; PMID:97105885; PMID:8948633

A:Accession: S73843

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-503 <HIM>

A:Cross-references: UNIPROT:P75462; UNIPARC:UPI00001394B1; EMBL:AE000051; GB:U00089; NID

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: gap1

A:Genetic code: SGC3

Query Match 28.2%; Score 57; DB 2; Length 503;
Best Local Similarity 61.1%; Pred. No. 10;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 22 VGSNKGATIGLMVGGVIT 39
DB 131 VKDNNGALIGLVGFFVL 148

RESULT 19

S61992

SLG1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein O2545; protein UNF378; protein YOR008c

C:Species: Saccharomyces cerevisiae

C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S61992; S66873; S72141

R:Sterky, F.; Uhlen, M.

submitted to the EMBL Data Library, December 1995

A:Reference number: S61981

A:Accession: S61992

A:Molecule type: DNA

A:Residues: 1-378 <STE>

A:Cross-references: UNIPROT:P54867; UNIPARC:UPI0000135A12; EMBL:U43491; NID:G1150992; PI

R:Petersson, B.; Sterky, F.; Uhlen, M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66682

A:Accession: S66873

A:Molecule type: DNA

A:Residues: 1-378 <PET>

A:Cross-references: UNIPARC:UPI0000135A12; EMBL:Z74916; NID:G1420101; PID:e252318; PID:9

A:Experimental source: strain S288C

R:Sterky, F.; Holmberg, A.; Petersson, B.; Uhlen, M.

Yeast 12, 1091-1095, 1996

A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacchar

A:Reference number: S72130; PMID:97051599; PMID:8696276

A:Accession: S72141

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-378 <STW>
A:Cross-references: UNIPARC:UPI0000135A12; EMBL:U43491; NID:G1150992; PIDN:AA049488.1;
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

C:Genetics:
A:Gene: SGD:SLG1
A:Cross-references: SGD:S0005534; MIPS:YOR008c
A:Map position: 15R
C:Keywords: transmembrane protein
F:270-286/Domain: transmembrane #status predicted <TM>

Query Match 28.0%; Score 56.5; DB 2; Length 378;
Best Local Similarity 42.4%; Pred. No. 8.8;
Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

QY 6 DSGYEVHOKLVFAEDVGSNKGATIGLMVGGV 38
DB 251 SSGSKTHKK-----ANVGATVGGVGVV 274

RESULT 20

F95015

glycosyl transferase, family 2 SP0136 (imported) - Streptococcus pneumoniae (strain TIGR

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C:Accession: F95015

R:Petcellin, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Helic

on, J.D.; Umayam, L.A.; White, O.; Salberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

neon, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.D.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; PMID:21357209; PMID:11463916

A:Accession: F95015

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-291 <KUR>

A:Cross-references: UNIPROT:Q97T23; UNIPARC:UPI00000512P6; GB:AE005672; PIDN:AAK74319.1,

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP0136

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 27.2%; Score 55; DB 2; Length 291;
Best Local Similarity 37.9%; Pred. No. 10;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 HDGYEVHOKLVFAEDVGSNKGATIGL 32
DB 58 HPGYVTHRIKILSNEDIGATNARNIGI 86

RESULT 21

H97888

glycosyl transferase, family 2 (imported) - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: H97888

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; P

e, R.; Leblanc, D.J.; Lee, L.N.; Lelkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Ballido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; PMID:21429245; PMID:11544234

A:Accession: H97888

A:Molecule type: DNA

A:Residues: 1-317 <KUR>

A:Cross-references: UNIPROT:Q8DRG7; UNIPARC:UPI00000833BF; GB:AE007317; PIDN:AAK98940.1,

C:Genetics:

A:Gene: glycosyltransferase

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 27.2%; Score 55; DB 2; Length 317;
 Best Local Similarity 37.9%; Pred. No. 11;
 Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
 QY 4 HDSGYEVHHQKLVFAEDVGSNKGAIIGL 32
 DB 58 HQGYTNHRKILNSNEDIGATNARNIGI 86

RESULT 22
 527652
 Probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) - Pseudomonas sp.
 C.Species: Pseudomonas sp.
 C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C.Accession: C42971; 527652
 R.Peterson, J.A.; Lu, J.Y.; Geiselsoder, J.; Graham-Lorence, S.; Carmona, C.; Witney, F.
 J. Biol. Chem. 267, 14193-14203, 1992
 A.Title: Cytochrome P-450exp. Isolation and purification of the protein and cloning and
 A.Reference number: A42971; MUID:92332528; PMID:1629218
 A.Accession: C42971
 A.Status: preliminary; not compared with conceptual translation
 A.Molecule type: nucleic acid; protein
 A.Residues: 1-488 <PEP>
 A.Cross-references: UNIPROT:P33008; UNIPARC:UPI000012928E; EMBL:M91440; NID:G151584; PID
 A.Note: sequence extracted from NCBI backbone (NCBIP:108473)
 C.Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
 C.Keywords: NAD; oxidoreductase

Query Match 27.2%; Score 55; DB 2; Length 488;
 Best Local Similarity 40.6%; Pred. No. 18;
 Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;
 QY 4 HDSGYEVHHQKLVFAEDV----GSNKGAIIGL 31
 DB 305 HESITYEAFRDKLVAAQNVVIGDSQPGVTWG 336

RESULT 23
 C81683
 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC061
 N.Alternate names: oxoisovalerate dehydrogenase
 C.Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
 C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C.Accession: C81683
 R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dobson, R.; Gaim, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A.Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
 A.Reference number: A81500; MUID:20150255; PMID:10684935
 A.Accession: C81683
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-678 <TEP>
 A.Cross-references: UNIPROT:Q9PK54; UNIPARC:UPI00000579G3; GB:AE002330; GB:AE002160; NID
 A.Experimental source: strain Nig9 (Mopn)
 C.Genetics:
 A.Gene: TC0618
 C.Keywords: oxidoreductase

Query Match 27.0%; Score 54.5; DB 2; Length 678;
 Best Local Similarity 44.0%; Pred. No. 31;
 Matches 11; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
 QY 9 EYVHOK-LVFAEDVGSNKGAIIGL 32
 DB 364 EHMGRDGVVVFGBDVAGNKGVGFGV 388

RESULT 24
 H84848
 phospholipase D [imported] - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-May-2004

C.Accession: H84848
 R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A.Reference number: A84420; MUID:20083487; PMID:10617197
 A.Accession: H84848
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-832 <STO>
 A.Cross-references: UNIPARC:UPI000004863E; GB:AE002093; NID:G1871182; PIDN:AA85342.1; G
 C.Genetics:
 A.Gene: At2g42010
 A.Map position: 2
 C.Superfamily: phospholipase D, plant type

Query Match 27.0%; Score 54.5; DB 2; Length 832;
 Best Local Similarity 48.1%; Pred. No. 39;
 Matches 13; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
 QY 11 HHQKLVFAEDVGSNKGAIIGLMVGV 37
 DB 344 HHQKXVIVDADAGNRKRIIA-FVGL 369

RESULT 25
 A13443
 Na+/H+ antiporter 1 / protease IV (EC 3.4.-.-) [imported] - Brucella melitensis (strain
 C.Species: Brucella melitensis
 C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C.Accession: A13443
 R.DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
 .; Marut, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee,
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A.Reference number: AD3252; PMID:11756688
 A.Accession: A13443
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-763 <KUN>
 A.Cross-references: UNIPROT:Q8YF15; UNIPARC:UPI00000580E5; GB:AE008917; PIDN:AA152716.1;
 A.Experimental source: strain 16M
 C.Genetics:
 A.Gene: BME11535
 A.Map position: 1
 C.Superfamily: Na(+)/H(+) antiporter 1/protease IV-related
 C.Keywords: hydrolase

Query Match 26.7%; Score 54; DB 2; Length 763;
 Best Local Similarity 40.0%; Pred. No. 41;
 Matches 16; Conservative 5; Mismatches 17; Indels 2; Gaps 2;
 QY 2 FRHDSGYEVHHQKLVF-PAEDVGSNKGAIIGLMVGVVIA 40
 DB 552 YRRIRDLAERHOKKVFVFEVDVAAGVYIAL-AGDEIIA 590

RESULT 26
 T24727
 hypothetical protein T09A5.12 - Caenorhabditis elegans
 C.Species: Caenorhabditis elegans
 C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C.Accession: T24727
 R.Lighting, J.
 submitted to the EMBL Data Library, August 1994
 A.Reference number: Z19928
 A.Accession: T24727
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-708 <WIL>
 A.Cross-references: UNIPROT:P45972; UNIPARC:UPI000013BBE3; EMBL:Z36753; PIDN:CAA85341.1;
 A.Experimental source: clone T09A5

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:51; Search time 130.224 Seconds
(without alignments)
284.130 Million cell updates/sec

Title: US-09-731-899-5

Perfect score: 202

Sequence: 1 XFRHDSGYEVHHQKLVFPAEDVGNKGAIIIGMGVAVIA 40

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: UniProt_7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202	100.0	42	2 Q56J06 GRAGR	Q56J16 girampus gri
2	202	100.0	42	2 Q56J07 TURTR	Q56J17 tursiops tr
3	202	100.0	42	2 Q7M088 CAVPO	Q7M088 cavia porce
4	202	100.0	57	1 A4_URSHA	Q29149 u amyloid b
5	202	100.0	58	1 A4_CANFA	Q28280 c amyloid b
6	202	100.0	58	1 A4_RABIT	Q28748 o amyloid b
7	202	100.0	58	1 A4_SHEEP	Q28757 o amyloid b
8	202	100.0	59	1 A4_BOVIN	Q28053 b amyloid b
9	202	100.0	113	2 Q8TH58 CHESE	Q8TH58 chelydra se
10	202	100.0	534	2 Q93296 CHICK	Q93296 gallus gall
11	202	100.0	569	2 Q9PVL1 CHICK	Q9PVL1 gallus gall
12	202	100.0	695	2 Q2XQAO PIG	Q2XQAO sus scrofa
13	202	100.0	695	2 Q56J03 CANFA	Q56J03 canis fami
14	202	100.0	695	2 Q5R477 PONPY	Q5R477 pongo pygma
15	202	100.0	695	2 Q6RH29 CANFA	Q6RH29 canis fami
16	202	100.0	695	2 Q9DGJ8 CHICK	Q9DGJ8 gallus gall
17	202	100.0	714	2 Q56J04 CANFA	Q56J04 canis fami
18	202	100.0	749	2 Q56J02 STECO	Q56J02 stenella co
19	202	100.0	751	1 A4_SALSC	Q95241 s amyloid b
20	202	100.0	751	2 Q6GSC0 HUMAN	Q6GSC0 homo sapien
21	202	100.0	751	2 Q4R4R8 CANFA	Q4R4R8 macaca fasc
22	202	100.0	751	2 Q56J05 CANFA	Q56J05 canis fami
23	202	100.0	751	2 Q6RH28 CANFA	Q6RH28 canis fami
24	202	100.0	751	2 Q2XQ99 PIG	Q2XQ99 sus scrofa
25	202	100.0	770	1 Q9DGJ7 CHICK	Q9DGJ7 gallus gall
26	202	100.0	770	1 A4_CAVPO	Q60495 c amyloid b
27	202	100.0	770	1 A4_HUMAN	P05067 h amyloid b
28	202	100.0	770	1 A4_MACFA	P53601 m amyloid b
29	202	100.0	770	1 A4_PANTR	P51880 p amyloid b
30	202	100.0	770	1 A4_PIG	P79307 s amyloid b
31	202	100.0	770	2 Q56J06 CANFA	Q56J06 canis fami

32	202	100.0	770	2 Q6RH30 CANFA	Q6RH30 canis fami
33	197	97.5	52	2 Q8W299 HUMAN	Q8W299 homo sapien
34	192	95.0	62	2 Q3WQ25 ANTST	Q3WQ25 antechinus
35	186	92.1	693	2 Q98S60 XENTIA	Q98S60 xenopus lae
36	186	92.1	747	2 Q91963 GPPI	Q91963 xenopus lae
37	186	92.1	749	2 Q6NRRI XENTIA	Q6NRRI xenopus lae
38	186	92.1	750	2 Q6DJB6 XENTR	Q6DJB6 xenopus tro
39	183	90.6	750	2 Q35463 CRIGR	Q35463 cricetus
40	183	90.6	218	2 Q8BPV5 MOUSE	Q8BPV5 mus musculu
41	183	90.6	384	2 Q8BPC7 MOUSE	Q8BPC7 mus musculu
42	183	90.6	695	2 Q6GR76 MOUSE	Q6GR76 mus musculu
43	183	90.6	695	2 Q7ZXQ0 XENTIA	Q7ZXQ0 xenopus lae
44	183	90.6	695	2 Q98F9 XENTIA	Q98F9 xenopus lae
45	183	90.6	733	2 Q6P605 RAT	Q6P605 rattus norv
46	183	90.6	752	2 Q3TWF3 MOUSE	Q3TWF3 mus musculu
47	183	90.6	752	2 Q3TX19 MOUSE	Q3TX19 mus musculu
48	183	90.6	770	1 A4_MOUSE	P12023 m amyloid b
49	183	90.6	770	1 A4_RAT	P08592 r amyloid b
50	183	90.6	770	2 Q532T3 MOUSE	Q532T3 mus musculu
51	183	90.6	770	2 Q547B7 RAT	Q547B7 rattus norv
52	181	89.6	699	2 Q57394 NARJA	Q57394 narke japon
53	171	84.7	754	2 Q4RY33 TERNG	Q4RY33 tetraodon n
54	171	84.7	780	1 A4_TERTL	Q73683 tetraodon f
55	170	84.2	737	1 A4_FUGRO	Q93379 fugu rubrip
56	170	84.2	759	2 Q4S0J4 TERNG	Q4S0J4 tetraodon n
57	161	79.7	33	2 Q9UCJ3 HUMAN	Q9UCJ3 homo sapien
58	149.5	74.0	357	2 Q8UUI8 BRARE	Q8UUI8 brachydanio
59	149.5	74.0	472	2 Q8UUSO BRARE	Q8UUSO brachydanio
60	149.5	74.0	612	2 Q919E7 BRARE	Q919E7 brachydanio
61	149.5	74.0	678	2 Q7ZZT1 BRARE	Q7ZZT1 brachydanio
62	149.5	74.0	738	2 Q6NUZ1 BRARE	Q6NUZ1 brachydanio
63	149.5	74.0	738	2 Q90WZ8 BRARE	Q90WZ8 brachydanio
64	149	73.8	149	2 Q8UUI7 BRARE	Q8UUI7 brachydanio
65	149	73.8	362	2 Q5XIV5 BRARE	Q5XIV5 brachydanio
66	149	73.8	694	2 Q8UUR9 BRARE	Q8UUR9 brachydanio
67	121	59.9	49	2 Q97917 BOVIN	Q97917 bos taurus
68	121	59.9	49	2 Q2XQ98 PIG	Q2XQ98 sus scrofa
69	64	31.7	328	2 Q9RPS4 ENTFA	Q9RPS4 enterococcu
70	63	31.2	321	2 Q8RG41 FUSNN	Q8RG41 fusobacteri
71	63	31.2	755	2 Q9R472 GRHIZ	Q9R472 agrobacteri
72	63	31.2	755	2 Q9R694 GRHIZ	Q9R694 agrobacteri
73	63	31.2	755	2 Q9R717 GRHIZ	Q9R717 agrobacteri
74	63	31.2	755	2 Q8U6A3 AGRT5	Q8U6A3 agrobacteri
75	62	30.7	755	1 TR2M AGRT4	P0A3V2 agrobacteri
76	62	30.7	755	1 TR2M AGRTU	P0A3V3 agrobacteri
77	62	30.7	755	2 Q443B8 GRHIZ	Q443B8 agrobacteri
78	61	30.2	755	2 TR2N AGRTV	P25017 agrobacteri
79	60.5	29.7	351	2 Q6LJ99 PHOPR	Q6LJ99 photobacter
80	60	29.7	252	2 Q8HMH7 SQUAC	Q8HMH7 squallus aca
81	60	29.7	419	2 Q441M5 SOLUS	Q441M5 solibacter
82	60	29.7	755	2 Q9MWAI GRHIZ	Q9MWAI agrobacteri
83	60	29.7	755	2 Q8IKEX PLAF7	Q8IKEX plasmodium
84	59	28.2	362	2 Q5K514 VTRU	Q5K514 bacterioph
85	58	28.7	288	2 Q441H4 CHRSL	Q441H4 chromolab
86	58	28.7	320	2 Q7P4H7 FUSNV	Q7P4H7 fusobacteri
87	58	28.7	368	2 Q8G2C8 BRUSU	Q8G2C8 bruceella su
88	58	28.7	491	2 Q411H0 GIBZE	Q411H0 gibberella
89	58	28.7	624	2 Q6Z4P2 ORYSA	Q6Z4P2 oryza sativ
90	58	28.7	763	2 Q2YMB3 BRUAS	Q2YMB3 bruceella ab
91	57.5	28.5	323	2 Q4UE56 THEPA	Q4UE56 thelletia a
92	57.5	28.5	405	2 Q4N5D6 THEPA	Q4N5D6 thelletia p
93	57.5	28.5	545	2 Q7NGT4 GLOVI	Q7NGT4 gloeobacter
94	57.5	28.5	895	2 Q9AMB6 LYCES	Q9AMB6 glycoepetico
95	57	28.2	195	2 Q2Z667 ARATH	Q2Z667 arabidopsis
96	57	28.2	324	2 Q4AS87 CHILI	Q4AS87 chlorobium
97	57	28.2	324	2 Q5WW16 LEGPL	Q5WW16 legionella
98	57	28.2	324	2 Q5X504 LEGPA	Q5X504 legionella
99	57	28.2	324	2 Q5ZV81 LEGPH	Q5ZV81 legionella
100	57	28.2	331	2 Q40FX5_9RHOB	Q40FX5 jannaschia

ALIGNMENTS

```

RESULT 1
SQ 056J06 GRAGR PRELIMINARY; PRT; 42 AA.
ID 056J06 GRAGR PRELIMINARY; PRT; 42 AA.
AC 056J06;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AY926589; AAX81918.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYL01D.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 42

RESULT 2
SQ 056J07 TURTR PRELIMINARY; PRT; 42 AA.
ID 056J07 TURTR PRELIMINARY; PRT; 42 AA.
AC 056J07;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
-----
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-----
DR EMBL; AY926588; AAX81917.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYL01D.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 42

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FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 42

RESULT 3
SQ 07M088 CAVPO PRELIMINARY; PRT; 42 AA.
ID 07M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC 07M088;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 11.
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognathhi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance P receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
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DR PIR; P00512; P00512.
DR HSSP; O16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYL01D.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNGKAIIGLMVGVVIA 42

RESULT 4
SQ A4 URSMA STANDARD; PRT; 57 AA.
ID A4 URSMA STANDARD; PRT; 57 AA.
AC 029149;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, entry version 1.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:289-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56128; CAA39593.1; -; mRNA.
DR FIR; B60045; B60045.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1> >57
FT /FTid=PRO_0000226244.
FT Soluble APP-beta (By similarity).
FT /FTid=PRO_0000000191.
FT CTF-alpha (By similarity).
FT /FTid=PRO_0000000192.
FT FT CHAIN 6 47
FT Beta-amyloid protein 42 (By similarity).
FT /FTid=PRO_0000000193.
FT Beta-amyloid protein 40 (By similarity).
FT /FTid=PRO_0000000194.
FT Gamma-CTF(59) (By similarity).
FT /FTid=PRO_0000000195.
FT FT CHAIN 6 45
FT Beta-amyloid protein 40 (By similarity).
FT /FTid=PRO_0000000194.
FT Gamma-CTF(59) (By similarity).
FT /FTid=PRO_0000000195.
FT FT CHAIN 48 >57
FT Gamma-CTF(57) (By similarity).
FT /FTid=PRO_0000000196.
FT FT CHAIN <1> 33
FT TOPO_DOM 34 57
FT TRANSMEM 34 57
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 202; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE CTF(57) (Gamma-secretase C-terminal fragment 57) (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Kidney;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56125; CAA39590.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR Ensembl; ENSCAP00000008557; Canis familiaris.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1> >58
FT /FTid=PRO_0000226241.
FT Soluble APP-beta (By similarity).
FT /FTid=PRO_0000000070.
FT CTF-alpha (By similarity).
FT /FTid=PRO_0000000071.
FT Beta-amyloid protein 42 (By similarity).
FT /FTid=PRO_0000000072.
FT FT CHAIN 7 46
FT Beta-amyloid protein 40 (By similarity).
FT /FTid=PRO_0000000073.
FT Gamma-CTF(59) (By similarity).
FT /FTid=PRO_0000000074.
FT FT CHAIN 47 >58
FT Gamma-CTF(57) (By similarity).
FT /FTid=PRO_0000000075.
FT FT CHAIN 49 >58
FT TOPO_DOM <1> 34
FT TRANSMEM 35 58
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 202; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 NC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 DR EMBL: X56129; CAA39594.1; -; mRNA.
 DR HSSP: P08592; INMD.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00204; BETAMYLOID.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4_INTRA; PARTIAL.
 KM Amyloid; Membrane; Transmembrane.
 FT CHAIN <1
 FT /FTid=PRO_0000226242.
 FT Soluble APP-beta (By similarity).
 FT /FTid=PRO_0000000153.
 FT CTF-alpha (By similarity).
 FT /FTid=PRO_0000000154.
 FT Beta-amyloid protein 42 (By similarity).
 FT /FTid=PRO_0000000155.
 FT Beta-amyloid protein 40 (By similarity).
 FT /FTid=PRO_0000000156.
 FT Gamma-CTF(59) (By similarity).
 FT /FTid=PRO_0000000157.
 FT Gamma-CTF(57) (By similarity).
 FT /FTid=PRO_0000000158.
 FT Extracellular (Potential).
 FT /FTid=PRO_0000000190.
 FT Cytoplasmic (Potential).
 SQ SEQUENCE 58 AA; 6300 MM; F434209D88BA82D CRC64;
 Query Match 100.0%; Score 202; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 A4 SHEEP
 ID A4_SHEEP

STANDARD; PRT; 58 AA.

QY 2 FRHDSGYEVHOKLVFPADVGSNGKAIIGLWVGIVIA 40
 |||||
 DB 9 FRHDSGYEVHOKLVFPADVGSNGKAIIGLWVGIVIA 47

Query Match 100.0%; Score 202; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC Q28757;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
 GN Name=APP;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 NC NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Heart;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 DR EMBL: X56130; CAA39595.1; -; mRNA.
 DR HSSP: P08592; INMD.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00204; BETAMYLOID.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4_INTRA; PARTIAL.
 KM Amyloid; Membrane; Transmembrane.
 FT CHAIN <1
 FT /FTid=PRO_0000226243.
 FT Soluble APP-beta (By similarity).
 FT /FTid=PRO_0000000185.
 FT CTF-alpha (By similarity).
 FT /FTid=PRO_0000000186.
 FT Beta-amyloid protein 42 (By similarity).
 FT /FTid=PRO_0000000187.
 FT Gamma-CTF(59) (By similarity).
 FT /FTid=PRO_0000000188.
 FT Gamma-CTF(57) (By similarity).
 FT /FTid=PRO_0000000189.
 FT Extracellular (Potential).
 FT /FTid=PRO_0000000190.
 FT Cytoplasmic (Potential).
 SQ SEQUENCE 58 AA; 6300 MM; F434209D88BA82D CRC64;
 Query Match 100.0%; Score 202; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPADVGSNGKAIIGLWVGIVIA 40
 |||||
 DB 9 FRHDSGYEVHOKLVFPADVGSNGKAIIGLWVGIVIA 47

Query Match 100.0%; Score 202; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5.6e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 8
A4 BOVIN STANDARD; PRT; 59 AA.
ID Q2E053;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
DE protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
GN Name:APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane, single-pass type I membrane
CC protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
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CC
DR EMBL, X56124; CAA39589.1; -; mRNA.
DR EMBL, X56126; CAA39591.1; -; mRNA.
DR HSSP, P08592; INMO.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR01255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Membrane; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT FTID=PRO_0000000064.
FT CHAIN 7 7 CTF-alpha (By similarity).
FT FTID=PRO_0000000065.
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT FTID=PRO_0000000066.
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT FTID=PRO_0000000067.
FT CHAIN 47 47 Gamma-CTF(59) (By similarity).
FT FTID=PRO_0000000068.
FT CHAIN 49 49 Gamma-CTF(57) (By similarity).
FT FTID=PRO_0000000069.
FT TOPO_DOM 35 34 Extracellular (Potential).
FT TOPO_DOM 59 59 Potential.
FT NON_TER 1 1 Cyttoplasmic (Potential).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 100.0%; Score 202; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.7e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40

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Db 10 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 48
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RESULT 9
O80H58_CHESE PRELIMINARY; PRT; 113 AA.
ID O80H58;
AC O80H58;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21876906; PubMed=11882478;
RX Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RA "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina."
RL Environ. Health Perspect. 110:269-275(2002).
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CC
DR EMBL, AF541917; AAN04908.1; -; mRNA.
DR HSSP, Q16019; I1YT.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; P:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
Db 18 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 56
|||||
RESULT 10
O93296_CHICK PRELIMINARY; PRT; 534 AA.
ID O93296;
AC O93296;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98337885; PubMed=9671674;
RX Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).

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DR EMBL: AF042098; AAC25052.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2B66D4C92 CRC64;

Query Match
Best Local Similarity 100.0%; Score 202; DB 2; Length 534;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 40
DB 439 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 477

RESULT 11
ID Q9PVL1_CHICK PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Amyloid protein (Fragment).
GN Name=APP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
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DR EMBL: AF030341; AAF12698.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR SMR: Q9PVL1; 1-64, 260-369.
DR Ensemble: ENSGALG00000015770; Gallus gallus.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2B66D4C92 CRC64;

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SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match
Best Local Similarity 100.0%; Score 202; DB 2; Length 569;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 40
DB 475 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 513

RESULT 12
ID Q2XOA0_PIG PRELIMINARY; PRT; 695 AA.
AC Q2XOA0;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Amyloid protein variant 1.
GN Name=APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein, APP: Cloning and characterization
RT of cDNAs."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL: DQ267684; ABB82033.1; -; mRNA.
SQ SEQUENCE 695 AA; 78615 MW; 825A7E4AC10B8F0B CRC64;

Query Match
Best Local Similarity 100.0%; Score 202; DB 2; Length 695;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 40
DB 600 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVGVIA 638

RESULT 13
ID Q56UK3_CANFA PRELIMINARY; PRT; 695 AA.
AC Q56UK3;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AY926582; AAX81911.1; -; mRNA.
DR SMR: Q56UK3; 28-123, 124-189, 385-494.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0005488; F:binding; IEA.

```

DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR012282; Cytochrome_C_R.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 100.0%; Score 202; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 7.1e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
 DB 600 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 14
 OSR477 PONPY PRELIMINARY; PRT; 695 AA.
 AC OSR477_ PONPY
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Hypothetical protein DKFp459D212.
 GN Name=DKFp459D212.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cortex;
 RC The German CDNA Consortium;
 RA Mambaut R., Heubner D., Mewes H.W., Weil B., Amid C., Osaenger A.,
 RA Fobio G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

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 CC -----
 DR EMBL; CR861380; CAH93439.1; -; mRNA.
 DR SMR; OSR477; 28-123, 124-189, 385-494.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR012282; Cytochrome_C_R.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 695 AA; 78627 MW; 0BF5DD9BA2213E49 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 7.1e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
 DB 600 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 15
 OSRH29 CANFA PRELIMINARY; PRT; 695 AA.
 ID OSRH29 CANFA
 AC OSRH29;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Beta amyloid protein isoform APP695.
 GN Name=Beta APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Nakata M.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AY498707; AAR97727.1; -; mRNA.
 DR HSSP; Q16019; 1BA4.
 DR SMR; OSRH29; 28-123, 124-189, 385-494.
 DR Ensembl; ENSGAF0000008557; Canis familiaris.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 7.1e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
 DB 600 FRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 16
 OS9DGJ8 CHICK PRELIMINARY; PRT; 695 AA.
 ID OS9DGJ8 CHICK
 AC OS9DGJ8;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Beta-amyloid protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=16039787; DOI=10.1016/j.neuroscience.2005.05.020;
 RX Carrodeguas J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,

Query Match 100.0%; Score 202; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 7.1e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RA  Perez-pe R., Lacosta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RA  Sorribes V., Sarasa M.,
RT  "The chick embryo appears as a natural model for research in beta-
RT  amyloid precursor protein processing."
RL  Neuroscience 134:1285-1300(2005).
CC  -----
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CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
CC  EMBL; AF289218; AAG00593.1; -; mRNA.
DR  HSSP; Q16019; 11YT.
DR  SMR; Q9DGJ8; 28-123, 124-189, 385-494.
DR  Ensembl; ENSGALG00000015770; Gallus gallus.
DR  GO; GO:0016021; C: integral to membrane; IEA.
DR  GO; GO:0005488; F: binding; IEA.
DR  InterPro; IPR008155; A4_APP.
DR  InterPro; IPR008154; A4_extra.
DR  InterPro; IPR001255; Beta-APP.
DR  PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR  Pfam; PF02177; A4_EXTRA; 1.
DR  Pfam; PF03494; Beta-APP; 1.
DR  PRINTS; PR00203; AMYLOIDA4.
DR  PRINTS; PR00204; BETAMYLOID.
DR  SMART; SM00006; A4_EXTRA; 1.
DR  PROSITE; PS00319; A4_EXTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
SQ  SEQUENCE 695 AA; 78566 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 695;
Beet Local Similarity 100.0%; Pred. No. 7, 1e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHMQLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 600 FRHDSGYEVHMQLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 17
O56JK4 CANFA PRELIMINARY; PRT; 714 AA.
AC O56JK4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DS Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBD databases.
CC -----
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CC -----
CC EMBL; AY926581; AAX81910.1; -; mRNA.
DR SMR; Q56JK4; 28-123, 124-189, 404-513.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0020037; F: heme binding; IEA.
DR GO; GO:0006118; P: electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome c R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.

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QY PRINTS; PRO0204; BETAAMYLOID.
DR SMART; SMO0006; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 714 AA; 80827 MW; 50DD51PB930E5 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 714;
Best Local Similarity 100.0%; Pred. No. 7,3e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFPADVDGSKGAIIIGLMVGGVIA 40
DB 619 FRHDSGYEVHHQKLVFPADVDGSKGAIIIGLMVGGVIA 657

RESULT 18
ID Q56JK2_STECO PRELIMINARY; PRT; 749 AA.
AC Q56JK2;
DT 10-MAY-2005, integrated into UniProtKB/TREMBL.
DT 07-FEB-2006, entry version 5.
DT 10-MAY-2005, sequence version 1.
DE Beta-amyloid protein 749.
DI Beta-amyloid protein 749.
DS Stenella coelestisalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Cetacea;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
OX NCBI_TaxID=9737;
OK [1]
RN NUCLEOTIDE SEQUENCE.
RP Gallego C., Sarasa M.;
RL "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC -1 SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
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DR EMBL; AY926583; AAX81912.1; mRNA.
DR SMK; Q56JK2; 28-123, 124-189, 284-339, 457-566.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:serine binding; IEA.
DR GO; GO:0004867; F:enzyme-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR01255; Beta-APP.
DR InterPro; IPR01282; Cytochrome c R.
DR InterPro; IPR002223; Prot_inh_Kunzt-m.
DR PANTHER; PTHR10083.SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYL0IDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SMO0006; A4_EXTRA; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84543 MW; 426599887C2A95D6 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 749;
Best Local Similarity 100.0%; Pred. No. 7,6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFPADVDGSKGAIIIGLMVGGVIA 40
DB 654 FRHDSGYEVHHQKLVFPADVDGSKGAIIIGLMVGGVIA 692
```

A4_SAIISC STANDARD; PRT; 751 AA.

ID A4_SAIISC

AC 095241;

DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.

DT 01-FEB-1997, sequence version 1.

DT 07-MAR-2006, entry version 60.

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid beta A4 protein precursor) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].

GN NameAPP;

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Placentalia; Cebidae; Cebinae; Saimiri.

OC NCBI_TaxID=9521;

OX [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Kidney, and Liver;

RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2; Levy E., Amornit A., Frangione B., Walker L.C.;

RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."

RT Neurobiol. Aging 16:805-808(1995).

RL

CC -1- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(O) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPH1, APPBP1, IBL, KNS2 (via its TPR domains) (By similarity), APPBP2 (via BASS) and DDB1. In vitro, it binds MAPT via the WT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized into endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=APP770;

CC Name=APP770;

CC IsoId=Q95241-1; Sequence=Displayed;

CC Name=APP695;

CC IsoId=Q95241-2; Sequence=Not described;

CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

CC -1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/icastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

CC -1- PTM: N- and O-glycosylated (By similarity).

CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can reduce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).

CC Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

CC -1- SIMILARITY: Belongs to the APP family.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC EMBL; S81024; AAD14347.1; -; mRNA.

CC PDB; 1RW6; X-ray; A=346-551.

CC SMR; Q95241; 28-123, 124-189, 287-342.

CC InterPro; IPR008155; A4 APP.

CC InterPro; IPR008154; A4 APP.

CC InterPro; IPR001255; Beta-APP.

CC InterPro; IPR002223; Prot_inh_Kunz-m.

CC PANTHER; PTHR10083:SF6; Beta-APP; 5.

CC Pfam; PF02177; A4 EXTRA; 1.

CC Pfam; PF03494; Beta-APP; 1.

CC Pfam; PF00014; Kunitz BPTI; 1.

CC PRINTS; PR00203; AMYLOID4.

CC PRINTS; PR00759; BASICPTASE.

CC PRINTS; PR00204; BETAMYLOID.

CC ProDom; PD000222; Prot_inh_Kunz-m; 1.

CC SMART; SM00006; A4 EXTRA; 1.

CC SMART; SM00131; KU; 1.

CC PROSITE; PS00319; A4 EXTRA; 1.

CC PROSITE; PS00320; A4_INTRA; 1.

CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.

CC 3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion;

DB 656 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 694

```
RESULT 21
ID Q6R4R8_MACFA PRELIMINARY; PRT; 751 AA.
AC Q6R4R8;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Brain cDNA, clone: Q61A-13524, similar to human amyloid beta (A4)
DE protein (protease nexin-II, Alzheimer disease) (APP), transcript
DE variant 2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15944441; DOI=10.1093/molbev/msl187;
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RT Mol. Biol. Evol. 22:1976-1982(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AB169826; BAE01907.1; -; mRNA.
DR SMR; Q6R4R8; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR012282; Cytochrome C_R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta_APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYLOID.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 751 AA; 84817 MW; 83C1CD96AD355158 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 656 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 694

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RESULT 22
ID Q56UK5_CANFA PRELIMINARY; PRT; 751 AA.
AC Q56UK5;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RT Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AY926580; AAX81909.1; -; mRNA.
DR SMR; Q56UK5; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR012282; Cytochrome C_R.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta_APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84920 MW; C1CD20377DFPF8550 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AY498708; AAR97728.1; -; mRNA.
DR HSSP; Q16019; 1AAP.
DR SMR; OGRH28; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSGACFG00000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004867; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta_APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 40
DB 656 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 694

RESULT 24
Q2X099_PIG PRELIMINARY; PRT; 751 AA.
ID Q2X099_PIG
AC Q2X099_
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 1.
DE Amyloid protein variant 2.
GN Name=APP;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
OX NCB1
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein, APP: Cloning and characterization
of cDNAs.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; DQ267685; ABB82034.1; -; mRNA.

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SQ SEQUENCE 751 AA; 84799 MW; 37868743880C369F CRC64;

Query Match 100.0%; Score 202; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 40
DB 656 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 694

RESULT 25
Q9DGJ7 CHICK
ID Q9DGJ7 CHICK PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed; 16039787; DOI-10.1016/j.neuroscience.2005.05.020;
RA Carrodeguaes J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,
RA Perez-Pe R., Lacosta A.M., Dominguez U., Monleon I., Sanchez-Diaz R.,
RA Sorribas V., Sarrasa M.;
RT "The chick embryo appears as a natural model for research in beta-
amyloid precursor protein processing.";
RL Neuroscience 134:1285-1300(2005).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC -----
DR EMBL; AF289219; AAG00594.1; -; mRNA.
DR HSSP; Q16019; 1IYT.
DR SMR; Q9DGJ7; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSGALG00000015701; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004867; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083:SF6; Beta_APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 751 AA; 84706 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 202; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 40
DB 656 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVWGVVIA 694

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RESULT 26
 A4 CAVPO STANDARD; PRT; 770 AA.
 AC Q60496; Q60496; integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 56.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN Name=APP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxId=10141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing."; *Biochim. Biophys. Acta* 1351:17-21(1997).
 RL Bioclim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Marel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta."; *J. Neurochem.* 69:1995-2004(1997).
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Gamma-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein."; *Neuroscience* 95:243-254(2000).
 RL Neuroscience 95:243-254(2000).
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;
 RA Pimix I., Mununuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative C-
 RT terminal fragment-gamma of amyloid beta protein precursor."; *J. Biol. Chem.* 276:481-487(2001).
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC ApoB4 appears to be the preferred amyloid binding isoform, while
 CC the ApoB4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTF8).

RT sequencing of a 300 kb region of human APP locus." ;
 RN Nucleic Acids Res. 25:1802-1808(1997).
 RN (8)
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639." ;
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN (9)
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LYS-501.
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gilderleeve H., Cassidy C.M., Johnson S.J.,
 RA Swanson J.E., McFarland I., Yoo B., Park C., Nickerson D.A.;
 RT "NIHNS-SNP, environmental genome project, NIHNS ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN (10)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).
 RC TISSUE=Eye, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant J.L., Schetz T.E.,
 RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosch S.A., Meban P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman W., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marrs M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (11)
 RP NUCLEOTIDE SEQUENCE OF 1-10.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide." ;
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN (12)
 RP NUCLEOTIDE SEQUENCE OF 1-75.
 RA La Faut G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene." ;
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN (14)
 RP PROTEIN SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts." ;
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN (15)
 RP PROTEIN SEQUENCE OF 18-40.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;

RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides." ;
 RL Nat. Biotechnol. 21:566-569(2003).
 RN (16)
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein." ;
 RL Science 245:651-653(1989).
 RN (17)
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN (18)
 RP NUCLEOTIDE SEQUENCE OF 286-366.
 RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
 RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease." ;
 RL Nature 331:528-530(1988).
 RN (19)
 RP NUCLEOTIDE SEQUENCE OF 287-367.
 RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
 RA Kikuchi N., Takahashi Y., Tokushima Y., Shoji S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
 RT inhibitory activity." ;
 RL Nature 331:530-532(1988).
 RN (20)
 RP NUCLEOTIDE SEQUENCE OF 507-770.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marcota C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN (21)
 RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT Query Match 100.0%; Score 202; DB 1; Length 770;
 RT Best Local Similarity 100.0%; Pred. No. 7.9e-18;
 RT Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHOKLVFPAEDVGSNGKAITGLWGVVIA 40
 Db 675 FRHDSGYEVHOKLVFPAEDVGSNGKAITGLWGVVIA 713
 AC P53601; Q60H17; Q95KN7;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 22-FEB-2003, sequence version 3.
 DT 07-FEB-2006, entry version 55.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DE secretase C-terminal fragment 50; C31].

CN Name=APP; ORFNames=OcCfe-15949;

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecoidea; Cercopithecinae; Macaca.

NCBI_Taxid=9541;

OK [1]

NP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS APP695 AND APP770).

RP TISSUE=Cerebellum;

RC MEDLINE=91273117; PubMed=1905108;

RA Podlasky M.B., Tolan D.R., Selkoe D.J.;

RT "Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease";

RT Am. J. Pathol. 138:1423-1435(1991).

RL [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).

RC TISSUE=Brain cortex;

RA Kuwada J., Osada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;

RT "Isolation and characterization of cDNA for macaque neurological disease genes.";

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G10 and JIP (By similarity). Inhibits G10 alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metalated APP induces neuronal death directly or its potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK3IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2 (via its TPR domains) (By similarity), APPB2 (via BaS5) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Comment=Additional isoforms seem to exist;

CC Name=APP770;

CC IsoId=P53601-1; Sequence=Displayed;

CC Name=APP695;

CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;

CC Name=3;

CC IsoId=P53601-3; Sequence=VSP_013360, VSP_013361;

CC -1- DOMAIN: The basolateral sorting signal (BaS5) is required for targeting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

CC -1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

CC -1- PTM: N- and O-glycosylated (By similarity).

CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

CC -1- SIMILARITY: Belongs to the APP family.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC EMBL: M58726; AAA36828.1; -; mRNA.

CC EMBL: M58727; AAA36829.1; -; mRNA.

CC EMBL: AB125150; BAD51938.1; -; mRNA.

CC HSSP: P08592; 1NWJ.

CC SMR: P53601; 28-123, 124-189, 287-342, 460-569.

CC InterPro: IPR008154; A4_APP.

CC InterPro: IPR008154; A4_extra.

CC InterPro: IPR001255; Beta-APP.

CC InterPro: IPR002223; Prot_inh_Kunz-m.

CC PANTHER: PTHR10083; SFe; Beta-APP; 6.

CC Pfam: PF02177; A4_EXTRA; 1.

CC Pfam: PF03494; Beta-APP; 1.

CC Pfam: PF00014; Kunitz BPTI; 1.

CC PRINTS: PR00203; AMYLOIDA4.

CC PRINTS: PR00759; BASICPRASE.

CC PRINTS: PR00204; BETAMYLOID.

CC PRODom: PD000222; Prot_inh_Kunz-m; 1.

CC SMART: SM00006; A4_EXTRA; 1.

CC SMART: SM00131; KJ; 1.

CC PROSITE: PS00319; A4_EXTRA; 1.

CC PROSITE: PS00320; A4_INTRA; 1.

CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE: PS02079; BPTI_KUNITZ_2; 1.

CC Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;

RN NCCTGCTTTC SEQUENCE [MRNA].
 RX PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
 RA Dorus S., Vulliamdier E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
 RA Mowbray M., Wyckoff G.J., Malm C.M., Lahn B.T.,
 RT "accelerated evolution of nervous system genes in the origin of Homo
 sapiens.";
 RL Cell 119:1027-1040(2004).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin I (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-induced low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPT1 domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
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 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAFK3/PI3, and SHC1, Numb and Dab1 (By similarity). Binding
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 CC interacts with GPCR-like protein BPP, PPR1L, APPB1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPB2 (via BASS) and DDB1
 CC In vitro, it binds MAPK via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of APP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via a clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CRF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields p3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin1/nicastrin-mediated

CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: AY665248; AAV74286.1; -, mRNA.
 CC SMR: Q51S80; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_APP.
 CC InterPro: IPR001255; Beta_APP.
 CC InterPro: IPR012282; Cytochrome C_R.
 CC InterPro: IPR002223; Prot_inh_Kunz7m.
 CC PANTHER: PTHR10083; SFe; Beta_APP; 6.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF00394; Beta_APP; 1.
 CC PRINTS: PR00203; Kunitz_BPT1; 1.
 CC PRINTS: PR00203; BASICPTASE.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC ProDom: PD000222; Prot_inh_Kunz-m; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPT1_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPT1_KUNITZ_2; 1.
 CC Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
 CC Glycoprotein; Heparin-binding; Iron; Membrane; Metal-binding;
 CC Notch signaling pathway; Phosphorylation; Protease inhibitor;
 CC Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 CC SIGNAL
 CC FT CHAIN 1 17 Amyloid beta A4 protein.
 CC FT FT /FTid=PRO_0000000127.
 CC FT CHAIN 18 687 Soluble APP-alpha (Potential).
 CC FT FT /FTid=PRO_0000000128.
 CC FT CHAIN 18 671 Soluble APP-beta (Potential).
 CC FT FT /FTid=PRO_0000000129.
 CC FT CHAIN 672 770 C99 (Potential).
 CC FT FT /FTid=PRO_0000000130.
 CC FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
 CC FT FT /FTid=PRO_0000000131.
 CC FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
 CC FT FT /FTid=PRO_0000000132.
 CC FT CHAIN 688 770 C83 (Potential).
 CC FT FT /FTid=PRO_0000000133.
 CC FT CHAIN 688 713 P3(42) (Potential).
 CC FT FT /FTid=PRO_0000000134.
 CC FT CHAIN 688 711 P3(40) (Potential).
 CC FT FT /FTid=PRO_0000000135.
 CC FT CHAIN 712 770 Gamma-CTF(59) (Potential).
 CC FT FT /FTid=PRO_0000000136.
 CC FT CHAIN 714 770 Gamma-CTF(57) (Potential).
 CC FT FT /FTid=PRO_0000000137.
 CC RP

FT CHAIN 721 770 Gamma-CTF(50) (Potential).
 FT FT /FTid=PRO_0000000138.
 FT CHAIN 740 770 C31 (Potential).
 FT FT /FTid=PRO_0000000139.
 FT TOPO_DOM 18 699 Extracellular (Potential).
 FT TRANSMEM 700 723 Potential.
 FT TOPO_DOM 724 770 Cytoplasmic (Potential).
 FT DOMAIN 291 341 BPT1/Kunitz inhibitor.
 FT REGION 96 110 Heparin-binding (By similarity).
 FT REGION 181 188 Zinc-binding (By similarity).
 FT REGION 331 423 Heparin-binding (By similarity).
 FT REGION 431 522 Heparin-binding (By similarity).
 FT REGION 523 540 Collagen-binding (By similarity).
 FT REGION 732 751 Interaction with G(o)-alpha (By similarity).
 FT MOTIF 724 734 Basolateral sorting signal (By similarity).
 FT MOTIF 759 762 NPXY motif; contains endocytosis signal.
 FT COMBIBS 230 260 Asp/Glu-rich (acidic).
 FT COMBIBS 274 280 Poly-Thr.
 FT METAL 137 137 Copper (By similarity).
 FT METAL 147 147 Copper (By similarity).
 FT METAL 149 149 Copper (By similarity).
 FT METAL 151 151 Copper (By similarity).
 FT METAL 677 677 Copper or zinc (By similarity).
 FT METAL 681 681 Copper or zinc (By similarity).
 FT METAL 684 684 Copper or zinc (By similarity).
 FT METAL 685 685 Copper or zinc (By similarity).
 FT SITE 144 144 Required for Cu(2+) reduction (By similarity).
 FT SITE 301 302 Reactive bond (By similarity).
 FT SITE 671 672 Cleavage (by beta-secretase) (By similarity).
 FT SITE 672 673 Cleavage (by caspase-6) (By similarity).
 FT SITE 687 688 Cleavage (by alpha-secretase) (By similarity).
 FT SITE 688 688

Query Match 100.0%; Score 202; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 7; 9e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGVGVIA 40
 DB 675 FRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGVGVIA 713
 ID A4_PIG STANDARD; PRT; 770 AA.
 AC P79307; Q29023; Q9TU10;
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 50.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid beta A4 protein precursor) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C93; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OC NCBI_TaxID=9823;
 RX NUCLEOTIDE SEQUENCE [MRNA].
 RA Kimura A., Takahashi T.;
 RL "Amyloid precursor protein 770.";
 RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.

RC TISSUE=Small intestine;
RA Winterer A.K., Friedholm M.;
RT "Evaluation and characterization of a porcine small intestine cDNA
library";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 667-723.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functions as a cell surface receptor and performs
physiological functions on the surface of neurons relevant to
neurite growth, neuronal adhesion and axonogenesis. Involved in
cell mobility and transcription regulation through protein-protein
interactions (By similarity). Can promote transcription activation
through binding to APBB1/Tip60 and inhibit Notch signaling through
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inducing pathways such as those mediated by G(O) and JIP (By
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CC Acts as a kinesin I membrane receptor, mediating the axonal
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ion reduction (By similarity). In vitro, copper-metallated APP
induces neuronal death directly or is potentiated through Cu(2+)-
mediated low-density lipoprotein oxidation (By similarity). Can
regulate neurite outgrowth through binding to components of the
extracellular matrix such as heparin and collagen I and IV (By
similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
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to Dab1 inhibits its serine phosphorylation (By similarity). Also
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(via its TPR domains) (By similarity), APPB2 (via BASS) and DBP1.
CC In vitro, it binds MAPT via the WT-binding domains (By
similarity). Associates with microtubules in the presence of ATP
and in a kinesin-dependent manner (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
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pits. During maturation, the immature APP (N-glycosylated in the
endoplasmic reticulum) moves to the Golgi complex where complete
maturation occurs (O-glycosylated and sulfated). After alpha-
secretase cleavage, soluble APP is released into the extracellular
space and the C-terminal is internalized to endosomes and
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leaving the late Golgi compartment and returns to the cell
surface. Gamma-CTF(59) peptide is located to both the cytoplasm
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CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
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CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
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residue. The NPXY site is also involved in clathrin-mediated
endocytosis (By similarity).
CC -1- PTM: Proteolytically processed under normal cellular conditions.
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leads to generation and extracellular release of soluble APP
peptides, S-APP-alpha and S-APP-beta, respectively, and the
retention of corresponding membrane-anchored C-terminal fragments,
C83 and C99. Subsequent processing of C83 by gamma-secretase
yields P3 peptides. This is the major secretory pathway and is
non-amyloidogenic. Alternatively, presenilin/secretase-mediated
gamma-secretase processing of C99 releases the amyloid beta
proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
major components of amyloid plaques, and the cytotoxic C-terminal
fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
similarity).
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
(By similarity). Cleavage at Asp-739 by either caspase-3, 8 or -9
results in the production of the neurotoxic C31 peptide and the
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CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
serine residues is neuron-specific. Phosphorylation can affect APP
processing, neuronal differentiation and interaction with other
proteins (By similarity).
CC -1- PTM: Extracellular binding and reduction of copper, results in a
corresponding oxidation of Cys-144 and Cys-158, and the formation
of a disulfide bond (By similarity).
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
zinc, can induce histidine-bridging between beta-amyloid molecules
resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
inhibits collagen-binding (By similarity).
CC -1- SIMILARITY: Belongs to the APP family.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial
CC License
CC -----
CC DR EMBL: AB032550; BAA84580.1; -; mRNA.
CC DR EMBL: Z84022; CAB06313.1; -; mRNA.
CC DR EMBL: X56127; CAA59592.1; -; mRNA.
CC DR HSSP: P08592; INMGJ.
CC DR SMR: P79307; 28-123, 124-189, 287-342, 460-569.
CC DR InterPro: IPR008155; A4_APP.
CC DR InterPro: IPR008154; A4_extra.
CC DR InterPro: IPR001255; Beta-APP.
CC DR InterPro: IPR002223; Prot_inh_Kunz-m.
CC DR PANTHER: PTHR10083:SF6; Beta-APP; 6.
CC DR Pfam: PF02177; A4_EXTRA; 1.
CC DR Pfam: PF03494; Beta-APP; 1.
CC DR Pfam: PF00014; Kunitz_BPTI; 1.
CC DR PRINTS: PR00203; AMYOTID4.
CC DR PRINTS: PR00759; BASICPTASE.
CC DR PRINTS: PR00204; BETAAMYLOID.
CC DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
CC DR SMART: SM00006; A4_EXTRA; 1.
CC DR SMART: SM00131; KU7; 1.
CC DR PROSITE: PS00319; A4_EXTRA; 1.
CC DR PROSITE: PS00320; A4_INTRA; 1.
CC DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
CC KW Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
KW Notch signaling pathway; Phosphorylation; Protease inhibitor;
KW Serine protease inhibitor; Signal; Transmembrane; Zinc.
CC FT SIGNAL 1 17
CC FT CHAIN 18 770
CC FT /FTId=PRO_0000000140.
CC FT CHAIN 18 687
CC FT /FTId=PRO_0000000141.
CC FT CHAIN 18 671
CC FT /FTId=PRO_0000000142.
CC FT CHAIN 672 770
CC FT /FTId=PRO_0000000143.
CC FT CHAIN 672 713
CC FT /FTId=PRO_0000000144.
CC FT CHAIN 672 711
CC FT /FTId=PRO_0000000145.

FT	CHAIN	688	770	C83 (By similarity).
FT				/FTId=PRO_0000000146.
FT	PEPTIDE	688	713	p3(42) (By similarity).
FT				/FTId=PRO_0000000147.
FT	PEPTIDE	688	711	p3(40) (By similarity).
FT				/FTId=PRO_0000000148.
FT	CHAIN	712	770	Gamma-CTF(59).
FT				/FTId=PRO_0000000149.
FT	CHAIN	714	770	Gamma-CTF(57).
FT				/FTId=PRO_0000000150.
FT	CHAIN	721	770	Gamma-CTF(50) (By similarity).
FT				/FTId=PRO_0000000151.
FT	CHAIN	740	770	C31 (By similarity).
FT				/FTId=PRO_0000000152.
FT	TOPO_DOM	18	699	Extracellular (Potential).
FT	TRANSMEM	700	723	Potential.
FT	TOPO_DOM	724	770	Cytoplasmic (Potential).
FT	DOMAIN	291	341	BPTI/Kunitz inhibitor.
FT	REGION	96	110	Heparin-binding (By similarity).
FT	REGION	135	155	Copper-binding (By similarity).
FT	REGION	181	188	Zinc-binding (By similarity).
FT	REGION	391	423	Heparin-binding (By similarity).
FT	REGION	491	522	Heparin-binding (By similarity).
FT	REGION	523	540	Collagen-binding (By similarity).
FT	REGION	732	751	Interaction with G(i)-alpha (By similarity).
FT	MOTIF	724	734	Basolateral sorting signal.
FT	MOTIF	759	762	NPXY motif; contains endocytosis signal.
FT	COMBIAS	230	260	Asp/Glu-rich (acidic).

Query Match 100.0%; Score 202; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 7,9e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40
 |||||
 DB 675 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 713

Search completed: September 28, 2006, 06:22:58
 Job time : 131.224 secs

100 202 100.0 43 2 US-08-996-422-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-07-744-767A-2

Sequence 2, Application US/07744767A

Patent No. 5434050

GENERAL INFORMATION:

APPLICANT: Magglio, John E.

APPLICANT: Manlyth, Patrick W.

TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods

TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/744,767A

FILING DATE: 13-AUG-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meeting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 600,226-US-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-0331

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-744-767A-2

Query Match 100.0%; Score 202; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,2e-23;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 40

Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2

US-08-179-574-1

Sequence 1, Application US/08179574

Patent No. 5506097

GENERAL INFORMATION:

APPLICANT: Huntman Potter

APPLICANT: Unamah Kayyali

TITLE OF INVENTION: Compounds and Methods for Inhibiting

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/179,574

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/819,361

FILING DATE: 13-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: HU90-03A3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-179-574-1

Query Match 100.0%; Score 202; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,2e-23;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 40

Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 3

US-08-347-144-1

Sequence 1, Application US/08347144

Patent No. 5589154

GENERAL INFORMATION:

APPLICANT: ANDERSON, STEPHEN

TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT

TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWREY & SIMON

STREET: 1299 PENNSYLVANIA AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,144

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: AUERBACH, JEFFREY I.

REGISTRATION NUMBER: 32,680

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 383-7451

TELEFAX: (202) 383-6610

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 40
DB 4 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 4
US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5652092

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids
TYPE: amino acid
STRADEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-19

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 40
DB 4 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 5
US-08-123-659A-19
Sequence 19, Application US/08123659A
Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-19

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 40
DB 4 FRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGSVIA 42

RESULT 6
US-08-464-247A-19
Sequence 19, Application US/08464247A
Patent No. 5693478

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-19

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 7
US-08-464-248A-19
Sequence 19, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSES: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/464,248A
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSES: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/476,464A
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSES: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 58415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 40
DB 4 FRHDSGEVHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 10
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhlro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRB
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-5

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 40
DB 4 FRHDSGEVHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 11
US-08-268-348A-1
Sequence 1, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobeil, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingstand Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-1

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 12
US-08-433-734-2
Sequence 2, Application US/08433734

Patent No. 5837473
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-2

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 13
US-08-609-090-9
Sequence 9, Application US/08609090

Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA

ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-9

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 14
US-07-737-371E-72
Sequence 72, Application US/07737371E

Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 40
DB 4 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 15
US-08-422-333-4
Sequence 4, Application US/08422333
Patent No. 5912410
GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 966-2438
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 40
DB 4 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 16
US-08-682-245A-4
Sequence 4, Application US/08682245A
Patent No. 5919631

GENERAL INFORMATION:
APPLICANT: GOYAL, SHEPALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHARABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-4

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 40
DB 4 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVIA 42

RESULT 17
US-08-986-948-5
Sequence 5, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317unhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRB
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-5

Query Match 100.0%; Score 202; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 18
US-08-717-551A-2
Sequence 2, Application US/08717551A
Patent No. 6071493
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
NUMBER OF SEQUENCES: 2
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESS: & No. 6071493rls LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,551A
FILING DATE: Sept-20-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-551A-2

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
DB 4 FRHDSGYEVHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-09-388-890-1
Sequence 1, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

ORGANISM: AMYLOID PEPTIDE
US-09-388-890-1

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 40
|||||
DB 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 42

RESULT 20
US-09-005-215-20
Sequence 20, Application US/09005215

PATENT NO. 6172063
GENERAL INFORMATION:
APPLICANT: Ingram, Vernon M.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0656/7035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

US-09-005-215-20

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 40
|||||
DB 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 42

RESULT 21
US-09-242-724-23
Sequence 23, Application US/09242724

PATENT NO. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-242-724-23

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 40
|||||
DB 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVIA 42

RESULT 22
US-08-922-930-2
Sequence 2, Application US/08922930

PATENT NO. 6451544
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,930
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori V. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-930-2

Query Match 100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-922-930-2


```

; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-922-889-2

Query Match          100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 26
US-09-731-460-1
; Sequence 1, Application US/09731460
; Patent No. 6495335
; GENERAL INFORMATION:
; APPLICANT: Choikier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOIKIER-04302
; CURRENT APPLICATION NUMBER: US/09/731,460
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-731-460-1

Query Match          100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 27
US-09-133-866-2
; Sequence 2, Application US/09133866
; Patent No. 6600017
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/09/133,866
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: 60/055,660
; EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
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```

; ORGANISM: Homo sapiens
; US-09-133-866-2

Query Match          100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 28
US-09-723-384-1
; Sequence 1, Application US/09723384
; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuraltab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152704-004740US
; CURRENT APPLICATION NUMBER: US/09/723,384
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-09-723-384-1

Query Match          100.0%; Score 202; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 29
US-09-724-961-42
; Sequence 42, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vaequez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152704-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
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```

; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
;
US-09-724-961-42

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Query Match	100.0%;	Score 202;	DB 2;	length 42;
Best Local Similarity	100.0%;	Pred. No. 1.2e-23;		
Matches 39; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 30
US-09-724-552-1
; Sequence 1, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Diseases
; FILE REFERENCE: 152707-004740US
; CURRENT APPLICATION NUMBER: US/09/724,552
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
; US-09-724-552-1

```

Query Match	100.0%	Score 202;	DB 2;	Length 42;
Best Local Similarity	100.0%	Pred. No. 1.2e-23;		
Matches 39; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Dy 2 FRHDSGYEYVHHQKLVFFADVDGSKKGALITGLMWGVVIA 400
Db 4 FRHDSGYEYVHHQKLVFFADVDGSKKGALITGLMWGVVIA 422

Search completed: September 28, 2006, 06:27:13
Job time : 28.1614 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:58:47 : Search time 91.6592 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-5
Perfect score: 202
Sequence: 1 XFRHDSGYEVNHQKLVFAEDVGSNKALIGMVGIVIA 40

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	100.0	42	2	US-08-922-930-2
2	202	100.0	42	2	US-08-923-055-2
3	202	100.0	42	3	US-09-867-847-1
4	202	100.0	42	3	US-09-956-625-26
5	202	100.0	42	3	US-09-731-460-1
6	202	100.0	42	3	US-09-962-955C-37
7	202	100.0	42	3	US-09-848-616-174
8	202	100.0	42	3	US-09-865-294-65
9	202	100.0	42	3	US-09-792-079-13
10	202	100.0	42	3	US-09-825-242-1
11	202	100.0	42	3	US-09-930-915A-293
12	202	100.0	42	4	US-10-051-496-2
13	202	100.0	42	4	US-10-082-804-7
14	202	100.0	42	4	US-10-217-584-2
15	202	100.0	42	4	US-10-169-580-2
16	202	100.0	42	4	US-10-278-181-1
17	202	100.0	42	4	US-10-143-534-2
18	202	100.0	42	4	US-10-190-548A-1
19	202	100.0	42	4	US-10-051-663-2
20	202	100.0	42	4	US-10-159-279-13
21	202	100.0	42	4	US-10-050-902-220
22	202	100.0	42	4	US-10-050-898-220
23	202	100.0	42	4	US-10-082-014-81
24	202	100.0	42	4	US-10-372-076-82
25	202	100.0	42	4	US-10-455-218-2
26	202	100.0	42	4	US-10-231-298B-15
27	202	100.0	42	4	US-10-231-470C-15

28	202	100.0	42	4	US-10-231-063C-15	Sequence 15, Appl
29	202	100.0	42	4	US-10-366-125-28	Sequence 28, Appl
30	202	100.0	42	4	US-10-411-544-2	Sequence 2, Appl
31	202	100.0	42	4	US-10-231-213D-15	Sequence 15, Appl
32	202	100.0	42	4	US-10-231-114C-15	Sequence 2, Appl
33	202	100.0	42	4	US-10-337-261-2	Sequence 15, Appl
34	202	100.0	42	4	US-10-363-082-1	Sequence 1, Appl
35	202	100.0	42	4	US-10-433-385-6	Sequence 6, Appl
36	202	100.0	42	4	US-10-423-047-1	Sequence 1, Appl
37	202	100.0	42	4	US-10-617-876-7	Sequence 7, Appl
38	202	100.0	42	4	US-10-429-216-1	Sequence 1, Appl
39	202	100.0	42	4	US-10-656-624-5	Sequence 5, Appl
40	202	100.0	42	4	US-10-622-087-91	Sequence 91, Appl
41	202	100.0	42	4	US-10-683-815-11	Sequence 11, Appl
42	202	100.0	42	4	US-10-732-862A-95	Sequence 95, Appl
43	202	100.0	42	4	US-10-806-006-293	Sequence 293, App
44	202	100.0	42	4	US-10-416-262B-6	Sequence 6, Appl
45	202	100.0	42	4	US-10-677-074-82	Sequence 82, Appl
46	202	100.0	42	4	US-10-805-913-293	Sequence 293, App
47	202	100.0	42	4	US-10-816-022-1	Sequence 1, Appl
48	202	100.0	42	4	US-10-816-529-1	Sequence 1, Appl
49	202	100.0	42	4	US-10-815-353-1	Sequence 1, Appl
50	202	100.0	42	4	US-10-815-391-1	Sequence 1, Appl
51	202	100.0	42	4	US-10-772-656-55	Sequence 55, Appl
52	202	100.0	42	4	US-10-478-308-3	Sequence 3, Appl
53	202	100.0	42	4	US-10-478-307-3	Sequence 3, Appl
54	202	100.0	42	4	US-10-402-420-1	Sequence 1, Appl
55	202	100.0	42	4	US-10-771-174A-1	Sequence 1, Appl
56	202	100.0	42	5	US-10-828-548-1	Sequence 1, Appl
57	202	100.0	42	5	US-10-864-107-2	Sequence 2, Appl
58	202	100.0	42	5	US-10-816-380-1	Sequence 1, Appl
59	202	100.0	42	5	US-10-485-310-19	Sequence 19, Appl
60	202	100.0	42	5	US-10-889-999-42	Sequence 42, Appl
61	202	100.0	42	5	US-10-890-070-42	Sequence 42, Appl
62	202	100.0	42	5	US-10-861-614-65	Sequence 65, Appl
63	202	100.0	42	5	US-10-481-387-2	Sequence 2, Appl
64	202	100.0	42	5	US-10-890-000-42	Sequence 42, Appl
65	202	100.0	42	5	US-10-788-666-1	Sequence 1, Appl
66	202	100.0	42	5	US-10-923-471-1	Sequence 1, Appl
67	202	100.0	42	5	US-10-823-463-42	Sequence 42, Appl
68	202	100.0	42	5	US-10-923-469-1	Sequence 1, Appl
69	202	100.0	42	5	US-10-933-559-1	Sequence 1, Appl
70	202	100.0	42	5	US-10-815-404-1	Sequence 1, Appl
71	202	100.0	42	5	US-10-934-609-1	Sequence 1, Appl
72	202	100.0	42	5	US-10-950-018-1	Sequence 1, Appl
73	202	100.0	42	5	US-10-883-150-3	Sequence 3, Appl
74	202	100.0	42	5	US-10-923-474-1	Sequence 1, Appl
75	202	100.0	42	5	US-10-884-892-1	Sequence 1, Appl
76	202	100.0	42	5	US-10-822-968-42	Sequence 42, Appl
77	202	100.0	42	5	US-10-933-206-37	Sequence 37, Appl
78	202	100.0	42	5	US-10-777-792-42	Sequence 42, Appl
79	202	100.0	42	5	US-10-825-958-1	Sequence 1, Appl
80	202	100.0	42	5	US-10-775-562-1	Sequence 1, Appl
81	202	100.0	42	5	US-10-852-950-1	Sequence 1, Appl
82	202	100.0	42	5	US-10-890-071-42	Sequence 42, Appl
83	202	100.0	42	5	US-10-903-279-1	Sequence 1, Appl
84	202	100.0	42	5	US-10-810-881A-50	Sequence 50, Appl
85	202	100.0	42	5	US-10-890-024-42	Sequence 42, Appl
86	202	100.0	42	5	US-10-934-819-1	Sequence 1, Appl
87	202	100.0	42	5	US-10-508-586-1	Sequence 1, Appl
88	202	100.0	42	5	US-10-505-313-27	Sequence 27, Appl
89	202	100.0	42	5	US-10-770-712-35	Sequence 35, Appl
90	202	100.0	42	5	US-10-923-267-1	Sequence 1, Appl
91	202	100.0	42	5	US-10-928-926-42	Sequence 42, Appl
92	202	100.0	42	5	US-10-923-605-1	Sequence 1, Appl
93	202	100.0	42	5	US-10-934-818-1	Sequence 1, Appl
94	202	100.0	42	5	US-10-945-133-1	Sequence 13, Appl
95	202	100.0	42	5	US-10-966-919B-3	Sequence 3, Appl
96	202	100.0	42	5	US-10-058-757-42	Sequence 42, Appl
97	202	100.0	42	6	US-11-004-053-37	Sequence 37, Appl
98	202	100.0	42	6	US-11-007-643-37	Sequence 37, Appl
99	202	100.0	42	6	US-11-007-644-37	Sequence 37, Appl
100	202	100.0	42	6	US-11-007-644-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-08-922-930-2

Sequence 2, Application US/08922930

Publication No. US20010016326A1

GENERAL INFORMATION:

APPLICANT: Dana Giulian

TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz

ADDRESSEE: & No. 6451541st LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT FOR WINDOWS 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/922,930

FILING DATE: Sept-03-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardell

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: BYLR-0039

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-922-930-2

Query Match 100.0%; Score 202; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 40

DB 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2

US-08-923-055-2

Sequence 2, Application US/08923055

Publication No. US20010016327A1

GENERAL INFORMATION:

APPLICANT: Dana Giulian

TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz

ADDRESSEE: & No. US20010016327A1st LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT FOR WINDOWS 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,055

FILING DATE: Sept-03-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardell

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: BYLR-0038

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-923-055-2

Query Match 100.0%; Score 202; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 40

DB 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 3

US-09-867-847-1

Sequence 1, Application US/09867847

Patent No. US20020094335A1

GENERAL INFORMATION:

APPLICANT: Chalifour, Robert

APPLICANT: Hebert, Lisa

APPLICANT: Kong, Xiangqi

APPLICANT: Gervais, Francine

TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S

TITLE OF INVENTION: AND AMYLOID RELATED DISEASES

FILE REFERENCE: 14445-501 CIP

CURRENT APPLICATION NUMBER: US/09/867,847

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: 60/168,594

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: 09/724,842

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 42

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: All D peptides

OTHER INFORMATION: or peptidomimetics

US-09-867-847-1

Query Match 100.0%; Score 202; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 40

DB 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

Db 4 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 4

US-09-956-625-26

Sequence 26, Application US/09956625

Patent No. US2002011926A1

GENERAL INFORMATION:

APPLICANT: Paaser, Paul

TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof

FILE REFERENCE: 14445-503

CURRENT APPLICATION NUMBER: US/09/956,625

CURRENT FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: 60/233,482

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 26

LENGTH: 42

TYPE: PRT

ORGANISM: Homo sapiens

US-09-956-625-26

Query Match 100.0%; Score 202; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 40

Db 4 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 5

US-09-731-460-1

Sequence 1, Application US/09731460

Patent No. US20020137112A1

GENERAL INFORMATION:

APPLICANT: Choikier, Mario

TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's

FILE REFERENCE: Disease

CURRENT APPLICATION NUMBER: US/09/731,460

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 42

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-731-460-1

Query Match 100.0%; Score 202; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 40

Db 4 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 6

US-09-962-955C-37

Sequence 37, Application US/09962955C

Publication No. US20030013648A1

GENERAL INFORMATION:

APPLICANT: Gerardo M. Castilho

APPLICANT: Alan D. Snow

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrick M. Dwyer

STREET: ProteoTech, Inc. 1818 Westlake Avenue N, Suite 114

CITY: Seattle

STATE: WA (Washington)

COUNTRY: United States of America

ZIP: 98109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC

OPERATING SYSTEM: Windows 98

SOFTWARE: WordPerfect 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,955C

FILING DATE: 24-September-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/938,275

FILING DATE: 22-August-2001

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dwyer, Patrick M.

REGISTRATION NUMBER: 32,411

REFERENCE/DOCKET NUMBER: PROTEO.P03CI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 343-7074

TELEFAX: (206) 343-7085

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

ORIGINAL SOURCE:

ORGANISM: MOUSE

FEATURE:

OTHER INFORMATION: Also referred to in the specification as "AB 1-42"

US-09-962-955C-37

Query Match 100.0%; Score 202; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 40

Db 4 FRHDSGYEVHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 7

US-09-848-616-174

Sequence 174, Application US/09848616

Publication No. US20030054010A1

GENERAL INFORMATION:

APPLICANT: Sebbel, Peter

APPLICANT: Dunant, Nicolas

APPLICANT: Bachmann, Martin

APPLICANT: Tisoc, Alain

APPLICANT: Lechner, Franziska

TITLE OF INVENTION: Molecular Antigen Array

FILE REFERENCE: 1700.0180002

CURRENT APPLICATION NUMBER: US/09/848,616

CURRENT FILING DATE: 2001-05-05

NUMBER OF SEQ ID NOS: 186

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 174

LENGTH: 42

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Amyloid Beta Peptide

US-09-848-616-174

Query Match 100.0%; Score 202; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,7e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 40
DB 4 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 42

RESULT 8
US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-65

Query Match 100.0%; Score 202; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 40
DB 4 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 42

RESULT 9
US-09-792-079-13
; Sequence 13, Application US/09792079
; Publication No. US20030083277A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Herish, Louis B.
; APPLICANT: Mukherjee, Atish
; TITLE OF INVENTION: Use of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzhei
; FILE REFERENCE: 050229-0261
; CURRENT APPLICATION NUMBER: US/09/792,079
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,826
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-079-13

Query Match 100.0%; Score 202; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 40
DB 4 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 42

RESULT 10
US-09-825-242-1
; Sequence 1, Application US/09825242
; Publication No. US20030092000A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152701-004720US
; CURRENT APPLICATION NUMBER: US/09/825,242
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-825-242-1

Query Match 100.0%; Score 202; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 40
DB 4 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 42

RESULT 11
US-09-930-915A-293
; Sequence 293, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 293
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-915A-293

Query Match 100.0%; Score 202; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 40
DB 4 FRHDSGEVHHQKLVFFAEDVGSNKGAIIIGLMVGGVIA 42

RESULT 12
US-10-051-496-2
; Sequence 2, Application US/10051496
; Publication No. US2002018260A1
; GENERAL INFORMATION:
; APPLICANT: Kei-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunocassays for
; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
; Abeta(1-41), Abeta(1-42) and Abeta(1-43)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Kei-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 Inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US20020182650A1epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183,407
FILING DATE: 18-February-2000
ATTORNEY/AGENT INFORMATION:
NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662
REFERENCE/DOCKET NUMBER: PBI-PT001.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1-42
IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42
US-10-051-496-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 42
RESULT 13
US-10-082-804-7
Sequence 7, Application US/10082804
Publication No. US20020194632A1
GENERAL INFORMATION:
APPLICANT: McConlogue, Lisa
APPLICANT: Gurney, Mark E.
TITLE OF INVENTION: Transgenic Knockouts of BACE-1
FILE REFERENCE: MBH 02-329-A
CURRENT APPLICATION NUMBER: US/10/082,804
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/271,092
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/271,514
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/293,762
PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7
Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 42
RESULT 14
US-10-217-584-2
Sequence 2, Application US/10217584
Publication No. US20030077261A1
GENERAL INFORMATION:
APPLICANT: Paris, Daniel
APPLICANT: Mullian, Michael
TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
FILE REFERENCE: USF-T161X1
CURRENT APPLICATION NUMBER: US/10/217,584
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,656
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(42)
OTHER INFORMATION: A-beta 1-42 peptide
US-10-217-584-2
Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVIA 42
RESULT 15
US-10-169-580-2
Sequence 2, Application US/10169580
Publication No. US20030100477A1
GENERAL INFORMATION:
APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR SUPPRESSING B-AMYLOID PRODUCTION
FILE REFERENCE: Q70898
CURRENT APPLICATION NUMBER: US/10/169,580
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 2000-131037
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: PCT/JP01/03555
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens

US-10-169-580-2

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 16
US-10-278-181-1
; Sequence 1, Application US/10278181
; Publication No. US20030104488A1
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOJKIER-04302
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/731,460
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-278-181-1

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 17
US-10-143-534-2
; Sequence 2, Application US/10143534
; Publication No. US20030105152A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M00656/70078
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 10/051,663
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-143-534-2

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 18
US-10-190-548A-1
; Sequence 1, Application US/10190548A
; Publication No. US20030109435A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Premier, Irene
; APPLICANT: Wright, Sarah
; APPLICANT: Yednock, Theodore
; APPLICANT: Rydel, Russell
; TITLE OF INVENTION: Methods of Inhibiting Amyloid Toxicity
; FILE REFERENCE: 08576.0030-00
; CURRENT FILING DATE: US/10/190,548A
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-548A-1

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 19
US-10-051-663-2
; Sequence 2, Application US/10051663
; Publication No. US20030114510A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M0656/7071
; CURRENT FILING DATE: US/10/051,663
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-051-663-2

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
DB 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 20
US-10-159-279-13
; Sequence 13, Application US/10159279
; Publication No. US20030165481A1

```

; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Herish, Louis B.
; APPLICANT: Mukherjee, Atish
; TITLE OF INVENTION: Use of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzhei
; FILE REFERENCE: 050229-0298
; CURRENT APPLICATION NUMBER: US/10/159,279
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/184,826
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/792,079
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-279-13

Query Match      100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 42

RESULT 21
US-10-050-902-220
; Sequence 220, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisbet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 220
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Amyloid Beta Peptide
US-10-050-902-220

Query Match      100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 42

RESULT 22
US-10-050-898-220
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; Sequence 220, Application US/10050898
; Publication No. US2003017511A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisbet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 220
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Amyloid Beta Peptide
US-10-050-898-220
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Query Match      100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 42

RESULT 23
US-10-082-014-81
; Sequence 81, Application US/10082014
; Publication No. US20030185858A1
; GENERAL INFORMATION:
; APPLICANT: Birrell, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
; FILE REFERENCE: ICG-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 81
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Alzheimer's disease b-Amyloid
US-10-082-014-81

Query Match      100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVIA 42

RESULT 24
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US-10-372-076-82
; Sequence 82, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Alzheimer's disease b-Amyloid
US-10-372-076-82

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 25
US-10-455-218-2
; Sequence 2, Application US/10455218
; Publication No. US20030204051A1
; GENERAL INFORMATION:
; APPLICANT: Garzon-Rodriguez, William
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-218-2

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 26
US-10-231-298B-15
; Sequence 15, Application US/10231298B
; Publication No. US20030219853A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Cross-Linking a Compound
; FILE REFERENCE: SAMG/0006

; CURRENT APPLICATION NUMBER: US/10/231,298B
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-298B-15

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 27
US-10-231-470C-15
; Sequence 15, Application US/10231470C
; Publication No. US20030219857A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Having Broad Substrate
; FILE REFERENCE: SAMG/0003
; CURRENT APPLICATION NUMBER: US/10/231,470C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-470C-15

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 28
US-10-231-063C-15
; Sequence 15, Application US/10231063C
; Publication No. US20030224476A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Reactive Compound
; FILE REFERENCE: SAMG/0004
; CURRENT APPLICATION NUMBER: US/10/231,063C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42

TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-063C-15

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 29
US-10-366-125-28
Sequence 28, Application US/10366125
Publication No. US20030228259A1
GENERAL INFORMATION:
APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: EASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
FILE REFERENCE: 416272003500
CURRENT APPLICATION NUMBER: US/10/366,125
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 60/356,008
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-366-125-28

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 30
US-10-411-544-2
Sequence 2, Application US/10411544
Publication No. US20030232758A1
GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter
APPLICANT: McLaurin, Joanne
TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzhe
FILE REFERENCE: L101547
CURRENT APPLICATION NUMBER: US/10/411,544
CURRENT FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-544-2

Query Match 100.0%; Score 202; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGGVIA 42

Search completed: September 28, 2006, 07:09:26
Job time : 92.8259 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 ; Search time 15.6054 Seconds
(without alignments)
199.066 Million cell updates/sec

Title: US-09-731-899-5

Perfect score: 202

Sequence: 1 XFRHDSGYEVHOKLVFPAEDVGSNKGAIGIMVGVVIA 40

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 285145 seqs, 77663843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published_Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	100.0	40	1	US-09-731-899-5
2	202	100.0	40	6	US-10-966-645-38
3	202	100.0	42	1	US-09-731-899-3
4	202	100.0	42	6	US-10-890-071-42
5	202	100.0	42	6	US-10-544-093-1
6	202	100.0	42	6	US-10-546-547-3
7	202	100.0	42	6	US-10-966-645-36
8	202	100.0	42	7	US-11-104-300-2
9	202	100.0	42	7	US-11-297-316-1
10	202	100.0	42	7	US-11-87-157A-49
11	202	100.0	43	1	US-09-731-899-4
12	202	100.0	43	7	US-11-348-091-1
13	202	100.0	56	6	US-10-544-093-16
14	202	100.0	56	6	US-10-544-093-19
15	202	100.0	58	6	US-10-515-919A-30
16	202	100.0	58	6	US-10-544-093-12
17	202	100.0	58	6	US-10-544-093-14
18	202	100.0	58	6	US-10-544-093-27
19	202	100.0	59	1	US-09-731-899-1
20	202	100.0	60	6	US-10-544-093-20
21	202	100.0	64	6	US-10-544-093-13
22	202	100.0	79	6	US-10-544-093-15
23	202	100.0	99	6	US-10-544-093-22
24	202	100.0	99	6	US-10-544-093-24
25	202	100.0	142	6	US-10-544-093-17

26	202	100.0	142	6	US-10-544-093-21	Sequence 21, Appl
27	202	100.0	142	6	US-10-544-093-23	Sequence 23, Appl
28	202	100.0	185	6	US-10-544-093-18	Sequence 18, Appl
29	202	100.0	203	6	US-10-544-093-26	Sequence 26, Appl
30	202	100.0	316	6	US-10-544-093-25	Sequence 25, Appl
31	202	100.0	695	6	US-10-515-919A-1	Sequence 1, Appl
32	202	100.0	695	6	US-10-511-269-7	Sequence 7, Appl
33	202	100.0	751	6	US-10-546-547-2	Sequence 2, Appl
34	202	100.0	770	6	US-10-511-269-9	Sequence 9, Appl
35	197	97.5	626	6	US-10-515-919A-13	Sequence 13, Appl
36	197	97.5	626	6	US-10-515-919A-18	Sequence 18, Appl
37	196	97.0	626	6	US-10-515-919A-15	Sequence 15, Appl
38	196	97.0	626	6	US-10-515-919A-20	Sequence 20, Appl
39	195	96.5	422	7	US-11-269-857-5	Sequence 5, Appl
40	195	96.5	626	6	US-10-515-919A-16	Sequence 14, Appl
41	195	96.5	626	6	US-10-515-919A-19	Sequence 19, Appl
42	195	96.5	626	6	US-10-515-919A-21	Sequence 21, Appl
43	195	96.5	626	6	US-10-515-919A-21	Sequence 21, Appl
44	194	96.0	38	6	US-10-966-645-39	Sequence 39, Appl
45	194	96.0	38	6	US-10-966-645-44	Sequence 44, Appl
46	194	96.0	40	1	US-09-731-899-2	Sequence 2, Appl
47	194	96.0	40	6	US-10-966-645-37	Sequence 37, Appl
48	194	96.0	626	6	US-10-515-919A-12	Sequence 12, Appl
49	194	96.0	626	6	US-10-515-919A-17	Sequence 17, Appl
50	189	93.6	422	6	US-10-515-919A-3	Sequence 3, Appl
51	189	93.6	42	6	US-10-515-919A-8	Sequence 8, Appl
52	188	93.1	42	7	US-11-104-300-3	Sequence 3, Appl
53	188	93.1	42	6	US-10-515-919A-5	Sequence 5, Appl
54	188	93.1	42	6	US-10-515-919A-10	Sequence 10, Appl
55	187	92.6	40	7	US-11-269-857-3	Sequence 3, Appl
56	187	92.6	42	6	US-10-515-919A-4	Sequence 4, Appl
57	187	92.6	42	6	US-10-515-919A-6	Sequence 6, Appl
58	187	92.6	42	6	US-10-515-919A-9	Sequence 9, Appl
59	187	92.6	42	6	US-10-515-919A-11	Sequence 11, Appl
60	186	92.1	42	6	US-10-515-919A-2	Sequence 2, Appl
61	186	92.1	42	6	US-10-515-919A-7	Sequence 7, Appl
62	183	90.6	42	6	US-10-515-919A-22	Sequence 22, Appl
63	183	90.6	42	6	US-10-515-919A-23	Sequence 23, Appl
64	183	90.6	695	6	US-10-538-410-96	Sequence 96, Appl
65	183	90.6	770	7	US-11-104-300-1	Sequence 1, Appl
66	155	76.7	32	1	US-09-731-899-6	Sequence 6, Appl
67	137	67.8	28	7	US-11-297-316-2	Sequence 2, Appl
68	125	61.9	26	1	US-09-731-899-7	Sequence 7, Appl
69	101	50.0	19	6	US-10-966-645-43	Sequence 43, Appl
70	101	50.0	19	6	US-10-966-645-45	Sequence 45, Appl
71	101	50.0	21	6	US-10-966-645-42	Sequence 42, Appl
72	84	41.6	19	6	US-10-890-071-75	Sequence 75, Appl
73	61	30.2	10	6	US-10-890-071-13	Sequence 13, Appl
74	61	30.2	10	6	US-10-890-071-14	Sequence 14, Appl
75	59	29.2	10	6	US-10-890-071-12	Sequence 12, Appl
76	58	28.7	10	6	US-10-890-071-15	Sequence 15, Appl
77	58	28.7	624	6	US-10-449-902-33879	Sequence 33879, A
78	56	27.7	1046	6	US-10-449-902-51230	Sequence 51230, A
79	56	27.7	10	6	US-10-890-071-16	Sequence 16, Appl
80	56	27.7	10	6	US-10-890-071-17	Sequence 17, Appl
81	56	27.7	10	6	US-10-890-071-18	Sequence 18, Appl
82	55	27.5	356	7	US-11-056-356B-51389	Sequence 51389, A
83	55	27.5	480	7	US-11-056-356B-51388	Sequence 51388, A
84	55	27.5	504	7	US-11-056-356B-51387	Sequence 51387, A
85	55	27.5	618	6	US-10-449-902-47542	Sequence 47542, A
86	55	27.2	10	6	US-10-890-071-19	Sequence 19, Appl
87	55	27.2	10	6	US-10-890-071-21	Sequence 21, Appl
88	55	27.2	429	7	US-11-056-356B-53789	Sequence 53789, A
89	55	27.2	556	7	US-11-056-356B-53788	Sequence 53788, A
90	55	27.2	826	7	US-11-056-356B-87461	Sequence 87461, A
91	54.5	27.0	862	7	US-11-056-356B-87460	Sequence 87460, A
92	54.5	27.0	1083	7	US-11-056-356B-87459	Sequence 87459, A
93	54.5	27.0	1083	7	US-10-890-071-20	Sequence 20, Appl
94	54	26.7	10	6	US-10-515-919A-6	Sequence 6, Appl
95	53.5	26.5	921	6	US-10-890-071-22	Sequence 22, Appl
96	53	26.2	10	6	US-10-890-071-27	Sequence 27, Appl
97	52	25.7	10	6	US-10-890-071-27	Sequence 27, Appl
98	52	25.7	10	6	US-10-890-071-28	Sequence 28, Appl

99 52 25.7 304 6 US-10-449-902-34773 Sequence 34773, A
100 52 25.7 534 6 US-10-953-349-22703 Sequence 22703, A

ALIGNMENTS

RESULT 1

US-09-731-899-5
; Sequence 5, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-5

Query Match 100.0%; Score 202; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 2e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

DB 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 2

US-10-966-645-38
; Sequence 38, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT FILING DATE: 2004-10-15
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 38
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-38

Query Match 100.0%; Score 202; DB 6; Length 40;

Best Local Similarity 100.0%; Pred. No. 2e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

DB 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 3
US-09-731-899-3
; Sequence 3, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is L-Asp, D-Asp, or L-Iso Asp
US-09-731-899-3

Query Match 100.0%; Score 202; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.1e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

DB 4 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 4

US-10-890-071-42
; Sequence 42, Application US/10890071
; Publication No. US20060121038A9
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT FILING DATE: 2004-07-12
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-890-071-42

Query Match 100.0%; Score 202; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.1e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

DB 4 FRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 5

US-10-544-093-1
; Sequence 1, Application US/10544093


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; Publication No. US2006018512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vazquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-544-093-1
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Query Match          100.0%; Score 202; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
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RESULT 6
US-10-546-547-3

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; Sequence 3, Application US/10546547
; Publication No. US20060188951A1
; GENERAL INFORMATION:
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; APPLICANT: Mook, In Hee
; APPLICANT: Hur, Ji Yeun
; TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
; TITLE OF INVENTION: Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Sam
; FILE REFERENCE: DE-1646
; CURRENT APPLICATION NUMBER: US/10/546,547
; CURRENT FILING DATE: 2005-08-23
; PRIOR APPLICATION NUMBER: PCT/KR2004/000371
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: 1-42 amino acid of amyloid a4 precursor protein (APP)
US-10-546-547-3
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Query Match          100.0%; Score 202; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
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RESULT 7
US-10-966-645-36

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; Sequence 36, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
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; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE JOHANNES
```

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; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-36
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Query Match          100.0%; Score 202; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
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RESULT 8
US-11-104-300-2

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; Sequence 2, Application US/11104300
; Publication No. US20060099211A1
; GENERAL INFORMATION:
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; APPLICANT: Monthe, Carmen
; APPLICANT: Szabo, Paul
; APPLICANT: Wekeler, Mark
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treating
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 1676.0270US1
; CURRENT APPLICATION NUMBER: US/11/104,300
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US 60/561,423
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-104-300-2
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Query Match          100.0%; Score 202; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42
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RESULT 9
US-11-297-316-1

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; Sequence 1, Application US/11297316
; Publication No. US20060141602A1
; GENERAL INFORMATION:
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; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-297-316-1

Query Match 100.0%; Score 202; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 10
US-11-287-157A-49
Sequence 49, Application US/11287157A
Publication No. US20060154863A1

GENERAL INFORMATION:
APPLICANT: SKURATCH, HANNA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
FILE REFERENCE: 32051-701.201
CURRENT FILING DATE: 2005-11-25
PRIOR APPLICATION NUMBER: US/11/287,157A
PRIOR FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 60/658,859
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/630,880
PRIOR FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn version 3.3
SEQ ID NO 49
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-287-157A-49

Query Match 100.0%; Score 202; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 11
US-09-731-899-4
Sequence 4, Application US/09731899
Publication No. US20060088548A1

GENERAL INFORMATION:
APPLICANT: Chaitin, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-731-899-4

Query Match 100.0%; Score 202; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2,1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 12
US-11-348-091-1
Sequence 1, Application US/11348091
Publication No. US20060211679A1

GENERAL INFORMATION:
APPLICANT: Han, Qi
TITLE OF INVENTION: Substituted Lactams as Inhibitors of ABeta Protein Production
FILE REFERENCE: BMS-PH-7164.1(C)
CURRENT FILING DATE: 2006-02-06
PRIOR APPLICATION NUMBER: US/11/348,091
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 09/832,455
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/196,549
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-11-348-091-1

Query Match 100.0%; Score 202; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 2,1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
Db 4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

RESULT 13
US-10-544-093-16
Sequence 16, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/544,093
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Padre-A-beta fragment fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-16

Query Match 100.0%; Score 202; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 17 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 55

RESULT 14

US-10-544-093-19
Sequence 19, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDGENIC DISEASE
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
PRIOR FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (46)..(46)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-19

Query Match 100.0%; Score 202; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 15

US-10-515-919A-30
Sequence 30, Application US/10515919A
Publication No. US20060160146A1

GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
FILE REFERENCE: 084952
CURRENT APPLICATION NUMBER: US/10/515,919A
PRIOR FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: PCT/JP03/06319
PRIOR FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: JP 2002-155472
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3

SEQ ID NO 30
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-515-919A-30

Query Match 100.0%; Score 202; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 20 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 58

RESULT 16

US-10-544-093-12
Sequence 12, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
PRIOR FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12

Query Match 100.0%; Score 202; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 17

US-10-544-093-14
Sequence 14, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
PRIOR FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31

```

; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-14
```

```

Query Match          100.0%; Score 202; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 40
Db      4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 42
```

```

RESULT 18
US-10-544-093-27
; Sequence 27, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Baird, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152700-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27
```

```

Query Match          100.0%; Score 202; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 40
Db      4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 42
```

```

RESULT 19
US-09-731-899-1
; Sequence 1, Application US/0971899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-1
```

```

Query Match          100.0%; Score 202; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 40
Db      8 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 46
```

```

RESULT 20
US-10-544-093-20
; Sequence 20, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Baird, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152700-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-20
```

```

Query Match          100.0%; Score 202; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.1e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 40
Db      4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVGVIA 42
```

```

RESULT 21
US-10-544-093-13
; Sequence 13, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
```

```

; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-00982005
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13

```

```

Query Match          100.0%; Score 202; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
         |||||
Db       4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

```

```

RESULT 22
US-10-544-093-15
; Sequence 15, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-15

```

```

Query Match          100.0%; Score 202; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
         |||||
Db       4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

```

```

RESULT 23
US-10-544-093-22
; Sequence 22, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)..(99)
; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-22

```

```

Query Match          100.0%; Score 202; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 40
         |||||
Db       4 FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

```

```

RESULT 24
US-10-544-093-24
; Sequence 24, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24

```

```

: LENGTH: 99
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Fusion protein
: NAME/KEY: MISC FEATURE
: LOCATION: (1)-(43)
: OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
: FEATURE: Preferred fragments are 5-10 or 7-10 residues in length.
: NAME/KEY: MISC FEATURE
: LOCATION: (44)-(86)
: OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-24
```

```

Query Match          100.0%; Score 202; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 5,3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 40
Db      4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 42
```

RESULT 25

```

US-10-544-093-17
: Sequence 17, Application US/10544093
: Publication No. US20060188512A1
: GENERAL INFORMATION:
: APPLICANT: Vednock, Ted
: APPLICANT: Vasquez, Nicki
: APPLICANT: Bard, Frederique
: APPLICANT: Seubert, Peter A.
: TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
: FILE REFERENCE: 15270J-009820US
: CURRENT FILING DATE: 2005-08-01
: PRIOR FILING DATE: 2004-01-31
: PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
: PRIOR FILING DATE: 2004-01-31
: PRIOR APPLICATION NUMBER: US 60/444,150
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 17
: LENGTH: 142
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: A-beta-A-beta-A-beta-Padre fusion protein
: NAME/KEY: MISC FEATURE
: LOCATION: (1)-(43)
: OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
: NAME/KEY: MISC FEATURE
: LOCATION: (44)-(86)
: OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
: FEATURE:
: NAME/KEY: MISC FEATURE
: LOCATION: (87)-(129)
: OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
: NAME/KEY: MISC FEATURE
: LOCATION: (132)-(132)
: OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-17
```

```

Query Match          100.0%; Score 202; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7,9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 40
Db      4 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 42
```

RESULT 26

```

US-10-544-093-21
: Sequence 21, Application US/10544093
: Publication No. US20060188512A1
: GENERAL INFORMATION:
: APPLICANT: Vednock, Ted
: APPLICANT: Vasquez, Nicki
: APPLICANT: Bard, Frederique
: APPLICANT: Seubert, Peter A.
: TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
: FILE REFERENCE: 15270J-009820US
: CURRENT FILING DATE: 2005-08-01
: PRIOR FILING DATE: 2004-01-31
: PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
: PRIOR FILING DATE: 2004-01-31
: PRIOR APPLICATION NUMBER: US 60/444,150
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 21
: LENGTH: 142
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Fusion protein
: NAME/KEY: MISC FEATURE
: LOCATION: (14)-(56)
: OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
: NAME/KEY: MISC FEATURE
: LOCATION: (57)-(99)
: OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
: FEATURE:
: NAME/KEY: MISC FEATURE
: LOCATION: (100)-(142)
: OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
: OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-21
```

```

Query Match          100.0%; Score 202; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7,9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 40
Db      17 FRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGSVVIA 55
```

RESULT 27

```

US-10-544-093-23
: Sequence 23, Application US/10544093
: Publication No. US20060188512A1
: GENERAL INFORMATION:
: APPLICANT: Vednock, Ted
: APPLICANT: Vasquez, Nicki
: APPLICANT: Bard, Frederique
: APPLICANT: Seubert, Peter A.
: TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
: FILE REFERENCE: 15270J-009820US
```

CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
FEATURE:
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
FEATURE:
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (87)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-23

Query Match 100.0%; Score 202; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 7.9e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVIA 40
Db 4 FRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVIA 42

RESULT 28
US-10-544-093-18
Sequence 18, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vaequez, Ted
APPLICANT: Yednock, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 152700-00982005
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)

OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (143)..(185)
OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-18

Query Match 100.0%; Score 202; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVIA 40
Db 17 FRHDSGYEVHHQKLVFPFADVGSNKGAIIGLMVGSVIA 55

RESULT 29
US-10-544-093-26
Sequence 26, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vaequez, Ted
APPLICANT: Yednock, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 152700-00982005
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 203
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (81)..(123)
OTHER INFORMATION: Only a contiguous fragment of residues 81-123 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (161)..(203)
OTHER INFORMATION: Only a contiguous fragment of residues 161-203 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-26

Query Match 100.0%; Score 202; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 30

US-10-544-093-25
; Sequence 25, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIORITY FILING DATE: 2005-08-01
; PRIORITY APPLICATION NUMBER: WO PCT/US2004/002856
; PRIORITY FILING DATE: 2004-01-31
; PRIORITY APPLICATION NUMBER: US 60/444,150
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; FEATURE:
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (109)..(151)
; OTHER INFORMATION: Only a contiguous fragment of residues 109-151 are present.
; FEATURE:
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (152)..(194)
; OTHER INFORMATION: Only a contiguous fragment of residues 152-194 are present.
; FEATURE:
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (195)..(237)
; OTHER INFORMATION: Only a contiguous fragment of residues 195-237 are present.
; FEATURE:
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (238)..(280)
; OTHER INFORMATION: Only a contiguous fragment of residues 238-280 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-25

Query Match 100.0%; Score 202; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.9e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 40
|||||
DB 4 FRHDSGYEVHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

Search completed: September 28, 2006, 07:10:56
Job time : 15.6054 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 85.5247 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
Sequence: 1 XVFHQKLVFAEDVGNKGALIGLVGVVIA 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	155	100.0	32	4 AAB84430	Aab84430 Partial s
2	155	100.0	40	4 AAB84429	Aab84429 Partial s
3	155	100.0	40	8 ADU24435	Adu24435 Novel glu
4	155	100.0	40	8 ADU46709	Adu46709 Amyloid b
5	155	100.0	40	9 ADZ71361	Adz71361 Human bet
6	155	100.0	40	9 AEA35194	Aea35194 Human OC
7	155	100.0	40	9 AEB92567	Aeb92567 Glutamin
8	155	100.0	42	2 AAR20330	Aar20330 Sequence
9	155	100.0	42	2 AAR60366	Aar60366 Beta-amy1
10	155	100.0	42	2 AAR95248	Aar95248 Beta/A4-a
11	155	100.0	42	2 AAR94591	Aar94591 Alzheimer
12	155	100.0	42	2 AAM12828	Aam12828 Beta A4 p
13	155	100.0	42	2 AAM64507	Aam64507 Neurotox
14	155	100.0	42	2 AAM42989	Aam42989 Full leng
15	155	100.0	42	2 AAM47230	Aam47230 Beta-amy1
16	155	100.0	42	2 AAY49691	Aay49691 Human bet
17	155	100.0	42	2 AAM95858	Aay95858 Mutant ag
18	155	100.0	42	2 AAM81474	Aam81474 Synthetic
19	155	100.0	42	2 AAY08607	Aay08607 Human bet
20	155	100.0	42	2 AAM29093	Aay29093 A-beta-b1
21	155	100.0	42	2 AAI25137	Aay25137 Human amy
22	155	100.0	42	2 AAM92726	Aay92726 Human tac
23	155	100.0	42	2 AAY33407	Aay33407 Human amy

24	155	100.0	42	3 AAY96956	Aay96956 Beta-amy1
25	155	100.0	42	4 AAB86134	Aab86134 Human Alz
26	155	100.0	42	4 AAB35589	Aab35589 Beta/A4-a
27	155	100.0	42	4 AAB49098	Aab49098 Human amy
28	155	100.0	42	4 AAB84427	Aab84427 Partial s
29	155	100.0	42	4 AAB48457	Aab48457 Human amy
30	155	100.0	42	4 AAB91779	Aab91779 Amyloid b
31	155	100.0	42	4 AAB91812	Aab91812 Amyloid b
32	155	100.0	42	4 AAB82622	Aab82622 Amyloid-b
33	155	100.0	42	4 AAB49395	Aab49395 Human amy
34	155	100.0	42	4 AAB48830	Aab48830 Human amy
35	155	100.0	42	4 AAE05484	Aae05484 Human pep
36	155	100.0	42	5 ABB81321	Abb81321 Amyloid p
37	155	100.0	42	5 AAU80961	Aau80961 Human amy
38	155	100.0	42	5 AAU98727	Aau98727 Human amy
39	155	100.0	42	5 ABB94281	Abb94281 Amyloid b
40	155	100.0	42	5 AAE21438	Aae21438 Human bet
41	155	100.0	42	5 ABB76029	Abb76029 Beta amy1
42	155	100.0	42	5 AAE25335	Aae25335 Modified
43	155	100.0	42	5 AA015848	Aa015848 Beta-amy1
44	155	100.0	42	5 AAU76483	Aau76483 Amino aci
45	155	100.0	42	5 AAE26080	Aae26080 Beta amy1
46	155	100.0	42	5 AAE68314	Aae68314 Human bet
47	155	100.0	42	5 AAU96896	Aau96896 Human Amy
48	155	100.0	42	5 AAU93988	Aau93988 Human bet
49	155	100.0	42	5 AAE26300	Aae26300 Human bet
50	155	100.0	42	5 ABB80593	Abb80593 Human amy
51	155	100.0	42	5 AAM51964	Aam51964 Neuronal
52	155	100.0	42	5 AAU75433	Aau75433 Amyloid p
53	155	100.0	42	5 ABB83306	Abb83306 Amyloid-b
54	155	100.0	42	5 ABB77990	Abb77990 Beta-amy1
55	155	100.0	42	6 AAE35671	Aae35671 Human bet
56	155	100.0	42	6 AAU08711	Aau08711 Amyloid b
57	155	100.0	42	6 AA016344	Aa016344 A-beta pr
58	155	100.0	42	6 ABB08506	Abb08506 Human amy
59	155	100.0	42	6 AAE33793	Aae33793 Beta-amy1
60	155	100.0	42	6 ABB99423	Abb99423 Beta-amy1
61	155	100.0	42	6 ABB82633	Abb82633 Beta fib
62	155	100.0	42	6 ABB96144	Abb96144 Human Abe
63	155	100.0	42	6 ABB72223	Abb72223 Human bet
64	155	100.0	42	6 AAE35428	Aae35428 Beta pro
65	155	100.0	42	6 AAE33218	Aae33218 Beta amy1
66	155	100.0	42	6 ABB97882	Abb97882 Amino aci
67	155	100.0	42	6 ABB63707	Abb63707 Rat amylo
68	155	100.0	42	6 ADA74126	Ada74126 Beta-amy1
69	155	100.0	42	6 ADA89912	Ada89912 Abeta42 a
70	155	100.0	42	7 ADA37267	Ada37267 Human bet
71	155	100.0	42	7 ADB37652	Adb37652 Human bet
72	155	100.0	42	7 ADB85562	Adb85562 Beta-amy1
73	155	100.0	42	7 ADB75176	Adb75176 Amyloid b
74	155	100.0	42	7 AAE38649	Aae38649 Human amy
75	155	100.0	42	7 ADC66002	Adc66002 Human Ab
76	155	100.0	42	7 ADC35181	Adc35181 Beta-amy1
77	155	100.0	42	7 ADD20743	Add20743 Human bet
78	155	100.0	42	7 ADE10848	Ade10848 Chimeric
79	155	100.0	42	7 ADF60932	Adf60932 Human bet
80	155	100.0	42	7 ADF55649	Adf55649 Human A b
81	155	100.0	42	7 ADM82703	Adm82703 Beta-amy1
82	155	100.0	42	7 ADM39753	Adm39753 B-cell pe
83	155	100.0	42	8 ADF53271	Adf53271 Amyloid A
84	155	100.0	42	8 ADE63948	Ad63948 Recombina
85	155	100.0	42	8 ADI40716	Adi40716 Human amy
86	155	100.0	42	8 ADK52267	Adk52267 Human amy
87	155	100.0	42	8 ADN00694	Adn00694 A42, SEQ
88	155	100.0	42	8 ADM97740	Adm97740 Native Am
89	155	100.0	42	8 ADN41875	Adn41875 Amino aci
90	155	100.0	42	8 ADP61369	Adp61369 Beta-amy1
91	155	100.0	42	8 ADP73482	Adp73482 Alzheimer
92	155	100.0	42	8 ADP64925	Adp64925 Beta-amy1
93	155	100.0	42	8 ADQ74960	Adq74960 Human bet
94	155	100.0	42	8 ADQ26240	Adq26240 Human amy
95	155	100.0	42	8 ADQ37252	Adq37252 Vaccine a
96	155	100.0	42	8 ADR16409	Adr16409 Human Abe

97	155	100.0	42	8	ADR04018	Human amy
98	155	100.0	42	8	ADR12775	Human bet
99	155	100.0	42	8	ADR43293	Abeta42 B
100	155	100.0	42	8	ADR30645	GPBP cata

ALIGNMENTS

RESULT 1
 AAB84430
 ID AAB84430 standard; peptide; 32 AA.
 XX
 AC AAB84430;
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 XX
 KW Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 XX vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "pyroglutamate"
 XX
 PN MO200142306-AA.
 PD 14-JUN-2001.
 XX
 PF 08-DEC-2000; 2000WO-US033203.
 XX
 PR 08-DEC-1999; 99US-0169687P.
 XX
 PA (MTND-) MTNDSET BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain B;
 DR MPI; 2001-381648/40.
 XX
 PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PR epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 XX
 PS Claim 3; Page 42-43; 47pp; English.
 XX
 CC The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal
 XX
 Q0 Sequence 32 AA:

Db 2 VHQLVFPAEDVGSNKGAIIGLMVGVIA 32

2 VHHQKL V FFAEDVGSNKGAI IGLMVGGVIA 32

RESULT 2

ID AAB84429 standard; peptide; 40 AA.
 AC AAB84429;
 DT 22-AUG-2001 (first entry)
 XX Partial sequence of a human beta-amyloid precursor protein.
 XX DE
 XX Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KM vaccine.
 XX
 OS Homo sapiens.
 FH Key
 FT Modified-site 1
 FT /note= "pyroglutamate"
 XX
 XX MO200142306-A2.
 PN
 PN 14-JUN-2001.
 PD
 PD 08-DEC-2000; 2000MO-USO33203.
 PF
 PF 08-DEC-1999; 99US-0169687P.
 XX
 XX (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 PA
 PA Chain B;
 PI
 PI WPI; 2001-381648/40.
 DR
 DR
 XX
 XX Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 PS
 PS Claim 3; Page 42; 47pp; English.
 XX
 XX The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal
 CC
 CC Sequence 40 AA;
 CC

Query Match	100.0%	Score 155	DB 4	Length 40;
Best Local Similarity	100.0%	Pred. No. 1.2e-16;		
Matches 31;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2 VHHOKLVFPADYVGSNNKGATIGLWVGGVIA 3
 |||||
 10 VHHOKLVFPADYVGSNNKGATIGLWVGGVIA 40
Db

RESULT 3

ADU24435
 ID ADU24435 standard; protein; 40 AA.
 XX
 AC ADU24435;
 XX
 DT 27-JAN-2005 (first entry)
 DT
 XX
 DE Novel glutaminyl cyclase (QC) inhibitor-related protein #3.
 XX
 KW Alzheimer's disease; Down's syndrome; Huntington's disease;
 KW glutaminyl cyclase inhibitor; QC inhibitor; nootropic; neuroprotective;
 KW antiparkinsonian; neuroleptic; antipyretic; antidepressant; hypotensive;
 KW eating-disorders-Gen; anticonvulsant; antialcoholic; antiaddictive;
 KW hypnotic; CNS-Gen; endocrine-Gen; tranquiliser; antulcer; cycostatic;
 KW antiinflammatory; antipsoriatic; antirheumatic; antiarthritic;
 KW antarteriosclerotic; pyroglutamic acid; neuronal disease;
 KW Parkinson's disease; Huntington's chorea; pathogenic psychotic condition;
 KW schizophrenia; impaired food intake; sleep-wakefulness;
 KW homeostatic regulation; energy metabolism; autonomic function;
 KW hormonal balance; body fluid regulation; hypertension; fever;
 KW sleep dysregulation; anorexia; anxiety related disorder; depression;
 KW seizure; epilepsy; drug withdrawal; alcoholism;
 KW neurodegenerative disorder; cognitive dysfunction; dementia; ulcer;
 KW gastric cancer; neoplasia; inflammatory host response; cancer; melanoma;
 KW malignant metastasis; psoriasis; rheumatoid arthritis; atherosclerosis;
 KW leukocyte adhesion.
 XX
 OS Unidentified.
 XX
 PN US2004224875-A1.
 XX
 PD 11-NOV-2004.
 XX
 PF 05-MAY-2004; 2004US-00838993.
 XX
 PR 05-MAY-2003; 2003US-0468014P.
 XX
 PA (SCHI/) SCHILLING S.
 PA (NIESTR/) NIESTROJ A J.
 PA (HEIS/) HEISER U.
 PA (BUCH/) BUCHHOLZ M.
 PA (DEMU/) DEMUTH H.
 XX
 PI Schilling S, Niestroj AJ, Heiser U, Buchholz M, Demuth H;
 DR MPI, 2004-813067/80.
 XX
 PT Use of glutaminyl cyclase inhibitor for the treatment of e.g. Alzheimer's
 PT disease, Down syndrome, pathogenic psychotic conditions, schizophrenia
 PT and Huntington's disease.
 XX
 PS Disclosure; Page 5; 34pp; English.
 XX
 CC This invention relates to a novel treatment of Alzheimer's disease,
 CC Down's syndrome or Huntington's disease which involves administering a
 CC glutaminyl cyclase (QC) inhibitor. The invention may be useful for the
 CC development of compounds with a nootropic, neuroprotective,
 CC antiparkinsonian, neuroleptic, antipyretic, antidepressant, hypotensive,
 CC eating-disorders-Gen, anticonvulsant, antialcoholic, antiaddictive,
 CC hypnotic, CNS-Gen, endocrine-Gen, tranquiliser, antulcer, cycostatic,
 CC antiinflammatory, antipsoriatic, antirheumatic, antiarthritic or
 CC antarteriosclerotic activity acting as glutaminyl cyclase inhibitors.
 CC Glutaminyl cyclase catalyzes both the intramolecular cyclisation of N-
 CC terminal glutamate residues into pyroglutamic acid with liberation of
 CC ammonia and the intramolecular cyclisation of N-terminal glutamate
 CC residues into pyroglutamic acid with liberation of water, the glutaminyl
 CC cyclase inhibitors are useful in the treatment of various neuronal
 CC diseases. The composition containing a QC inhibitor is useful for the
 CC treatment of neuronal disorders such as Alzheimer's disease, Down
 CC syndrome, Parkinson's disease, Chorea Huntington, pathogenic psychotic
 CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,
 CC impaired homeostatic regulation of energy metabolism, impaired autonomic
 CC function, impaired hormonal balance, impaired regulation of body fluids,

CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
 CC disorders (including depression, seizures including epilepsy, drug
 CC withdrawal and alcoholism), and neurodegenerative disorders (such as
 CC cognitive dysfunction and dementia). The compositions may also be useful
 CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host
 CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid
 CC arthritis, atherosclerosis and leukocyte adhesion and migration processes
 CC in the endothelium. The present sequence is that of a protein which is
 CC related to the treatment method of the invention.
 CC
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 155; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
 DB 10 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 40
 RESULT 4
 ID ADU46709 standard; peptide; 40 AA.
 XX
 AC ADU46709;
 XX
 DT 10-FEB-2005 (first entry)
 DT
 XX
 DE Amyloid beta peptide (3-42), substrate of glutaminyl cyclase.
 DE
 XX
 KW Amyloid-beta peptide (3-42); glutaminyl cyclase; nootropic;
 KW neuroprotective; anticonvulsant; antulcer; cycostatic; neuroleptic;
 KW antifertility; antipsoriatic; antirheumatic; antiarthritic;
 KW antarteriosclerotic; Alzheimer's disease; human.
 XX
 OS Homo sapiens.
 OS
 PN WO2004098625-A2.
 XX
 PD 18-NOV-2004.
 XX
 PF 05-MAY-2004; 2004WO-EP004778.
 XX
 PR 05-MAY-2003; 2003US-0468014P.
 PR 05-MAY-2003; 2003US-0468043P.
 PR 15-OCT-2003; 2003US-0512038P.
 XX
 PA (PROB-) PROBIODRUG AG.
 XX
 PI Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U;
 DR MPI, 2004-805062/79.
 XX
 PT Use of effectors of glutaminyl cyclase (QC) for treating diseases and/or
 PT for modulating physiological processes based on the action of pglu-
 PT containing peptides.
 XX
 PS Disclosure; Page 12; 106pp; English.
 XX
 CC The present sequence is that of amyloid beta peptide (3-42).
 CC Pyroglutamate (pglu)-containing isoforms of amyloid beta peptides in
 CC represent the prominent forms of N-truncated amyloid beta peptides in
 CC senile plaques. The pglu modification exacerbates the toxic properties of
 CC amyloid beta peptides. The invention shows that glutaminyl cyclase (QC,
 CC EC 2.3.2.5) is involved in the cyclisation of Glu to pglu, making this
 CC enzyme a target in drug development. The invention relates to the
 CC identification, screening and use of effectors of QC for the preparation
 CC of a medicament for: (a) the treatment of diseases that can be treated by
 CC modulation of QC activity in vivo; and/or (b) the modulation of
 CC physiological processes based on the action of pglu-containing peptides
 CC caused by modulation of QC activity. The QC effectors are used to alter
 CC the conversion of N-terminal Glu or Gln residues to pglu residues in a QC

CC substrate such as amyloid beta3-40/42. They can be used to treat
 CC Alzheimer's disease, Down Syndrome, Huntington's disease, Kennedy's
 CC disease, ulcer disease and gastric cancer with or without Helicobacter
 CC pylori infections, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, melanoma, psoriasis, rheumatoid arthritis, atherosclerosis,
 CC impaired humoral and cell-mediated immune responses, leukocyte adhesion
 CC and migration processes in the endothelium, impaired food intake, sleep-
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids. The effectors of QC are also useful for:
 CC regulating and/or controlling male fertility; stimulating
 CC gastrintestinal tract cell proliferation, preferably proliferation of
 CC gastric mucosal cells, epithelial cells, acute acid secretion and for
 CC differentiating acid-producing parietal cells and histamine-secreting
 CC enterochromaffin-like cells (all claimed). Amyloid beta peptides were
 CC also shown to be substrates of dipeptidyl peptidase IV (DP IV) and DP IV-
 CC like enzymes, and preferred effector compositions additionally comprise
 CC inhibitors of these enzymes.

XX Sequence 40 AA:

Query Match 100.0%; Score 155; DB 8; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
 DB 10 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 5
 ADZ71361

ID ADZ71361 standard; peptide; 40 AA.

XX ADZ71361;

XX 14-JUL-2005 (first entry)

XX Human beta-amyloid peptide #3.

XX Zollinger-Elison syndrome; gastrointestinal disease; neoplasm;

XX colorectal tumor; gastrointestinal tumor; Helicobacter pylori infection;

XX antibacterial; infection; beta-amyloid.

XX Homo sapiens.

XX WO2005039548-A2.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011630.

XX 15-OCT-2003; 2003US-0512038P.

XX (PROB-) PROBIODRUG AG.

XX Schilling S, Hoffmann T, Niestroj AJ, Demuth H, Heiser U;

XX WPI; 2005-346574/35.

XX Use of glutaminyl cyclase effectors in the manufacture of a medicament

XX for modulating conversion of glutamic acid/glutamine residue to

XX pyroglutamic acid residue at the N-terminus of glutaminyl cyclase

XX substrate in the treatment e.g. cancer.

XX Disclosure; Page 13; 105pp; English.

XX The invention relates to the use of a glutaminyl cyclase effector (EI)

XX for modulating conversion of glutamic acid/glutamine residue to

XX pyroglutamic acid residue at the N-terminus of a glutaminyl cyclase (QC)

XX substrate. The glutaminyl cyclase effector is useful for treating a

XX condition mediated by modulation of QC enzyme activity e.g. Familial

CC British Dementia (FBD) and Familial Danish Dementia (FDD), ulcer disease
 CC and duodenal cancer with or without Helicobacter pylori infections,
 CC colorectal cancer, Zollinger-Elison syndrome, gastric cancer, Alzheimer's
 CC disease, Down's syndrome, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, psoriasis, rheumatoid arthritis, atherosclerosis, impaired
 CC humoral and cell-mediated immunity responses, leukocyte adhesion and
 CC migration processes in the endothelium, impaired food intake, sleep
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids, for the preparation of contraceptive
 CC medicaments for males. The amino acid sequence of the human beta-amyloid
 CC peptide.

XX Sequence 40 AA:

Query Match 100.0%; Score 155; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
 DB 10 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 6
 AEA35394

ID AEA35394 standard; peptide; 40 AA.

XX AEA35394;

XX 11-AUG-2005 (first entry)

XX Novel QC inhibitor composition-related Abeta(3-42) polypeptide.

XX pharmaceutical; nootropic; neuroprotective; antiparkinsonian;

XX neuroleptic; hypotensive; antipsychotic; tranquilizer; antidepressant;

XX antialcoholic; anticonvulsant; anabolic; eating-disorders-Gen.; hypnotic;

XX amyloid; neurological disease; Alzheimer's disease; Downs Syndrome;

XX Parkinson's disease; Huntingtons chorea; psychotic disorders;

XX schizophrenia; sleep disorder; hypertension; anorexia nervosa;

XX anxiety disorder; major depressive disorder; epilepsy; alcoholism;

XX neurodegenerative disease; cognitive disorder; dementia.

XX Unidentified.

XX WO2005049027-A2.

XX 02-JUN-2005.

XX 29-OCT-2004; 2004WO-EP012301.

XX 03-NOV-2003; 2003US-0516717P.

XX (PROB-) PROBIODRUG AG.

XX Schilling S, Niestroj AJ, Demuth H, Rosner S;

XX WPI; 2005-395979/40.

XX Composition used for treating neuronal diseases e.g. Alzheimer's disease,

XX Down Syndrome, Parkinson disease, Chorea Huntington comprises glutaminyl

XX cyclase inhibitor.

XX Disclosure; Page 15; 123pp; English.

XX This invention relates to a novel composition which comprises at least

XX one glutaminyl cyclase (QC) inhibitor and optionally at least one of

XX prolyl endopeptidase (PEP) inhibitors, inhibitors of dipeptidyl

XX aminopeptidase (DP), neuropeptide Y (NPY) receptor ligands, NPY agonists

XX or antagonists, acetylcholinesterase (AChE) inhibitors, protein

XX isopartate carboxymethyl transferase (PMT) enhancers, inhibitors of

XX beta or gamma secretases and inhibitors of neutral endopeptidase. The

CC or the A695 sequence. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
 |||
 DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 9
 AAR60366
 ID AAR60366 standard; peptide; 42 AA.

AC AAR60366;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1995 (first entry)
 XX
 DE Beta-amyloid (1-42).
 XX
 KM Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 KM anti-beta-amyloid antibody; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9417197-A1.
 XX
 PD 04-AUG-1994.
 XX
 PF 24-JAN-1994; 94WO-UP000089.
 XX
 PR 25-JAN-1993; 93JP-00010132.
 PR 05-FEB-1993; 93JP-0019035.
 PR 16-NOV-1993; 93JP-00286985.
 PR 28-DEC-1993; 93JP-00334773.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Suzuki N, Odaka A, Kitada C;
 DR WPI, 1994-264110/32.
 XX
 PT Antibodies recognising specific parts of beta-amyloid - can be used for
 PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
 PT disease.
 XX
 PS Disclosure; Page 83; 116pp; Japanese.
 XX
 CC Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
 CC the C-terminal portion. The antibodies are useful for assaying beta-
 CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
 |||
 DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 10

AAR95248
 ID AAR95248 standard; peptide; 42 AA.
 XX
 AC AAR95248;
 XX
 DT 20-JAN-1997 (first entry)
 XX
 DE Beta/A4-amyloid peptide.
 XX

KM Beta/A4-amyloid peptide; tissue plasminogen activator;
 KM Alzheimer's disease; stimulation; investigation; pathogenesis;
 KM hereditary cerebral haemorrhage with amyloidosis-Dutch type; control;
 KM cerebral amyloid angiopathy; cerebral; haemorrhage; hemorrhage.
 XX
 OS Homo sapiens.
 XX
 PN WO9615799-A1.
 XX
 PD 30-MAY-1996.
 XX
 PF 22-NOV-1995; 95WO-US015007.
 XX
 PR 22-NOV-1994; 94US-00347144.
 XX
 PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Anderson S;
 XX
 DR WPI, 1996-268332/27.
 XX
 PT Use of agents which bind beta-amyloid peptide - for diagnosis, prevention
 PT and treatment of vascular damage caused by amyloid deposits, partic. in
 PT haemorrhaging and Alzheimer's disease.
 XX
 PS Example 1; Fig 1; 52pp; English.
 XX
 CC To investigate the effects of beta-amyloid peptide (BAP) on tissue
 CC plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide
 CC contained 42 amino acids and corresp. to the full length BAP (AAR95248).
 CC The other 2 peptides (AAR95249 and 50) contained the 28 N-terminal
 CC residues of the BAP found in Alzheimer's disease and hereditary cerebral
 CC haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an
 CC assay to determine the effect of the peptides on t-PA activation, each
 CC peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation
 CC (k(app)) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and
 CC 7.8 for null and fibrinogen controls. The results demonstrate that the
 CC BAP are able to stimulate t-PA activity in vitro, which is significant in
 CC that it provides a means for investigating and controlling the
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
 CC angiopathy related cerebral haemorrhage
 XX

SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
 |||
 DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11

AAR94591
 ID AAR94591 standard; peptide; 42 AA.

AC AAR94591;
 XX

DT 25-MAR-2003 (revised)
 DT 21-AUG-1996 (first entry)
 XX
 DE Alzheimer amyloid beta-protein active site sequence.
 XX

KW Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;
 KW serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;
 KW complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.
 XX
 OS Synthetic.
 XX
 PN USS506097-A.
 XX
 PD 09-APR-1996.
 XX
 PF 10-JAN-1994; 94US-00179574.
 XX
 PR 24-AUG-1990; 90US-00572671.
 PR 13-JAN-1992; 92US-00819361.
 PR 13-JAN-1993; 93WO-US000325.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Kayyali U, Potter H;
 XX
 DR WPI; 1996-2002/0/20.
 XX
 PT Inhibiting enzymatic activity of Alzheimer amyloid beta-protein - using p
 PT -amidino:phenyl:methanesulphonyl fluoride or ebelactone A, for treatment,
 PT study and diagnosis of Alzheimer's disease, etc.
 XX
 PS Disclosure; Fig 1; 17pp; English.
 XX
 CC This is the sequence of a fragment of the beta-amyloid protein associated
 CC with Alzheimer's disease. The protein contains esterase (cholinesterase
 CC and lipase) activities based on active site similarities with serine
 CC proteases (see AAR94592-96). The esterase activity of the beta-amyloid
 CC protein is inhibited by the cpds. of the invention i.e. ebelactone A or
 CC para-amidinophenylmethanesulphonyl fluoride. Inhibition of these
 CC activities prevent complex formation between the beta-amyloid protein and
 CC alpha(1)-antichymotrypsin, thus can be used to treat, study or diagnose
 CC Alzheimer's or Down's diseases or normal ageing. (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42
 XX
 RESULT 12
 AAW12828
 ID AAW12828 standard; peptide; 42 AA.
 XX
 AC AAW12828;
 XX
 DT 08-DEC-1997 (first entry)
 XX
 DE Beta A4 peptide.
 XX
 DE Beta A4 peptide.
 XX
 KW Beta A4 peptide; Alzheimer's disease; peptide aggregation; brain;
 KW therapy; inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO9707403-A1.
 XX
 PD 27-FEB-1997.
 XX
 PF 23-JUL-1996; 96WO-US012034.
 XX
 PR 16-AUG-1995; 95US-00515606.
 XX

PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Goyal S, Paul J, Riedel NG, Sahasrabudhe SR;
 XX
 DR WPI; 1997-165447/15.
 XX
 PT Determn. of the degree of betaA4 peptide aggregation using binding agent
 PT - used to screen cpds. for possible use in Alzheimer's disease treatment.
 XX
 PS Disclosure; Page 10; 18pp; English.
 XX
 CC This sequence represents the beta A4 peptide. The degree of aggregation
 CC of this peptide is determined using the method of the invention. The beta
 CC A4 peptide is present in the brain of Alzheimer's disease patients, but
 CC not in the brain of non-Alzheimer's disease individuals. The peptide
 CC clumps or aggregates in the brain of Alzheimer's disease patients, where
 CC it may be responsible for the destruction of normal brain cells. Once the
 CC clumps or aggregates form, the formulation is almost irreversible. The
 CC method of the invention comprises reacting this sequence with a binding
 CC reagent capable of binding to it only in its non-aggregated state, to
 CC form an amount of a beta A4 peptide-bound reagent and an amount of
 CC protein free reagent. The amount of the beta A4 peptide, binding reagent
 CC complex is then measured. Compounds which inhibit aggregation of beta A4
 CC peptide are potentially useful for treatment of Alzheimer's disease
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42
 XX
 RESULT 13
 AAW64507
 ID AAW64507 standard; peptide; 42 AA.
 XX
 AC AAW64507;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Neurotoxic beta-amyloid peptide decoy peptide #20.
 XX
 KW Beta-amyloid peptide; beta-A₄ neuropeptide; neurotoxin; calcium influx;
 KW aggregate; Alheimers disease; decoy; treatment.
 XX
 OS Synthetic.
 XX
 PN WO9830229-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 09-JAN-1998; 98WO-US000653.
 XX
 PR 10-JAN-1997; 97US-0035847P.
 PR 29-OCT-1997; 97US-00960188.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Ingram VM, Blanchard BJ;
 XX
 DR WPI; 1998-398795/34.
 XX
 PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor, useful
 PT for, e.g. treating Alzheimer's disease.
 XX
 PS Example 8, Page 46; 68pp; English.
 XX
 CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid

CC peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates
 CC that increase calcium influx into neuronal cells. Such peptides can be
 CC used in the treatment of diseases associated with neurotoxic aggregates
 CC of beta-AP specifically Alzheimer's disease. The peptides are
 CC administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and
 CC orally, or from slow-release implants

XX Sequence 42 AA:

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 14

AAW42989 standard; peptide; 42 AA.

AC AAW42989;

DT 01-MAY-1998 (first entry)

XX Full length beta-amyloid peptide (BAP).

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KW cerebrovascular deposit; Alzheimer's disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

XX abnormal proteolytic cleavage.

OS Homo sapiens.

XX US5703209-A.

PD 30-DEC-1997.

PF 05-JUN-1995; 95US-00464248.

XX 01-MAY-1992; 92US-00877675.

PR 20-SEP-1993; 93US-00123659.

XX (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

XX WPI; 1998-076482/07.

DR Amyloid precursor protein fusion polypeptides - comprising APP fragment

PT and marker, useful for research and drug screening.

XX Disclosure; Col 7; 84pp; English.

XX The present sequence represents a beta-amyloid peptide (BAP). Abnormal

CC accumulation of extracellular BAP in plaques and cerebrovascular deposits

CC is characteristic in brains of individuals suffering from Alzheimer's

CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating

CC protein which is derived from a larger amyloid precursor protein (APP).

CC APP is expressed as an integral membrane protein, and is cleaved by

CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes

CC amyloidogenesis and results in the release of the amino-terminal APP

CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-

CC 770. These isoforms are derived by alternative splicing. APP-APP 751 is a

CC deletion construct of APP-751, which has a deletion of 276 amino acids to

CC within 15 amino acids of the BAP domain. APP can be used as a substrate

CC for studying abnormal proteolytic cleavage which results in the release

CC of BAP, and also to screen for drugs that will inhibit such cleavage

XX Sequence 42 AA;

QY Query Match 100.0%; Score 155; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 15

AAW47230 standard; peptide; 42 AA.

AC AAW47230;

DT 22-MAY-1998 (first entry)

XX Beta-amyloid peptide residues 1-42.

KW Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;

KW Alzheimer's disease.

XX Homo sapiens.

XX US5721106-A.

PD 24-FEB-1998.

XX 12-SEP-1994; 94US-00304585.

PR 13-AUG-1991; 91US-00744767.

XX (MINN) UNIV MINNESOTA.

PA (HARD) HARVARD COLLEGE.

PI Mantyh PW, Maggio JE;

XX WPI; 1998-168404/15.

DR New in vitro screening assay for Alzheimer's disease drugs - comprises

PT assessing binding of labelled beta-amyloid peptide to silk sample.

XX Claim 8; Col 29-30; 36pp; English.

PS The present sequence was used in the development of a novel in vitro

CC screening assay for agents capable of affecting the deposition of beta-

CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk

CC sample with labelled BAP, optionally in the presence of a test agent,

CC detecting the amount of label bound to the silk and assessing the effect

CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP

CC to silk are potentially useful for treating amyloidosis diseases,

CC especially Alzheimer's disease

XX Sequence 42 AA;

QY Query Match 100.0%; Score 155; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.3e-16;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 32

DB 12 VHHOKLVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 16

AAW49691 standard; peptide; 42 AA.

ID AAW49691

AC AAW49691;

DT 13-JAN-2000 (first entry)

XX Human beta amyloid precursor protein peptide.

XX

XX

KW Human; beta amyloid precursor protein; APP; beta secretase inhibition;
 KM alpha secretase; neurological disorder; Alzheimer's disease;
 KM Down syndrome; mutation.
 XX
 OS Homo sapiens.
 XX
 PN WO9951752-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-JP001701.
 XX
 PR 31-MAR-1998; 98JP-00101821.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ozawa K, Ikeda S, Tabira T;
 XX
 DR WPI; 1999-620208/53.
 XX
 PT A cell line which produces beta amyloid precursor protein, used in the
 XX investigation of neurological disorders such as Alzheimer's disease.
 PS Disclosure; Page 41; 70pp; Japanese.
 XX
 CC The present invention describes a cell line which produces beta amyloid
 CC precursor protein (APP) and expresses alpha secretase activity but
 CC expresses beta secretase activity only under an external stimulus. Also
 CC described is a cloning method for DNA encoding beta secretase,
 CC comprising: (1) inserting a DNA library into the cell line, expressing
 CC the inserted DNA, and selecting cells expressing beta secretase then
 CC isolating the beta secretase DNA from them; or (2) isolating nucleic acid
 CC from the cell line with or without external stimulation and performing
 CC subtractive cloning to identify DNA expressed only under stimulation.
 CC Products from the present invention may be used in the investigation of
 CC neurological disorders such as Alzheimer's disease and Down syndrome and
 CC in particular the association of mutations of the beta APP with them. The
 CC present sequence represents a human beta APP peptide
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 XX
 RESULT 17
 AAW99585
 ID AAW99585 standard; peptide; 42 AA.
 XX
 AC AAW99585;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE Mutant aggregating amyloid-beta peptide.
 XX
 KM Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KM diagnosis; Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9908695-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 13-AUG-1998; 98WO-US016809.
 XX
 PR 14-AUG-1997; 97US-0055660P.

XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Glabe C, Garzon-Rodriguez W;
 XX
 DR WPI; 1999-190112/16.
 XX
 PT New fluorescent labeled amyloid A-beta peptides.
 XX
 PS Example 1; Page 21; 50pp; English.
 XX
 CC This sequence corresponds to a mutant aggregating amyloid-beta peptide
 CC which can be covalently labeled with a fluorescent group. The detection
 CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
 CC or detect a predisposition to Alzheimer's disease. The screening assays
 CC can be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid-beta peptide are also useful for exploring other aspects of
 CC amyloid structure
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42
 XX
 RESULT 18
 AAW81474
 ID AAW81474 standard; peptide; 42 AA.
 XX
 AC AAW81474;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (A-beta) peptide 9 (residues 1-42).
 XX
 KM Amyloid beta; A-beta; deoxygenated solvent; evaporative deposition;
 KM research; neurotoxicity; free-radical; glutamine synthetase.
 XX
 OS Synthetic.
 XX
 PN US5840838-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-00609090.
 XX
 PR 29-FEB-1996; 96US-00609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Aksenov M, Carney JM, Hensley K, Butterfield DA;
 XX
 DR WPI; 1999-034120/03.
 XX
 PT Process for treating synthetic amyloid beta peptides - by organic solvent
 PT treatment, useful for studying neurotoxicity.
 XX
 PS Claim 5; Col 11-12; 14pp; English.
 XX
 CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (A-beta)
 CC peptides. The invention provides a process for treating a synthetic A-beta
 CC peptide that comprises dissolving the peptide in a deoxygenated solvent
 CC selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/mL, incubating the solution
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by "evaporative
 CC deposition," in 5-10 minutes. Synthetic amyloid beta peptides are useful

CC as research tools for studying neurotoxicity resulting from Abeta peptide
 CC enhanced free-radical production. The treatment increases the activity
 CC of the synthetic Abeta peptides in tests to determine free-radical
 CC generating capacity and glutamine synthetase inactivation
 CC
 SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1,3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 42

RESULT 19
 AAY08607
 ID AAY08607 standard; protein; 42 AA.

AC AAY08607;

DT 05-AUG-1999 (first entry)

DE Human beta-amyloid precursor core protein A42.

KM APP, beta-amyloid precursor protein; human; transgenic mice; pathology;
 KM Alzheimer's disease; model; therapeutic compound; brain; mechanism;
 KM nerve tissue specific promoter; synthesis; inhibitor; deposition;
 KM plaque formation; treatment; A42.

OS Homo sapiens.

PN US5912410-A.

PD 15-JUN-1999.

PF 13-APR-1995; 95US-00422333.

PR 15-JUN-1990; 90US-00538857.

PR 17-JUN-1991; 91US-00716725.

PR 21-OCT-1994; 94US-00327381.

PA (SCIO-) SCIOS INC.

PI Cordell B;

DR WPI; 1999-357231/30.

PT Transgenic mice useful for studying compounds potentially useful in the
 PT treatment of Alzheimer's disease.

PS Disclosure; Fig 3; 72pp; English.

CC This invention describes novel transgenic mice expressing proteins
 CC related to the pathology of Alzheimer's disease and which provide models
 CC for studying potentially therapeutic compounds. The transgenic mice
 CC contain a DNA sequence encoding a beta-amyloid precursor protein (APP)
 CC and a nerve tissue specific promoter operably linked to the beta-APP
 CC allowing its expression to form beta-amyloid protein deposits in the
 CC animal's brain. The transgenic mouse is useful for elucidating the
 CC molecular mechanisms involved in the synthesis of and, more importantly,
 CC inhibiting the synthesis and deposition of beta-amyloid proteins (most
 CC importantly in the brain where plaque formation is associated with
 CC Alzheimer's disease) by inhibiting production and/or increasing cleavage
 CC after production. The transgenic animals provide useful models for
 CC studying the in vivo relationships of the proteins to each other and to
 CC other compounds being tested for their usefulness in treating Alzheimer's
 CC disease

SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1,3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 42

RESULT 20

ID AAM29093
 ID AAM29093 standard; peptide; 42 AA.

AC AAM29093;

DT 20-JUL-1999 (first entry)

DE A-beta-binding peptide 1-42.

KM Cyclosporin; A-beta peptide; conjugate; neurological disease; Alzheimer;
 KM multiple sclerosis; amyotrophic lateral sclerosis; ALS;
 KM non-immunosuppressive; amyloid plaque formation.

OS Homo sapiens.

PN WO9910374-A1.

PD 04-MAR-1999.

PF 25-AUG-1998; 98WO-US017544.

PR 26-AUG-1997; 97US-0057751P.

PA (MISC) WISCONSIN ALUMNI RES FOUND.

PI Rich DH, Solomon ME;

DR WPI; 1999-276928/23.

PT New A-b-binding peptide conjugates and Caa analogs - useful in treatment
 PT of neurological diseases e.g. Alzheimer's disease, Multiple Sclerosis
 PT etc.

PS Claim 5; Page 98; 129pp; English.

CC New conjugates are disclosed which are of formula A-Z, in which: A is (1)
 CC a cyclosporin A analogue described in AAM29087 or (2) an FK506 binding
 CC peptide inhibitor; and Z is a polypeptide comprising 5 or more contiguous
 CC residues of A-beta peptide. The compounds are novel chemical inducers of
 CC dimerization which are non-immunosuppressive and which are inhibitors of
 CC A-beta peptide aggregation and deposition in amyloid plaques. The adverse
 CC consequences of amyloid plaque formation can be prevented or ameliorated
 CC by sequestering the A-beta peptide in monomeric form with a conjugate
 CC which links the A-beta to cyclophilin or FKBP, therefore providing a
 CC mechanism to minimize the amount of free A-beta available for fibril
 CC formation and deposition. The compounds can be used for the treatment of
 CC Alzheimer's disease, multiple sclerosis and amyotrophic lateral sclerosis

SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1,3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 32
 DB 12 VHHOKLVFFAEVDVGSNKGAIIGLMVGVVIA 42

RESULT 21

ID AAY25137
 ID AAY25137 standard; peptide; 42 AA.

AC AAY25137;

XX 26-AUG-1999 (first entry)
 XX
 DE Human amyloid beta-A4 peptide 5.
 XX
 KW Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KW therapeutic drug; brain; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN US5919631-A.
 PD 06-JUL-1999.
 XX
 PF 17-JUL-1996; 96US-00682245.
 XX
 PR 17-JUL-1996; 96US-00682245.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Sahaerabudhe SR, Paul JW, Goyal S, Riedel NG;
 DR WPI, 1999-403957/34.
 XX
 PT Determination of degree of aggregation of a peptide, useful for
 PT identifying therapeutic drugs for treating Alzheimer's disease.
 XX
 PS Claim 1; Col 7-8; 8pp; English.
 XX
 CC This invention describes a novel method for the determination of the
 CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
 CC Determination comprises: (a) incubating a sample of unaggregated (I) with
 CC Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated
 CC (I); (b) measuring the amount of (II) bound to (I) to obtain a value (i);
 CC (c) repeating steps (a) and (b) with a second sample at a different time
 CC to obtain a second value (ii); and (d) determining the difference between
 CC (i) and (ii) which is inversely related to the degree of aggregation of
 CC (I). This method may be applied to a screen for compounds that inhibit
 CC aggregation of (I). These inhibitors may be used as therapeutic drugs to
 CC inhibit the formation of these aggregates in the brains of patients
 CC suffering from Alzheimer's disease
 CC
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 VHHQKLVFAEDVGSNKGATIGLMVGCVIA 32
 DB 12 VHHQKLVFAEDVGSNKGATIGLMVGCVIA 42
 RESULT 22
 AAW92726
 ID AAW92726 standard; peptide; 42 AA.
 XX
 AC AAW92726;
 XX
 DT 20-MAR-2003 (revised)
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #72.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 PD 02-MAR-1999.

XX 29-JUL-1991; 91US-00737371.
 PF
 XX
 PR 27-JUL-1990; 90US-00559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 DR WPI, 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
 XX
 PS Disclosure; Col 41-42; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)
 CC
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 155; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 VHHQKLVFAEDVGSNKGATIGLMVGCVIA 32
 DB 12 VHHQKLVFAEDVGSNKGATIGLMVGCVIA 42
 RESULT 23
 AAY33407
 ID AAY33407 standard; peptide; 42 AA.
 XX
 AC AAY33407;
 XX
 DT 03-DEC-1999 (first entry)
 DE Human amyloidogenic A-beta peptide 1.
 XX
 KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
 KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
 KW Down's Syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WC0941279-A2.
 PD 19-AUG-1999.
 XX
 PF 12-FEB-1999; 99WO-US003231.
 PR 13-FEB-1998; 98US-0074658P.
 XX
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI Lynn DG, Meredith SC, Burkoth TS;
 DR WPI, 1999-561326/47.
 XX
 PT Inhibiting amyloid plaque formation in humans suffering from amyloidosis,
 PT Alzheimer's disease or Down's Syndrome.
 XX
 PS Claim 21; Page 140; 141pp; English.
 XX

CC This invention describes a novel method for inhibiting amyloid
CC fibrillogenesis which comprises contacting tissue with a composition
CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC at an end terminal or a side chain, by conjugation to polyethylene
CC glycol, by conjugation to a second compound and a pharmaceutically
CC acceptable buffer, solvent or diluent. The methods are used to inhibit
CC amyloid plaque formation in humans suffering from amyloidosis,
CC Alzheimer's disease or Down's Syndrome. This sequence represents a
CC fragment of the beta-amyloid peptide described in the method of the
CC invention
CC
SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
|||
DB 12 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 24

AA96956
ID AA96956 standard; peptide; 42 AA.

XX AA96956;

DT 31-OCT-2000 (first entry)

XX Beta-amyloid 1-42 peptide.

XX PRUBX3; polyhistidine; tag; rubredoxin; antigen; vaccine; carrier;
XX immunogenic; flag tag; beta-amyloid; fusion.

XX Homo sapiens.

PN MO200039310-A1.

PD 06-JUL-2000.

PF 29-DEC-1999; 99MO-US031176.

PR 29-DEC-1998; 98US-00114034.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

PI Przybyla A, Menon N;

DR MPI; 2000-452403/39.

XX Nucleic acids encoding fusion peptides comprising rubredoxin, useful as
XX vaccines.

PS Example 2; Page 63; 67pp; English.

CC Fusion proteins comprising rubredoxin and fused antigens and/or haptens
CC may be used as vaccines to initiate immune responses. In this case, the
CC rubredoxin acts as a carrier. The fusion protein is capable of binding
CC iron (Fe-2+) when properly folded, giving it a red color that makes it
CC easy to identify following or during purification. The C-terminal fused
CC protein may be insoluble or known to form inclusion bodies in a host
CC cell. The rubredoxin serves as the carrier molecule to yield immunogenic
CC fusion products. As rubredoxin is itself only negligibly antigenic, there
CC is no need to include a cleavage site in the fusion product to allow
CC cleavage of the N-terminal and C-terminal constituents

XX Sequence 42 AA;

Query Match 100.0%; Score 155; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
|||
DB 12 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 25

AA86134
ID AA86134 standard; protein; 42 AA.

XX AA86134;

DT 31-JUL-2001 (first entry)

XX Human Alzheimer-Beta-peptide (1-42).

XX Beta-peptide; subunit-containing molecular associate; gene therapy;
XX neurodegenerative disorder; amyloidogenic disorder; Alzheimer's disease;
XX Huntington's disease; Parkinson's disease; type II diabetes mellitus;
XX transmissible spongiform encephalopathy; muscular dystrophy;
XX virus-like protein shell.

XX Homo sapiens.

PN MO200132694-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-EP010877.

PR 03-NOV-1999; 99DE-01052955.

PA (ACGT-) ACGT PROGENOMICS AG.

PI Boehm G, Schmidt U;

DR MPI; 2001-316418/33.

XX Characterizing molecular associates of subunits, useful e.g. for
XX diagnosis of neurodegenerative diseases, by fluorescence-activated cell
XX sorting of associates containing labeled subunits.

PS Disclosure; Page 45; 45pp; German.

CC This invention describes a novel method for characterizing subunit (SU)-
CC containing molecular associates (A) by: (i) labeling non-associated SU
CC with a fluorescent dye (I); (ii) contacting labeled SU, with each other
CC or with unlabeled SU or with (A), so that labeled (A) are formed by
CC attachment of labeled SU; (iii) characterizing the labeled (A) by
CC fluorescence-activated cell sorting (FACS); and (iv) optionally
CC separating (A) by known methods. The method is used to characterize (and
CC optionally separate) (A): (i) associated with a wide range of
CC neurodegenerative or other amyloidogenic disorders, e.g. Alzheimer's,
CC Huntington's or Parkinson's diseases, transmissible spongiform
CC encephalopathies, type II diabetes mellitus and muscular dystrophy, for
CC diagnosis and prediction of such diseases; or (ii) produced during
CC recombinant protein production (inclusion bodies). It may also be used to
CC detect homologous subunits and for measuring kinetics of
CC aggregate/associate formation. A particular application is determining
CC the packaging efficiency of virus-like protein shells for therapeutic
CC proteins and nucleic acid, for use as gene therapy vectors. Separated (A)
CC are useful experimentally, e.g. in cell cultures or animal models. The
CC method has high specificity and sensitivity for detection/quantification
CC of disease-related associates, and can provide an unequivocal diagnosis,
CC at an early stage to allow treatment to start before symptoms are
CC evident. Fluorescence-activated cell sorting (FACS) is a standardizable
CC and generally applicable method, suitable for automation and high
CC throughput screening. This sequence represents the human Alzheimer's
CC disease associated beta-peptide (1-42) which is used to illustrate the
CC method of the invention

XX Sequence 42 AA;

Query Match 100.0%; Score 155; DB 4; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 32
12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

DB 12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

RESULT 26
AAB35589
ID AAB35589 standard; peptide; 42 AA.
XX
AC AAB35589;
XX
DT 15-FEB-2001 (first entry)
XX
DE Beta/A4-amyloid peptide.
XX
KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
XX
OS Unidentified.
XX
PN US6136548-A.
XX
PD 24-OCT-2000.
XX
PF 02-SEP-1999; 99US-00388890.
XX
PR 22-NOV-1994; 94US-00347144.
PR 22-NOV-1995; 95WO-US015007.
PR 26-JUL-1996; 96US-00686599.
XX
PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Anderson S;
XX
DR WPI; 2001-030939/04.
XX
PT Identifying mutant tissue-type plasminogen activator (t-PA) for improving
PT thrombolytic therapy or treating vascular hemorrhaging, by determining
PT whether t-PA binds to fibrin but not to a beta amyloid peptide.
XX
PS Disclosure; Col 10; 23pp; English.
XX
CC The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 32
12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

DB 12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

RESULT 27
AAB49098
ID AAB49098 standard; peptide; 42 AA.
XX
AC AAB49098;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human amyloid beta peptide A-beta 42, SEQ ID NO:1.

XX
KW Amyloid disease; amyloid fibril deposition; amyloid plaque; immunogenic;
KW antibody; vaccine; Alzheimer's disease; type 2 diabetes;
KW reactive system amyloidosis; systemic senile amyloidosis;
KW familial amyloid cardiomyopathy; transmissible spongiform encephalopathy;
KW Creutzfeld-Jakob disease; Kuru;
KW haemodialysis-associated beta-2-microglobulin deposition;
KW amyloid beta peptide; A-beta 42.
XX
OS Homo sapiens.
XX
PN WO200072876-A2.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US015239.
XX
PR 01-JUN-1999; 99US-0137010P.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB;
XX
DR WPI; 2001-070921/08.
XX
PT Pharmaceutical composition comprising immunogen against amyloid component
PT such as fibril peptide or protein, or antibody against amyloid component
PT useful for treating amyloid diseases or amyloidoses.
XX
PS Disclosure; Page 24; 140pp; English.
XX
CC The invention relates to a novel pharmaceutical composition for
CC preventing or treating a disease characterised by amyloid fibril deposits
CC (amyloid plaques) in a patient. The pharmaceutical composition comprises
CC an agent that will induce an immune response against an amyloid
CC component, or an antibody or antibody fragment that binds to an amyloid
CC component. The invention also relates to a method for determining the
CC prognosis of a patient undergoing treatment for an amyloid disorder which
CC involves measuring a patient serum amount of immunoreactivity against a
CC selected amyloid component. A patient serum immunoreactivity of at least
CC four times a base line serum immunoreactivity control level indicates a
CC prognosis of improved status with respect to the disorder. The
CC pharmaceutical compositions of the invention are useful for treating a
CC wide variety of disorders characterised by amyloid fibril deposition in a
CC patient. Such disorders include Alzheimer's disease characterised by
CC amyloid beta peptide fibril deposits, type 2 diabetes characterised by
CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
CC amyloidosis associated with systemic inflammatory diseases (e.g. '
CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
CC fibrils derived from transthyretin (TTR); transmissible spongiform
CC encephalopathies (e.g. Creutzfeld-Jakob disease, Kuru) characterised by
CC prion protein deposits; and beta-2-microglobulin deposits which form as a
CC result of long term haemodialysis treatment. The present sequence
CC represents human amyloid beta peptide A-beta 42
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 32
12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

DB 12 VHHQKLVFPADVGNKGAIIIGLMVGAVIA 42

RESULT 28
AAB84427
ID AAB84427 standard; peptide; 42 AA.
XX
AC AAB84427;

XX 22-AUG-2001 (first entry)
DT Partial sequence of a human beta-amyloid precursor protein.
XX
XX
DE Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
KM vaccine.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 1
FT /note= "L-Asp, D-Asp or L-Iso-Asp"
XX
XX WO200142306-A2.
XX
XX 14-JUN-2001.
PD
XX 08-DEC-2000; 2000WO-US033203.
PF
XX 08-DEC-1999; 99US-0169687P.
PR
XX (MIND-) BIOPHARMACEUTICALS USA INC.
PA
XX Chain B:
PI
XX WPI; 2001-381648/40.
DR
XX Novel chimeric peptide containing N- or C-terminal end-specific B cell
PT epitope from naturally occurring internal peptide cleavage product (such
PT as beta amyloid peptide) of a precursor protein, joined to T cell
PT epitope.
XX
XX Claim 3; Page 42; 47pp; English.
PS
XX The present sequence represents a partial sequence of a human beta-
CC amyloid precursor protein (APP). The peptide is used to create chimeric
CC peptides of the invention. The chimeric peptides contain a N- or C-
CC terminal end-specific B cell epitope from a naturally occurring internal
CC peptide cleavage product of a precursor or mature protein, as a free N-
CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
CC reduce or prevent the accumulation of amyloid beta peptide in the
CC extracellular space, interstitial fluid and cerebrospinal fluid of the
CC brain, and aggregation into senile amyloid deposits or plaques. They also
CC block the interaction of amyloid beta peptides with other molecules that
CC contribute to the neurotoxicity of amyloid beta. The chimeric peptides are
CC useful for immunizing humans against the free N- or C-terminus of an
CC internal self peptide cleavage product (e.g. APP peptide) derived from a
CC precursor protein or a mature protein. The internal peptide cleavage
CC product is the self molecule of the mammal
XX
SQ Sequence 42 AA;
XX
XX Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 29
AAB48497
ID AAB48497 standard; protein; 42 AA.
XX
XX AAB48497;
AC
XX 02-MAR-2001 (first entry)
DT
XX Human amyloid protein.
DE
XX

KM Neurotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KM Alzheimer's disease; human; amyloid protein.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200068263-A2.
PN
XX 16-NOV-2000.
PD
XX
XX 04-MAY-2000; 2000WO-CA000515.
PF
XX
XX 05-MAY-1999; 99US-0132592P.
PR
XX (NEUR-) NEUROCHEM INC.
PA
XX
XX Chalfour R, Gervais F, Gupta A;
PI
XX WPI; 2001-031852/04.
DR
XX
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
XX Disclosure; Fig 1; 46pp; English.
PS
XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein (the present sequence)
XX
XX
SQ Sequence 42 AA;
XX
XX Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 30
AAB91779
ID AAB91779 standard; peptide; 42 AA.
XX
XX AAB91779;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:955.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US013576.
PF
XX
XX 17-MAY-1999; 99US-0134406P.
PR
XX 10-SEP-1999; 99US-0153406P.
PR
XX 15-OCT-1999; 99US-0159783P.
PA
XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX

PS Disclosure; Page 506; 733pp; English.

XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases.
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 42 AA;

Query Match 100.0%; Score 155; DB 4; Length 42;

Best Local Similarity 100.0%; Pred No. 1,3e-16;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPFADVGSNKGAIIGLMVGVYIA 32
 |||||
 Db 12 VHHQKLVFPFADVGSNKGAIIGLMVGVYIA 42

Search completed: September 28, 2006, 06:10:41
 Job time : 91.5247 secs

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OM protein - protein.search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 13.2018 Seconds
(without alignments)
233.221 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
Sequence: 1 XVHQKLVFPAEDVGNKGAITGLMWGVVIA 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	155	100.0	42	2 PN0512	beta-amyloid prote
2	155	100.0	57	2 A60045	Alzheimer's diseas
3	155	100.0	57	2 F60045	Alzheimer's diseas
4	155	100.0	57	2 D60045	Alzheimer's diseas
5	155	100.0	57	2 E60045	Alzheimer's diseas
6	155	100.0	57	2 G60045	Alzheimer's diseas
7	155	100.0	57	2 B60045	Alzheimer's diseas
8	155	100.0	82	2 P00438	Alzheimer's diseas
9	155	100.0	695	1 A49795	Alzheimer's diseas
10	155	100.0	770	1 QRH044	Alzheimer's diseas
11	151	97.4	747	2 JH0773	Alzheimer's diseas
12	147	94.8	695	2 A27485	Alzheimer's diseas
13	147	94.8	695	2 S00550	Alzheimer's diseas
14	82	52.9	33	2 S23094	beta-amyloid prote
15	60	38.1	755	2 A13228	tryptophan 2-mono
16	59	38.1	755	1 QOAG4T	tryptophan 2-mono
17	58	37.4	755	1 DAAGWT	general amino acid
18	57	36.8	503	2 S73843	phospholipase D [i
19	54.5	35.2	832	2 H84848	na+/h+ antiporter
20	53	34.2	390	2 C75103	Na+/H+ antiporter
21	53	34.2	763	2 A13443	conserved hypochet
22	52	33.5	527	2 T18232	3-methyl-2-oxobuta
23	52	33.5	678	2 G71526	conserved hypochet
24	52	33.5	678	2 C81683	conserved hypochet
25	52	33.5	738	2 C95936	probable xanthine
26	51.5	33.2	1364	2 T51920	sugr protein - Del
27	51	32.9	103	2 D75449	probable dimethyl
28	51	32.9	257	2 AC1024	probable transport
29	51	32.9	611	2 S19434	

30	50.5	32.6	245	2 AH1098	a probable phospho
31	50.5	32.6	245	2 AG1461	probable phospho-b
32	50.5	32.6	833	2 T01547	probable phosphol
33	50	32.3	234	2 G95989	hypothetical glyci
34	50	32.3	296	2 A69856	polysugar degradin
35	50	32.3	390	2 H71083	probable Na+/H+-ex
36	50	32.3	487	2 T49424	hypothetical prote
37	50	32.3	1286	2 T49424	probable ABC trans
38	50	32.3	1286	2 T49424	P-glycoprotein hom
39	49.5	31.9	1292	2 T48007	hypothetical prote
40	49	31.6	316	2 G86324	hypothetical prote
41	49	31.6	316	2 D97865	hypothetical prote
42	49	31.6	322	2 E71647	hypothetical prote
43	49	31.6	403	2 S61992	SLG1 protein - yea
44	49	31.6	403	2 T36019	phosphoglycerate k
45	49	31.6	469	2 C90446	permease, multidr
46	49	31.6	649	2 S58064	hdc protein - fru
47	48.5	31.3	674	2 S39476	kinase-like transm
48	48.5	31.3	144	2 AC2572	hypothetical prote
49	48	31.0	337	2 E95288	aromatic amino aci
50	48	31.0	337	2 E95288	membrane zinc-bind
51	48	31.0	409	2 S29124	hypothetical prote
52	48	31.0	415	2 G72335	hypothetical prote
53	48	31.0	523	2 UC7556	linoleoyl-CoA des
54	48	31.0	656	2 B86289	probable serine/th
55	48	31.0	701	2 S64599	probable membrane
56	47.5	30.6	159	2 D86278	hypothetical prote
57	47	30.3	159	2 D86278	sigma-E factor reg
58	47	30.3	139	2 P50133	H-2 class I histoc
59	47	30.3	119	2 C70027	multidrug-efflux t
60	47	30.3	135	2 G87686	hypothetical prote
61	47	30.3	249	2 A61087	myelin P0 glycopro
62	47	30.3	303	2 D69114	conserved hypochet
63	47	30.3	314	2 F66805	cation transporter
64	47	30.3	330	2 AD0305	probable sugar tra
65	47	30.3	406	2 T23496	hypothetical prote
66	47	30.3	492	1 E69114	lumarate reductase
67	47	30.3	543	2 B97092	ABC-type transport
68	47	30.3	771	2 AB2160	hypothetical prote
69	47	30.3	1278	2 E86155	probable ABC trans
70	46.5	30.0	1362	2 T41534	leptomycin B resis
71	46.5	30.0	159	2 B85903	sigma-E factor, ne
72	46.5	30.0	159	2 D91058	sigma-E factor reg
73	46.5	30.0	375	2 A49336	hemolysin B1 precu
74	46.5	30.0	464	2 D71219	probable L-asparta
75	46.5	30.0	510	1 A35251	histidine ammonia-
76	46.5	30.0	681	2 T23811	hypothetical prote
77	46.5	30.0	1014	2 T17275	hypothetical prote
78	46.5	30.0	1035	2 T42093	phospholipase D (E
79	46.5	30.0	1036	2 T18530	phospholipase D (E
80	46.5	30.0	1074	2 T17203	phospholipase (EC
81	46.5	30.0	1215	2 S50428	probable Ca2+-tran
82	46	29.7	223	2 T21437	hypothetical prote
83	46	29.7	254	2 F90107	60S ribosomal prot
84	46	29.7	317	2 G64408	hypothetical prote
85	46	29.7	322	1 JQ1028	6-phosphofructokin
86	46	29.7	331	2 A71365	probable Lambda CI
87	46	29.7	417	2 F97789	ampc protein limo
88	46	29.7	446	2 B63744	sucrose phosphotra
89	46	29.7	448	2 T41145	probable amine tra
90	46	29.7	471	2 B90269	multidrug resistan
91	46	29.7	585	2 H83199	phosphotransferase
92	46	29.7	609	2 H82039	GRP-binding protei
93	46	29.7	678	2 C86495	hypothetical prote
94	46	29.7	678	2 H72128	3-methyl-2-oxobuta
95	46	29.7	769	1 UC1121	leukocyte adhesion
96	46	29.7	821	2 A49881	beta-glucosidase (
97	46	29.7	827	1 S66094	stage II sporulati
98	46	29.7	976	2 B84659	probable receptor-
99	45.5	29.4	3519	2 S43048	polyketide synthas
100	45.5	29.4	288	2 AC2654	proteinas
			289	2 C97436	probable proteins

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PN0512
R:Shimomura, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A:Reference number: PN0512; MUID:93290653; PMID:7685598
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <J0H>
A:Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031558
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid

Query Match

Best Local Similarity 100.0%; Score 155; DB 2; Length 42;
Pred. No. 9.1e-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
17 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

DB

RESULT 2

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <J0H>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 155; DB 2; Length 57;
Pred. No. 1.3e-14;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
17 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 47

DB

RESULT 3

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <J0H>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIRN:CAA39592.1; PID:
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 155; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
17 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 47

DB

RESULT 4

D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <J0H>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 155; DB 2; Length 57;
Pred. No. 1.3e-14;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
17 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 47

DB

RESULT 5

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <J0H>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 155; DB 2; Length 57;
Pred. No. 1.3e-14;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
17 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 47

DB

RESULT 6

G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <J0H>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 155; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 17 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 47

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #ext_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:92165; PIDN:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 155; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 17 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 47

RESULT 8
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #ext_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, U.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: P00438; MUID:93075180; PMID:1445331
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 155; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 28 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 58

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: UNIPARC:UPI00002A2F2; GB:M58727; NID:9342062; PIDN:AAA36829.1; PID
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 155; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 608 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 10
Q8RUH4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhib;
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #ext_change 15-Sep-2000
C:Accession: S02260; S05194; A33260; A35486; I39452; I39453; I59562; A4
4668; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252; S
R:Lemaire, H.G.; Salbaum, J.M.; Mulhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Be
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: UNIPARC:UPI00016A5FC; EMBL:X13466; NID:935598; PIDN:CAA31830.1; PII
A:Note: alternative splice form APP(695)
R:Li, F.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similar
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:9178863; PIDN:AAA51768.1; PID
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Cross-references: UNIPARC:UPI0000148176
A>Note: 693-Gln was found in DNA isolated from HCHNA-D patients
R.Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: UNIPARC:UPI00000202B1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, QMLMPVLPAPMEAKYGR, <YOS2>
A:Cross-references: UNIPARC:UPI00001654Y; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:
R.Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A>Note: revised physical map for reference I39451
R.Levy, E.; Carman, M.D.; Fernandez-Madrid, I.U.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260603; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AAA51727.1; PID:
A>Note: a mutation with 693-Gln is presented
R.Murrell, U.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: UNIPARC:UPI00001177EA; GB:S57665; NID:G236720; PIDN:AAB3991.1; PID:
R.Kamino, K.; Orr, H.T.; Payami, H.; Wjisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, R.
Arakis, S.E.; Kornberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, A.M.
Hum. Gene. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <RAM1>
A:Cross-references: UNIPARC:UPI00001177EB; GB:S45135; NID:G257377; PIDN:AAB3645.1; PID:
A:Experimental source: Familial Alzheimer disease family SB
A>Note: sequence extracted from NCBI backbone (NCBIF:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:G257379; PIDN:AAB3646.1; PID:
A:Experimental source: Familial Alzheimer disease family LT
A>Note: sequence extracted from NCBI backbone (NCBIF:115376)
A>Note: this sequence has a silent mutation
R.Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1997
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfaced
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:
A>Note: alternative splice form AP(695)
R.Robkiss, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030, MUID:87231971, PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <RDB>
A:Cross-references: UNIPARC:UPI000016A55; GB:M16765; NID:G178539; PIDN:AA51722.1; PID:
A:Note: The authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:G178706; PIDN:AAA5540.1; PID
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:G177957; PIDN:AA51564.1; PID
R:Dyck, T.; Wiedemann, A.; Multhaup, G.; Salbaum, J.M.; Lemstra, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
A:Cross-references: UNIPARC:UPI0000035AB0
R:Tanzi, R.E.; McClatchey, A.I.; Lampertl, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 311, 528-530, 1988
A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: UNIPARC:UPI0000121B0; EMBL:X06582; NID:G28817; PIDN:CAA30042.1; PIL
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Demilte, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 311, 525-527, 1988
A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: UNIPARC:UPI000002A26; GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA3
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 311, 530-532, 1988
A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashcor
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three i
A:Reference number: A30320
A:Accession: A30320
A:Molecule type: mRNA
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: B30320
A:Molecule type: mRNA
A>Status: not compared with conceptual translation

A:Residues: 122-288, 'V', 365-770 <VRT2>
A:Cross-references: UNIPARC:UPI0000174094
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VRT3>
A:Cross-references: UNIPARC:UPI0000174094
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

Query Match 100.0%; Score 155; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 683 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 713

RESULT 11
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid beta proteinase inhibitor homology <BPI>
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 97.4%; Score 151; DB 2; Length 747;
Best Local Similarity 96.8%; Pred. No. 6.9e-13;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 660 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 690

RESULT 12
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochem. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA

A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: UNIPARC:UPI0000003B7; GB:D10603; NID:g220328; PIDN:BA01456.1; PID:
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 94.8%; Score 147; DB 2; Length 695;
Best Local Similarity 96.8%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 608 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 13
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hlilich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2PB; EMBL:X07648; NID:g55616; PID:
R:Schubert, D.; Schroeder, R.; Lacotiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2966652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Cross-references: UNIPARC:UPI00001777FD
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Pompaska, A.; Styles, J.; Mentha, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Cross-references: UNIPARC:UPI00001777FE
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is c
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 94.8%; Score 147; DB 2; Length 695;
Best Local Similarity 96.8%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
 Db 608 VRHOKLVFAEDVGSNKGAIIGLMVGVVIA 638

RESULT 14

S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Otori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A:Reference number: S23094; MUID:92316198; PMID:1618299
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 A:Cross-references: UNIPARC:UPI00001777FB
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 52.9%; Score 82; DB 2; Length 33;
 Best Local Similarity 94.1%; Pred. No. 8.8e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VHHOKLVFAEDVGSNK 18
 Db 17 VRHOKLVFAEDVGSNK 33

RESULT 15

A13228
 tryptophan 2-monooxygenase tms1 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
 C:Accession: A13228
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyav, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: A13228
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-755 <KUR>
 A:Cross-references: UNIPROT:O8U6A3; UNIPARC:UPI00000D274E; GB:AE008690; PIDN:AAL46247.1;
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: tms1
 A:Genome: plasmid
 C:Superfamily: tryptophan 2-monooxygenase

Query Match 38.7%; Score 60; DB 2; Length 755;
 Best Local Similarity 48.1%; Pred. No. 2.7;
 Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 KLVFAEDVGSNKGAIIGLMVGVVIA 32
 Db 226 RIGFFEDVPRKVAIVIGAGISGLVVA 252

RESULT 16

OAG4T
 tryptophan 2-monooxygenase (EC 1.13.12.3) - Agrobacterium tumefaciens plasmids pTiAch5,
 C:Species: Agrobacterium tumefaciens
 C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 05-Oct-2004
 C:Accession: A04497; S28687; A20966
 R:Giesen, U.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, M.;
 EMBO J. 3, 835-846, 1984

A:Title: The complete nucleotide sequence of the T1-DNA of the Agrobacterium tumefaciens
 A:Reference number: A01001; MUID:84207942; PMID:6327292

A:Accession: A04497
 A:Molecule type: DNA
 A:Residues: 1-755 <GIB>
 A:Cross-references: UNIPROT:P04029; UNIPARC:UPI00001372AD
 A:Genetics: G1
 R:Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
 Plant Mol. Biol. 2, 335-350, 1983

A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
 A:Reference number: S28683

A:Accession: S28687
 A:Status: translation not shown

A:Molecule type: DNA
 A:Residues: 1-362, 'H', 364-596, 'S', 598-717, 'IO', 720, 'A', 722-755 <BAR>

A:Cross-references: UNIPARC:UPI00000B759D; EMBL:X00493; NID:g939062; PIDN:CAA25167.1; PID

A:Experimental source: strain octopine

A:Genetics: G2
 R:Klee, H.; Montoya, A.; Horodyaki, F.; Lichtenstein, C.; Garfinkel, D.; Fuller, S.; Flo
 proc. Natl. Acad. Sci. U.S.A. 81, 1728-1732, 1984

A:Title: Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti plasmid: two ge
 A:Reference number: A20966; MUID:84170374; PMID:6584906

A:Accession: A20966
 A:Molecule type: DNA

A:Residues: 1-717, 'IO', 720, 'A', 722-755 <KLE>
 A:Cross-references: UNIPARC:UPI0000170D07; GB:K02554; NID:g154747; PIDN:AAA92550.1; PID

A:Experimental source: strain octopine

A:Genetics: G3

C:Genetics: <G1>
 A:Genome: plasmid

C:Genetics: <G2>
 A:Genome: plasmid

A:Note: plasmid pTi15955
 C:Genetics: <G3>

A:Gene: tms1

A:Genome: plasmid

C:Function:
 A:Note: plasmid pTiA6NC

A:Pathway: tryptophan metabolism; auxin biosynthesis
 A:Note: catalyzes the first step in the biosynthesis of auxins from tryptophan

C:Superfamily: tryptophan 2-monooxygenase
 C:Keywords: monooxygenase; oxidoreductase

Query Match 38.1%; Score 59; DB 1; Length 755;
 Best Local Similarity 44.4%; Pred. No. 3.7;
 Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 6 KLVFAEDVGSNKGAIIGLMVGVVIA 32
 Db 226 RIGFFEDVPRKVAIVIGAGISGLVVA 252

RESULT 17

DAGMT
 tryptophan 2-monooxygenase (EC 1.13.12.3) TA - Agrobacterium tumefaciens plasmid pTiTm4
 C:Species: Agrobacterium tumefaciens
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
 C:Accession: S15002; S15450
 R:Bonnard, G.; Vincent, F.; Otten, L.
 Plant Mol. Biol. 16, 733-738, 1991
 A:Title: Sequence of Agrobacterium tumefaciens bioType III auxin genes.
 A:Reference number: S15001; MUID:91329707; PMID:1868204
 A:Accession: S15002
 A:Molecule type: DNA
 A:Residues: 1-755 <BO2>
 A:Cross-references: UNIPARC:UPI00001372B1; EMBL:X56185; NID:g39133; PIDN:CAA39646.1; PID
 A:Experimental source: strain Tm4; strain octopine
 C:Genetics:
 A:Gene: taam
 A:Genome: plasmid pTiTm4
 C:Function:
 A:Pathway: tryptophan metabolism; auxin biosynthesis

A>Note: catalyzes the first step in the biosynthesis of auxins from tryptophan
C:Superfamily: tryptophan 2-monooxygenase
C:Keywords: monooxygenase; oxidoreductase

Query Match 37.4%; Score 58; DB 1; Length 755;
Best Local Similarity 44.4%; Pred. No. 5.1;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 6 KLVFPAEDVGSNGKATIGLWGVVIA 32
DB 226 RIGFPEEDVPRKAVIIGAGISGLVVA 252

RESULT 18

S7843
general amino acid permease GAP1 homolog F10_orf503 - Mycoplasma pneumoniae (strain ATCC
N/A16ternate names: hypothetical protein F10_orf503
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S7843
R:Himmelfrich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633

A:Accession: S7843

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-503 <HIM>

A:Cross-references: UNIPROT:P75462; UNIPARC:UPI0000139481; EMBL:AE000051; GB:U00089; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: gap1

A:Genetic code: SGC3

Query Match 36.8%; Score 57; DB 2; Length 503;
Best Local Similarity 61.1%; Pred. No. 4.6;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 VGSNGKATIGLWGVVIA 31
DB 131 VKDNGALIGLWGVFL 148

RESULT 19

H84848

phospholipase D [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-May-2004

C:Accession: H84848

R:Julin, K.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84848

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-832 <STO>

A:Cross-references: UNIPARC:UPI000004863E; GB:AE002093; NID:G1871182; PIDN:AA63542.1; C

C:Genetics:

A:Gene: Atg942010

A:Map position: 2

C:Superfamily: phospholipase D, plant type

Query Match 35.2%; Score 54.5; DB 2; Length 832;
Best Local Similarity 48.1%; Pred. No. 17;

Matches 13; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 3 HHOKLVFPAEDVGSNGKATIGLWGVV 29
DB 344 HHOKNIVDADAGNRKRITA-FVGG 369

RESULT 20

C75103

Na+/H+ antiporter (napa-4) PAB0809 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: C75103

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A:Reference number: A75001

A:Accession: C75103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-330 <RAW>

A:Cross-references: UNIPROT:Q9U2D1; UNIPARC:UPI0000034520; GB:AJ248286; GB:AL096836; NID

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: napa-4; PAB0809

C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napa1

Query Match 34.2%; Score 53; DB 2; Length 390;
Best Local Similarity 46.2%; Pred. No. 13;

Matches 12; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 7 LVFPAEDVGSNGKATIGLWGVVIA 32
DB 225 LVFPAEDVGSNGKATIGLWGVVIA 248

RESULT 21

A13443

Na+/H+ antiporter 1 / protease IV (EC 3.4.-.-) [imported] - Brucella melitensis (stra

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A13443

R:Belvecchio, V.G.; Kapratel, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella meliten

A:Reference number: AD3252; PMID:11756688

A:Accession: A13443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-763 <KUR>

A:Cross-references: UNIPROT:Q8YF15; UNIPARC:UPI00000580B5; GB:AE008917; PIDN:AAU52716.1

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11535

A:Map position: I

C:Superfamily: Na(+)/H(+) antiporter 1/protease IV-related

C:Keywords: hydrolase

Query Match 34.2%; Score 53; DB 2; Length 763;
Best Local Similarity 50.0%; Pred. No. 26;

Matches 15; Conservative 4; Mismatches 9; Indels 2; Gaps 2;

QY 4 HOKLVFPAEDVGSNGKATIGLWGVVIA 32
DB 562 HOKLVFPAEDVGSNGKATIGLWGVVIA 590

RESULT 22

T18232

conserved hypothetical protein - yeast (Candida albicans)

C:Species: Candida albicans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18232

R:Barrell, B.G.; Ralband, M.A.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z18831

A:Accession: T18232

RESULT 27

D75449

sugE protein - *Deinococcus radiodurans* (strain R1)C:Species: *Deinococcus radiodurans*

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: D75449

R:White, O.; Eiken, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: D75449

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-103 <WHI>

A/Cross-references: UNIPROT:Q9RW3; UNIPARC:UPI00000D3DA8; GB:AE001952; GB:AE000513; NID

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR1004

A/Map position: 1

C/Superfamily: sugE protein

Query Match 32.9%; Score 51; DB 2; Length 103;

Best Local Similarity 39.1%; Pred. No. 5.7;

Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 8 VFPAEDVGSNKGAIIIGLWGVV 30

Db 75 VFEGQLGRKLLALVWVAAL 97

RESULT 28

AC1024

probable dimethyl sulfoxide reductase chain C dmsC [imported] - *Salmonella enterica* subsp.C:Species: *Salmonella enterica* subsp. *enterica* serovar TyphiA/Note: this species has also been called *Salmonella typhi*

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AC1024

R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Mole, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AC1024

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-257 <PAR>

A/Cross-references: UNIPARC:UPI000005A877; GB:AL513382; PIDN:CAD09292.1; PID:gl6505294;

C/Genetics:

A/Gene: dmsC

C/Superfamily: probable dimethylsulfoxide reductase chain C

Query Match 32.9%; Score 51; DB 2; Length 257;

Best Local Similarity 41.4%; Pred. No. 15;

Matches 12; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 2 VHHQKLVFPAEDVGSNKGAIIIGLWGVV 30

Db 1 MHHLPVFFVTFTQSAVGAFFILLIGAM 29

RESULT 29

S19434

probable transport protein YCR023c - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein YCR241

C:Species: *Saccharomyces cerevisiae*

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C/Accession: S19434; S22273

R:Berben, G.; Bolle, P.A.; Gilliquet, V.; Hilger, F.
submitted to the Protein Sequence Database, March 1992

A/Reference number: S19433

A/Accession: S19434

A/Molecule type: DNA

A/Residues: 1-611 <BER>

A/Cross-references: UNIPROT:P25351; UNIPARC:UPI000013A706; EMBL:X59720; NID:91907116; P

R:Bolle, P.A.; Gilliquet, V.; Berben, G.; Dumont, J.; Hilger, F.

Yeast 8, 205-213, 1992

A>Title: The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chrom

A/Reference number: S22273; MUID:92245758; PMID:1574926

A/Accession: S22273

A>Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-611 <BOL>

A/Cross-references: UNIPARC:UPI000013A706; GB:X59720; GB:S43845; GB:S49180; GB:S58084;

C/Genetics:

A/Cross-references: SGD:S0000617

A/Map position: 3R

C/Keywords: transmembrane protein

F:18-34/Domain: transmembrane #status predicted <TM1>

F:89-109/Domain: transmembrane #status predicted <TM2>

F:116-132/Domain: transmembrane #status predicted <TM3>

F:155-173/Domain: transmembrane #status predicted <TM4>

F:202-221/Domain: transmembrane #status predicted <TM5>

F:354-371/Domain: transmembrane #status predicted <TM6>

F:412-438/Domain: transmembrane #status predicted <TM7>

F:447-464/Domain: transmembrane #status predicted <TM8>

F:475-491/Domain: transmembrane #status predicted <TM9>

F:543-559/Domain: transmembrane #status predicted <TM10>

Query Match 32.9%; Score 51; DB 2; Length 611;

Best Local Similarity 35.7%; Pred. No. 38;

Matches 10; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 4 HQKLVFPAEDVGSNKGAIIIGLWGVV 31

Db 145 HQALAFSTWPLIFQGAIVGPMIGFLV 172

RESULT 30

AH1098

a probable phospho-beta-glucosidase homolog lmo0191 [imported] - *Listeria monocytogenes*C:Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AH1098

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A>Title: Comparative genomics of *Listeria species*.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AH1098

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-245 <GLA>

A/Cross-references: UNIPROT:Q8YAE0; UNIPARC:UPI0000055789; GB:NC_003210; PIDN:CAC98406.1

A/Experimental source: strain EGD-e

C/Genetics:

A/Gene: lmo0191

C/Superfamily: cellobiose phosphotransferase system celC

Query Match 32.6%; Score 50.5; DB 2; Length 245;

Best Local Similarity 39.3%; Pred. No. 17;

Matches 11; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 6 KLVFPAEDVGSNKGAIIIGLWGVV 30

Db 2 KLIFFNADFGISPGAVYGLBSYKRGV 29

Thu Sep 28 14:21:13 2006

us-09-731-899-6.rpr

Page 10

Search completed: September 28, 2006, 06:24:29
Job time : 16.2018 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:51; Search time 104.179 Seconds
(without alignments)
284.130 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
Sequence: 1 XVHQKLVFADVGSKNGALIGLVGVVIA 32

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	42	056J06_GRAGR	056J06 girampus gri
2	155	100.0	42	056J07_TURTR	056J07 turrops tr
3	155	100.0	42	07M088_CAYPO	07M088 cavia porce
4	155	100.0	52	08W299_HUMAN	08W299 homo sapien
5	155	100.0	57	A4_URSA	029149 u amyloid b
6	155	100.0	58	A4_CANPA	028280 c amyloid b
7	155	100.0	58	A4_PABIT	028748 o amyloid b
8	155	100.0	58	A4_GHEBP	028757 o amyloid b
9	155	100.0	59	A4_BOVIN	028053 b amyloid b
10	155	100.0	113	08DH58_CHESE	08J158 chelydra se
11	155	100.0	534	093296_CHICK	093296 gallus gall
12	155	100.0	569	09PVL1_CHICK	09PVL1 gallus gall
13	155	100.0	695	02X0A0_PIG	02X0A0 sus scrofa
14	155	100.0	695	056JK3_CANPA	056JK3 canis fami
15	155	100.0	695	05R477_PONPY	05R477 pongo pygma
16	155	100.0	695	06RH29_CANPA	06RH29 canis fami
17	155	100.0	695	09DGJ8_CHICK	09DGJ8 gallus gall
18	155	100.0	714	056JK4_CANPA	056JK4 canis fami
19	155	100.0	749	056JK2_STECO	056JK2 stenella co
20	155	100.0	751	A4_SAISC	095241 s amyloid b
21	155	100.0	751	06GSC0_HUMAN	06GSC0 homo sapien
22	155	100.0	751	04R4R8_MACPA	04R4R8 macaca fasc
23	155	100.0	751	056JK5_CANPA	056JK5 canis fami
24	155	100.0	751	06RH28_CANPA	06RH28 canis fami
25	155	100.0	751	02X099_PIG	02X099 sus scrofa
26	155	100.0	751	09DGJ7_CHICK	09DGJ7 gallus gall
27	155	100.0	754	04R733_TETNG	04R733 tetraodon n
28	155	100.0	770	A4_CAVPO	060495 c amyloid b
29	155	100.0	770	A4_HUMAN	050507 h amyloid b
30	155	100.0	770	A4_MACPA	P53601 m amyloid b
31	155	100.0	770	A4_PANTR	051680 p amyloid b

32	155	100.0	770	1	A4_PIG	P79307 s amyloid b
33	155	100.0	770	2	056JK6_CANPA	056JK6 canis fami
34	155	100.0	770	2	06RH30_CANPA	06RH30 canis fami
35	155	100.0	780	1	A4_TETFL	073683 tetraodon f
36	151	97.4	693	2	09SGG0_XENTLA	09SGG0 xenopus lae
37	151	97.4	747	2	091963_PPIPT	091963 xenopus lae
38	151	97.4	749	2	06NRRI_XENTLA	06NRRI xenopus lae
39	151	97.4	750	2	06RDB6_XENTLA	06RDB6 xenopus tro
40	148	95.5	695	2	07ZXO0_XENTLA	07ZXO0 xenopus lae
41	148	95.5	695	2	0988F9_XENTLA	0988F9 xenopus lae
42	147	94.8	79	2	035463_CRICR	035463 cricetus
43	147	94.8	218	2	08BPV5_MOUSE	08BPV5 mus musculu
44	147	94.8	384	2	08BPV7_MOUSE	08BPV7 mus musculu
45	147	94.8	695	2	06GR78_MOUSE	06GR78 mus musculu
46	147	94.8	733	2	06P605_RAT	06P605 rattus norv
47	147	94.8	752	2	03TWP3_MOUSE	03TWP3 mus musculu
48	147	94.8	752	2	03TXI9_MOUSE	03TXI9 mus musculu
49	147	94.8	770	1	A4_MOUSE	P12023 m amyloid b
50	147	94.8	770	1	A4_RAT	P08592 r amyloid b
51	147	94.8	770	2	0532T3_MOUSE	0532T3 mus musculu
52	147	94.8	770	2	0547B7_RAT	0547B7 rattus norv
53	146	94.2	699	2	057394_NARJA	057394 narke japon
54	146	94.2	737	1	A4_FUGRU	093279 fuga rubrip
55	146	94.2	759	2	04S0J4_TETNG	04S0J4 tetraodon n
56	145	93.5	64	2	03MQ25_ANTST	03MQ25 antechinus
57	143	92.3	357	2	08UUI8_BRARE	08UUI8 brachydantio
58	143	92.3	472	2	08UUS0_BRARE	08UUS0 brachydantio
59	143	92.3	612	2	0919E7_BRARE	0919E7 brachydantio
60	143	92.3	678	2	07ZZT1_BRARE	07ZZT1 brachydantio
61	143	92.3	738	2	06NUZ1_BRARE	06NUZ1 brachydantio
62	143	92.3	738	2	090W28_BRARE	090W28 brachydantio
63	121	78.1	49	2	097917_BOVIN	097917 bos taurus
64	121	78.1	49	2	02X098_PIG	02X098 sus scrofa
65	119	76.8	239	2	08UUI7_BRARE	08UUI7 brachydantio
66	119	76.8	362	2	05X1Y5_BRARE	05X1Y5 brachydantio
67	119	76.8	694	2	08UUR9_BRARE	08UUR9 brachydantio
68	114	73.5	33	2	09UCJ3_HUMAN	09UCJ3 homo sapien
69	64	41.3	328	2	09RPS4_ENTFA	09RPS4 enterococcu
70	60	38.7	755	2	09R472_PRRIZ	09R472 agrobacteri
71	60	38.7	755	2	09R694_PRRIZ	09R694 agrobacteri
72	60	38.7	755	2	09R717_PRRIZ	09R717 agrobacteri
73	60	38.7	755	2	09WMA1_PRRIZ	09WMA1 agrobacteri
74	60	38.7	755	2	08U6A3_AGR75	08U6A3 agrobacteri
75	59	38.1	755	1	TR2M_AGR74	P0A3V2 agrobacteri
76	59	38.1	755	1	TR2M_AGR75	P0A3V2 agrobacteri
77	59	38.1	755	2	044388_PRRIZ	044388 agrobacteri
78	58	37.4	252	2	06LJ99_PHRP	06LJ99 photobacter
79	58	37.4	755	1	TR2N_AGR71	P25017 agrobacteri
80	57.5	37.1	323	2	04UE56_THEAN	04UE56 thelleria a
81	57.5	37.1	405	2	04NSD6_THEPA	04NSD6 thelleria p
82	57.5	37.1	895	2	09AMB6_TYCES	09AMB6 lycopersio
83	57	36.8	368	2	08G2C8_BRUSU	08G2C8 bruceella su
84	57	36.8	503	1	Y319_MYCPN	P75462 mycoplasma
85	57	36.8	763	2	02YMB3_BRUVA	02YMB3 bruceella ab
86	56.5	36.5	327	2	06LIB3_PHRP	06LIB3 photobacter
87	56.5	36.5	845	2	0710M6_ORYSA	0710M6 oryza sativ
88	56.5	36.5	1046	2	08H093_ORYSA	08H093 oryza sativ
89	56	36.1	361	2	06BWL2_DESHA	06BWL2 deberyomyce
90	56	36.1	915	2	06FM18_CANGA	06FM18 candida gla
91	56	36.1	969	2	04C795_CROMT	04C795 crocospaer
92	55.5	35.8	904	2	08SAG7_ORYSA	08SAG7 oryza sativ
93	55.5	35.8	904	2	08H048_ORYSA	08H048 oryza sativ
94	55	35.5	344	2	041SK2_FBRAC	041SK2 ferroplasma
95	55	35.5	602	2	02SR05_MYCCA	02SR05 mycoplasma
96	54.5	35.2	324	2	05WMI6_LBEPV	05WMI6 legionella
97	54.5	35.2	324	2	05X504_LEGPA	05X504 legionella
98	54.5	35.2	322	2	05ZVBI_LEGPH	05ZVBI legionella
99	54.5	35.2	524	2	08H6B8_GOSHP	08H6B8 gossypium h
100	54.5	35.2	829	2	09XGTO_GOSHI	09XGTO gossypium h

ALIGNMENTS

```

RESULT 1
OS6J76 GRACR PRELIMINARY; PRT; 42 AA.
AC OS6J76;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83553;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
-----
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-----
DR EMBL; AY926589; AAX81918.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2
OS6J77 TURTR PRELIMINARY; PRT; 42 AA.
AC OS6J77;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE Amyloid beta protein (Fragment).
OS Turstrops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Turstrops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
-----
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-----
DR EMBL; AY926588; AAX81917.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

```

```

FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 3
ID 07M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC 07M088;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.;
RA Kamuya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
protein fragment for NK-1 substance P receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
-----
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-----
DR PIR; P05012; PNO512.
DR HSSP; Q16019; ILYT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 4
ID 08WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
AC 08WZ99;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 2.
DE Amyloid protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
 RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
 RA Nishimura H., Saito T.C., Hashimoto T., Iwatsubo T., Nakashima K.,
 RT "Novel amyloid precursor protein gene missense mutation (D678N) in
 RT probable familial Alzheimer's disease.";
 RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
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 CC
 CC EMBL; AB06441; BAB71958.2; -, mRNA.
 DR Ensembl; ENSG00000142192; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083; SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON-TER 1
 FT NON-TER 52
 SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;
 Query Match 100.0%; Score 155; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.1e-13;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGNKGAIIIGLMVGVVIA 32
 DB 12 VHHQKLVFPAEDVGNKGAIIIGLMVGVVIA 42
 RESULT 5
 A4_URSMA STANDARD; PRT; 57 AA.
 ID A4_URSMA
 AC Q29149;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) (Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)) (Fragment).
 GN Name=APP;
 OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
 OC Ursus.
 OC NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.,
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC
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 CC
 CC EMBL; X56128; CAA39593.1; -, mRNA.
 DR ETR; B60045; B60045.
 DR HSSP; P08592; INMU.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.

DR PANTHER; PTHR10083; SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR02004; BETAMYOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Amyloid; Membrane; Transmembrane.
 FT CHAIN <1
 FT CHAIN >57
 FT CHAIN <1
 FT CHAIN 5
 FT CHAIN >57
 FT CHAIN 6
 FT CHAIN >57
 FT CHAIN 6
 FT CHAIN 47
 FT CHAIN 6
 FT CHAIN 45
 FT CHAIN >57
 FT CHAIN 46
 FT CHAIN >57
 FT CHAIN 48
 FT CHAIN >57
 FT TOPO_DOM <1
 FT TRANSMEM 34
 FT NON-TER 34
 FT NON-TER 57
 FT NON-TER 1
 FT NON-TER 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;
 Query Match 100.0%; Score 155; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.3e-13;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGNKGAIIIGLMVGVVIA 32
 DB 17 VHHQKLVFPAEDVGNKGAIIIGLMVGVVIA 47
 RESULT 6
 A4_CANFA STANDARD; PRT; 58 AA.
 ID A4_CANFA
 AC Q28280;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 37.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) (Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)) (Fragment).
 GN Name=APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.,
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC
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 CC
 CC EMBL; X56125; CAA39590.1; -, mRNA.

RL	Brain Res.	Mol.	Brain Res.	10:299-305(1991).			
CC	-i-	FUNCTION:	Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).				
CC	-i-	SUBCELLULAR LOCATION:	Membrane; single-pass type I membrane protein.				
CC	-i-	SIMILARITY:	Belongs to the APP family.				
CC	-----						
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CC	-----						
DR	EMBL;	X56124;	CAA39589.1;	-; mRNA.			
DR	EMBL;	X56126;	CAA39591.1;	-; mRNA.			
DR	HSSP;	P08592;	INMJ				
DR	InterPro;	IPR008155;	A4_APP				
DR	InterPro;	IPR001255;	Beta-APP				
DR	PANTHER;	PTHR10083:SF6;	Beta-APP,	1.			
DR	Pfam;	PF03494;	Beta-APP,	1.			
DR	PRINTS;	PR00204;	BETAMAYLOID				
DR	PROSITE;	PS00319;	A4_EXTRA;	PARTIAL.			
DR	PROSITE;	PS00320;	A4_INTRA;	PARTIAL.			
KW	Amyloid;	Membrane;	Transmembrane.				
FT	CHAIN	<1	6	Soluble APP-beta (By similarity).			
FT			/Frtid=PRO_000000064.				
FT	CHAIN	7	>59	CTF-alpha (By similarity).			
FT			/Frtid=PRO_000000065.				
FT	CHAIN	7	48	Beta-amyloid protein 42 (By similarity).			
FT			/Frtid=PRO_000000066.				
FT	CHAIN	7	46	Beta-amyloid protein 40 (By similarity).			
FT			/Frtid=PRO_000000067.				
FT	CHAIN	47	>59	Gamma-CTF(59) (By similarity).			
FT			/Frtid=PRO_000000068.				
FT	CHAIN	49	>59	Gamma-CTF(57) (By similarity).			
FT			/Frtid=PRO_000000069.				
FT	TOPO_DOM	<1	34	Extracellular (Potential).			
FT	TRANSMEM	35	58	Potential.			
FT	TOPO_DOM	59	>59	Cytoplasmic (Potential).			
FT	NON_TER	1	1				
FT	NON_TER	59	59				
SQ	SEQUENCE	59 AA;	6414 MW;	F43469D488A2B12D CRC64;			
<hr/>							
Query March 100.0%; Score 155; DB 1; Length 59;							
Best local Similarity 100.0%; Pred. No.2.4e-13;							
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
OY	2	VHOKLVFFADVGSNKGAIIGLMVGCVIA	32				
DB	18	VHOKLVFFADVGSNKGAIIGLMVGCVIA	48				
<hr/>							
RESULT 10							
OQJHS8_CHESE PRELIMINARY; PRT; 113 AA.							
AC	OQJHS8;						
DT	01-OCT-2002,	integrated into UniProtKB/TrEMBL.					
DT	01-OCT-2002,	sequence version 1.					
DT	07-FEB-2006,	entry version 10.					
DE	Amyloid beta protein (Fragment).						
OS	Chalydra serpentina serpentina (common snapping turtle).						
OC	Eukaryota;	Metazoa;	Chordata;	Cranialta; Vertebrata; Euteleostomi;			
CC	Tetrapoda;	Cryptodira;	Testudinoidae;	Chelydridae;			
OX	NCBI_TaxID=134619;						
RN	[1]						
RP	NUCLEOTIDE SEQUENCE.						
RX	MEDLINE=21876906;	PubMed=11882478;					
RA	Trudeau V.L.,	Chiu S.,	Kennedy S.W.,	Brooke R.J.;			
RT	"Occyphenol (OP)	alters the expression of members of the amyloid					
RT	protein family in the hypothalamus of the snapping turtle, Chelydra	serpentina serpentina."					
RL	Environ. Health Perspect.	110:269-275(2002).					

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CC -----
DR EMBL: AF541917; AAN04908.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON TER
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4,5e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 32
DB 26 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 56

RESULT 11
ID 093296_CHICK PRELIMINARY; PRT; 534 AA.
AC 093296;
DT 01-NOV-1998; Integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998; sequence version 1.
DT 07-FEB-2006; entry version 20.
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxId=9031;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.B.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
CC -----
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CC -----
DR EMBL: AF042098; AAC25052.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR SMR: Q93296; 224-333.
DR Ensemble: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON TER
SQ SEQUENCE 534 AA; 60597 MW; FB53BC2E6D4C92 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 2e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 32

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DB 447 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 477

RESULT 12
ID 09PVL1_CHICK PRELIMINARY; PRT; 569 AA.
AC 09PVL1;
DT 01-MAY-2000; Integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000; sequence version 1.
DT 07-FEB-2006; entry version 19.
DE Amyloid protein (Fragment).
DE Name=APP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxId=9031;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor superegene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
CC -----
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CC -----
DR EMBL: AF030341; AAF12698.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR SMR: Q9PVL1; 1-64; 260-369.
DR Ensemble: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON TER
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B85163A19D CRC64;

Query Match 100.0%; Score 155; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 32
DB 483 VHHQKLVFAEDVGNKGAIIIGLMVGGVIA 513

RESULT 13
ID 02XQAO_PIG PRELIMINARY; PRT; 695 AA.
AC 02XQAO;
DT 20-DEC-2005; Integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005; sequence version 1.
DT 07-FEB-2006; entry version 3.
DE Amyloid protein variant 1.
DE Name=APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
OC Sub. NCBI_TaxId=9823;
RN [1]
RX NUCLEOTIDE SEQUENCE.

```


RA Oerum M.A., Larsen K., Bendixen C.;
 RT "Porcine amyloid precursor protein, APP: Cloning and characterization
 of cDNAs.";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; DQ267684; AB882033.1; -; mRNA.
 SQ SEQUENCE 695 AA; 78615 MW; 825A7E4AC10E8F0B CRC64;

Query Match 100.0%; Score 155; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 2.5e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
 DB 608 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 638

RESULT 14

OS6UK3 CANFA
 ID OS6UK3_CANFA PRELIMINARY; PRT; 695 AA.
 AC OS6UK3;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Beta-amyloid protein 695.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;

RN [1] NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
 RT "Relationship between canine dementia and Alzheimer's disease.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC -----

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DR EMBL; AY926582; AAX81911.1; -; mRNA.
 DR SMR; OS6UK3; 28-123, 124-189, 385-494.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR012282; Cytochrome C_R.
 DR PANTHER; PTHR10083; SF6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAMYL0ID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78748 MW; 5A253B0DB677875A CRC64;

Query Match 100.0%; Score 155; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 2.5e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
 DB 608 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 638

RESULT 15
 OSR477_PONPY PRELIMINARY; PRT; 695 AA.
 ID OSR477_PONPY

AC OSR477;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein DKFZp459D212.
 GN Name=DKFZp459D212.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.

OX NCBI_TaxID=9600;

RN [1] NUCLEOTIDE SEQUENCE.
 RP TISSUE-Cortex;
 RC The German cDNA Consortium;
 RA Mamuit R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fob G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CR861380; CAH93439.1; -; mRNA.
 DR SMR; OSR477; 28-123, 124-189, 385-494.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_EXTRA.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR012282; Cytochrome C_R.
 DR PANTHER; PTHR10083; SF6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAMYL0ID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 695 AA; 78627 MW; 0BF5D9BA2213E49 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 2.5e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
 DB 608 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 638

RESULT 16

Q6RH29 CANFA
 ID Q6RH29_CANFA PRELIMINARY; PRT; 695 AA.
 AC Q6RH29;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Beta amyloid protein isoform APP695.
 GN Name=Beta APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.

OX NCBI_TaxID=9615;

RN [1] NUCLEOTIDE SEQUENCE.
 RA Nakata M.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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 CC -----

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CC -----
DR EMBL: AY498707; AAR97727.1; -; mRNA.
DR HSSP: O16019; 1BA4.
DR SMR: Q6RH23; 28-123, 124-189, 385-494.
DR Ensembl: ENSGAFG0000008557; Canis familiaris.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 608 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 638

RESULT 17
ID Q9DGJ8 CHICK PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:16039787; DOI:10.1016/j.neuroscience.2005.05.020;
RA Carrodeguas J.A., Rodolasse A., Garza M.V., Sanz-Clemente A.,
RA Perez-Pe R., Lacoeta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
RA Sorribas V., Sarasa M.;
RT "The chick embryo appears as a natural model for research in beta-
RT amyloid precursor protein processing.";
RL Neuroscience 134:1285-1300(2005).

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CC -----
DR EMBL: AF289218; AAG00593.1; -; mRNA.
DR HSSP: O16019; 11YT.
DR SMR: Q9DGJ8; 28-123, 124-189, 385-494.
DR Ensembl: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78566 MW; F201ED02AEC86D95 CRC64;

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Query Match 100.0%; Score 155; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 608 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 638

RESULT 18
ID Q56JK4 CANFA PRELIMINARY; PRT; 714 AA.
AC Q56JK4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL: AY26581; AAX81910.1; -; mRNA.
DR SMR: Q56JK4; 28-123, 124-189, 404-513.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR012282; Cytochrome C-R.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 714 AA; 80827 MW; 50DDE51FB9E90EC5 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 714;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 627 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 657

RESULT 19
ID Q56JK2 STECO PRELIMINARY; PRT; 749 AA.
AC Q56JK2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Beta-amyloid protein 749.
OS Stenella coeruleoalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
OX NCBI_TaxID=9737;

```

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RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Gallego C., Sarasa M.;
RT      "The molecular machinery of Alzheimer's disease in the dolphin." ;
RL      Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL, AY925583; AX81912.1; -, mRNA.
DR      SMR; Q56UK2; 28-123, 124-189, 284-339, 457-566.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005488; F:binding; IEA.
DR      GO; GO:0020037; F:heme binding; IEA.
DR      GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR012282; Cytochrome c R.
DR      InterPro; IPR002223; Prot_inh_Kunz-m.
DR      PANTHER; PTHR10083; SFE; Beta-APP; 5.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOID4.
DR      PRINTS; PR00204; BETAAMYLOID.
DR      SMART; SM00066; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ      SEQUENCE 749 AA; 84543 MW; 426599867C2A95D6 CRC64;

Query Match      100.0%; Score 155; DB 2; Length 749;
Best Local Similarity 100.0%; Pred. No. 2; 7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFPFADVGNKGAIIIGLMVGVVIA 32
          |||||
          662 VHHOKLVFPFADVGNKGAIIIGLMVGVVIA 692

RESULT 20
A4_SAISC      STANDARD; PRT; 751 AA.
AC      Q95241;
DT      15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT      01-FEB-1997, sequence version 1.
DT      07-MAR-2006, entry version 60.
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
DE      amyloid beta A4 protein precursor) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
GN      Name=APP;
OS      Saimiri sciureus (Common squirrel monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC      Cebinae; Saimiri.
OX      NCBI_TaxID=9521;
RN      1
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      TISSUE=Kidney, and Liver;
RX      MEDLINE=96108482; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
RA      Levy E., Amourin A., Frangione B., Walker L.C.;
RT      "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
RT      amyloid angiopathy." ;
RL      Neurobiol. Aging 16:805-808(1995).

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CC      -1- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in
CC      cell mobility and transcription regulation through protein-protein
CC      interactions (By similarity). Can promote transcription activation
CC      through binding to APBB1/Tip60 and inhibit Notch signaling through
CC      interaction with Numb (By similarity). Couples to apoptosis-
CC      inducing pathways such as those mediated by G10 and JIP (By
CC      similarity). Inhibits G10 alpha ATPase activity (By similarity).
CC      Acts as a kinesin I membrane receptor, mediating the axonal
CC      transport of beta-secretase and presenilin 1 (By similarity). May
CC      be involved in copper homeostasis/oxidative stress through copper
CC      ion reduction. In vitro, copper-metalated APP induces neuronal
CC      death directly or is potentiated through Cu(2+)-mediated low-
CC      density lipoprotein oxidation (By similarity). Can regulate
CC      neurite outgrowth through binding to components of the
CC      extracellular matrix such as heparin and collagen I and IV (By
CC      similarity). The splice isoforms that contain the BPTI domain
CC      possess protease inhibitor activity (By similarity).
CC      -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC      with metal-reducing activity. Bind transient metals such as
CC      copper, zinc and iron (By similarity).
CC      -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC      peptides, including C31, are potent enhancers of neuronal
CC      apoptosis (By similarity).
CC      -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC      cytoplasmic proteins, including APBB family members, the APPA
CC      family, MAPKAP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC      to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC      interacts with GPCR-like protein BPP, FRL1, APPBP1, IBL, KNS2
CC      (via its TPR domain) (By similarity), APPB2 (via BaS5) and DDB1.
CC      In vitro, it binds MAP7 via the WT-binding domains (By
CC      similarity). Associates with microtubules in the presence of ATP
CC      and in a kinesin-dependent manner (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC      protein that rapidly becomes internalized via a clathrin-coated
CC      pits. During maturation, the immature APP (N-glycosylated in the
CC      endoplasmic reticulum) moves to the Golgi complex where complete
CC      maturation occurs (O-glycosylated and sulfated). After alpha-
CC      secretase cleavage, soluble APP is released into the extracellular
CC      space and the C-terminal is internalized to endosomes and
CC      lysosomes. Some APP accumulates in secretory transport vesicles
CC      leaving the late Golgi compartment and returns to the cell
CC      surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC      and nuclei of neurons (By similarity).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=APP770;
CC      Comment=Additional isoforms seem to exist;
CC      Name=APP695;
CC      IsoId=Q95241-1; Sequence=Displayed;
CC      IsoId=Q95241-2; Sequence=Not described;
CC      -1- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC      sorting of membrane proteins to the basolateral surface of
CC      epithelial cells (By similarity).
CC      -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC      phosphorylated proteins is required for the specific binding of
CC      the PID domain. However additional amino acids either N- or C-
CC      terminal to the NPXY motif are often required for complete
CC      interaction. The PID domain-containing proteins which bind APP
CC      require the YENPTY motif for full interaction. These interactions
CC      are independent of phosphorylation on the terminal tyrosine
CC      residue. The NPXY site is also involved in clathrin-mediated
CC      endocytosis (By similarity).
CC      -1- PTM: Proteolytically processed under normal cellular conditions.
CC      Cleavage by alpha-secretase or alternatively by beta-secretase
CC      leads to generation and extracellular release of soluble APP
CC      peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC      retention of corresponding membrane-anchored C-terminal fragments,
CC      C83 and C99. Subsequent processing of C83 by gamma-secretase
CC      yields P3 peptides. This is the major secretory pathway and is
CC      nonamyloidogenic. Alternatively, presenilinnicastatin-mediated
CC      gamma-secretase processing of C99 releases the amyloid beta

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CC		proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC		major components of amyloid plaques, and the cytotoxic C-terminal
CC		fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC		similarity).
CC	-1-	PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC		(By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC		results in the production of the neurotoxic C31 peptide and the
CC		increased production of beta-amyloid peptides (By similarity).
CC	-1-	PTM: N- and O-glycosylated (By similarity).
CC	-1-	PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC		serine residues is neuron-specific. Phosphorylation can affect APP
CC		processing, neuronal differentiation and interaction with other
CC		proteins (By similarity).
CC	-1-	MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC		zinc, can induce histidine-bridging between beta-amyloid molecules
CC		resulting in beta-amyloid-metal aggregates (By similarity).
CC		Extracellular zinc-binding increases binding of heparin to APP and
CC		inhibits collagen-binding (By similarity).
CC	-1-	SIMILARITY: Belongs to the APP family.
CC	-1-	SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC		-----
CC		Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC		Distributed under the Creative Commons Attribution-NoDerivs License
CC		-----
DR	EMBL:	S81024; AAD14347.1; - mRNA.
DR	PDB:	1RM6; X-ray; A=346-551.
DR	SMR;	G95241; 28-123, 124-189, 287-342.
DR	InterPro:	IPIR008155; A4_APP.
DR	InterPro:	IPIR008154; A4_extra.
DR	InterPro:	IPIR001255; Beta_APP.
DR	InterPro:	IPIR002223; Prot_inh_Kunz-m.
DR	PANTHER:	PTHR10083:SF6; Beta_APP; 5.
DR	pfam:	PF02177; A4_EXTRA; 1.
DR	pfam:	PF03494; Beta_APP; 1.
DR	pfam:	PF000014; Kunitz_BPTI; 1.
DR	PRINTS:	PR00203; AMYLOIDA4.
DR	PRINTS:	PRO0759; BASICPTASE.
DR	PRINTS:	PRO0204; BETAMYLOID.
DR	ProDom:	PD000222; Prot_inh_Kunz-m; 1.
DR	SMART:	SMO0006; A4_EXTRA; 1.
DR	SMART:	SMO0131; KU_1.
DR	PROSITE:	PS00319; A4_EXTRA; 1.
DR	PROSITE:	PS00320; A4_INTRA; 1.
DR	PROSITE:	PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE:	PS50279; BPTI_KUNITZ_2; 1.
KM		3D-structure: Alternative splicing: Amyloid; Apoptosis; Cell adhesion;
KM		Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
KM		Membrane; Metal-binding; Notch signaling pathway; Phosphorylation;
KM		Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
KW		Transmembrane; Zinc.
FT	SIGNAL	1..17
FT	CHAIN	16..751
FT		By similarity.
FT	CHAIN	18..668
FT		/FTId=PRO_0000000172.
FT	CHAIN	18..652
FT		Soluble APP-alpha (Potential).
FT	CHAIN	653..751
FT		/FTId=PRO_0000000173.
FT	CHAIN	653..694
FT		Soluble APP-beta (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000174.
FT	CHAIN	653..694
FT		C99 (Potential).
FT	CHAIN	653..694
FT		/FTId=PRO_0000000175.
FT	CHAIN	653..692
FT		Beta-amyloid protein 42 (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000176.
FT	CHAIN	653..692
FT		Beta-amyloid protein 40 (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000177.
FT	CHAIN	653..694
FT		C63 (Potential).
FT	CHAIN	653..694
FT		/FTId=PRO_0000000178.
FT	CHAIN	653..692
FT		p3(42) (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000179.
FT	CHAIN	653..692
FT		p3(40) (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000180.
FT	CHAIN	653..692
FT		Gamma-CTF(59) (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000181.
FT	CHAIN	653..692
FT		Gamma-CTF(57) (Potential).
FT	CHAIN	653..692
FT		/FTId=PRO_0000000182.

FT	CHAIN	702	751		Gamma-CRF(50) (Potential).
FT	CHAIN	721	751		/C31 (Potential).
FT	TOPO_DOM	18	680		/Frid=PRO_0000000183.
FT	TRANSMEM	681	704		C31 (Potential).
FT	TOPO_DOM	705	751		/Frid=PRO_0000000184.
FT	DOMAIN	291	341		Extracellular (Potential).
FT	REGION	96	110		Potential.
FT	REGION	181	188		BPT/Kunitz inhibitor.
FT	REGION	316	344		Heparin-binding (By similarity).
FT	REGION	363	428		Heparin-binding (By similarity).
FT	REGION	504	521		Collagen-binding (By similarity).
FT	REGION	713	732		Interaction with G(o)-alpha (By similarity).
FT	MOTIF	705	715		Basolateral sorting signal (By similarity).
FT	MOTIF	740	743		NPKX motif, contains endocytosis signal.
FT	COMPBIAS	230	260		Asp/Glu-rich (acidic).
FT	COMPBIAS	274	280		Poly-Thr.
FT	METAL	137	137		Copper (By similarity).
FT	METAL	147	147		Copper (By similarity).
FT	METAL	149	149		Copper (By similarity).
FT	METAL	151	151		Copper (By similarity).
FT	METAL	658	658		Copper or zinc (By similarity).
FT	METAL	662	662		Copper or zinc (By similarity).
FT	METAL	665	665		Copper or zinc (By similarity).
FT	METAL	666	666		Copper or zinc (By similarity).
Query Match					100.0%; Score 155; DB 1; Length 751;
Best Local Similarity					Pred. NO. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Oy	2 VHOKLVFFADVGSNKGAIIIGLWGVVIA 32				
Db	664 VHKQTVFFADVGSNKGAIIIGLWGVVIA 694				
RESULT 21					
OGSGCO HUMAN	PRELIMINARY; PRT; 751 AA.				
ID OGSGCO_HUMAN					
AC OGSGCO_T	Integrated into UniProtKB/TRMBL.				
DT 10-MAY-2005,	sequence version 1.				
DT 07-FEB-2006,	entry version 7.				
DE Amyloid beta A4 protein,, isoform b.					
CN Name=APP;					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrate; Euteleostomi;					
OC Mamalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;					
CC Homo.					
OX NCBI_Taxid=9606;					
RN [1]					
RP NUCLEOTIDE SEQUENCE.					
RC TISSUE=Eye;					
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA Steiner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,					
RA Alechni S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bat N.K.,					
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,					
RA Diatchenko L., Marruina K., Farmer A.A., Rubin G.M., Hong L.,					
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,					
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carvicut P., Prange C.,					
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA Roark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,					
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,					
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA Butcherfield Y.S.N., Krzywinski M.T., Skalske U., Smalhus D.E.,					

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG NIH MGC Project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: BC065529; AAH65529.1; -, mRNA.
DR SMR: Q6GSC0: 28-123, 124-189, 287-342, 441-550.
DR Ensembl: ENSG00000142192; Homo sapiens.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR012282; Cytochrome_C_R.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYOLOID.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84819 MW; C987C557C5A3714E CRC64;

Query Match 100.0%; Score 155; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVDGSKGAIIGLMVGGVIA 32
DB 664 VHHQKLVFPADVDGSKGAIIGLMVGGVIA 694

RN [2]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing and analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: AB169826; BAE01907.1; -, mRNA.
DR SMR: Q4R4R8: 28-123, 124-189, 287-342, 441-550.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR012282; Cytochrome_C_R.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETAMYOLOID.
DR PRODOM: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM
SQ SEQUENCE 751 AA; 84817 MW; 83C1CD96AD355158 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVDGSKGAIIGLMVGGVIA 32
DB 664 VHHQKLVFPADVDGSKGAIIGLMVGGVIA 694

RESULT 23
Q56CK5 CANFA PRELIMINARY; PRT; 751 AA.
ID Q56CK5 CANFA PRELIMINARY; PRT; 751 AA.
AC Q56CK5;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Beta-amyloid protein 751.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.,
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
EMBL: AY926580; AAX81909.1; -, mRNA.

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DR SMR; Q56J5; 28-123, 124-189, 287-342, 441-550.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR022223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083; SFe; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_Bpt1; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAMLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84920 MW; C1CD20377DFE8550 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 32
DB 664 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 694

RESULT 24
Q6RH28 CANFA PRELIMINARY; PRT; 751 AA.
ID Q6RH28;
AC Q6RH28;
DT 05-JUL-2004; Integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004; sequence version 1.
DE 07-FEB-2006; entry version 13.
DE Beta amyloid protein isoform APP751.
GN Name-beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Pisces; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RU Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC
CC EMBL; AY498708; AAR97728.1; -; mRNA.
DR HSSP; Q16019; IAP.
DR SMR; Q6RH28; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSGACG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR022223; Prot_inh_Kunz-m.
DR PANTHER; PTHR10083; SFe; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_Bpt1; 1.
DR PRINTS; PR00203; AMYLOIDA4.

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DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMAMLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;

Query Match 100.0%; Score 155; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 32
DB 664 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 694

RESULT 25
Q2XQ99_PIG PRELIMINARY; PRT; 751 AA.
ID Q2XQ99_PIG;
AC Q2XQ99;
DT 20-DEC-2005; Integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005; sequence version 1.
DT 07-MAR-2006; entry version 4.
DE Amyloid protein variant 2.
GN Name-APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein, APP: Cloning and characterization
RT of cDNAe.";
RU Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC
CC EMBL; DQ267685; ABB82034.1; -; mRNA.
SQ SEQUENCE 751 AA; 84799 MW; 37668743880C369F CRC64;

Query Match 100.0%; Score 155; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 32
DB 664 VHHQKLVFAEDVGNKGAIIIGLVGVVIA 694

RESULT 26
Q9DGJ7_CHICK PRELIMINARY; PRT; 751 AA.
ID Q9DGJ7_CHICK;
AC Q9DGJ7;
DT 01-MAR-2001; Integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001; sequence version 1.
DT 07-FEB-2006; entry version 22.
DE Beta-amyloid protein 751 isoform.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed; 16039787; DOI=10.1016/j.neuroscience.2005.05.020;

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RA Cardeguas J.A., Rodolose A., Garza M.V., Sanz-Clemente A.,
 RA Perez-Pe R., Lacosta A.M., Dominguez L., Monleon I., Sanchez-Diaz R.,
 RA Sarrias V., Sarasa M.;
 RT "The chick embryo appears as a natural model for research in beta-
 RT amyloid precursor protein processing.",
 RL Neuroscience 134:1285-1300(2005).
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
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 CC
 CC EMBL: AF289219; AAG00594.1; -; mRNA.
 DR HSSP: Q16019; 11YT.
 DR SMR: Q9DGJ7; 28-123, 124-189, 287-342, 441-550.
 DR Ensembl: ENSGALG0000015770; Gallus gallus.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0005488; F: binding; IEA.
 DR GO: GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR008154; A4 APP.
 DR InterPro: IPR008154; A4 extra.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Prot_inh_Kunz-m.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOID4.
 DR PRINTS: PR00759; BASICTPASE.
 DR PRINTS: PR00204; BETAMYLOID.
 DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 DR SEQUENCE 751 AA; 84706 MW; E78E9413A803D84 CRC64;
 SQ
 Query Match 100.0%; Score 155; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGNKGAIIIGLMVGGVIA 32
 DB 664 VHHQKLVFPAEDVGNKGAIIIGLMVGGVIA 694
 RESULT 27
 QARY33_TETNG PRELIMINARY; PRT; 754 AA.
 ID QARY33_TETNG
 AC QARY33;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Chromosome 3 SCAP14978, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSREN00027170001;
 OS Tetradon nigrivittidis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetradon.
 OC NCBI_TaxId=99883;
 OX [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Maucali E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Antichaud V., Jubin C., Castellino V., Katinka M., Vacherie B.,
 RA Biemont C., Skali Z., Catolico L., Poulain Y., De Bernardis V.,
 RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "genome duplication in the teleost fish Tetradon nigrivittidis reveals
 RT the early vertebrate proto-karyotype.",
 RL Nature 431:946-957(2004).
 CC (2)
 CC NUCLEOTIDE SEQUENCE.
 RP GenomeScope: Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: CAEB0104978; CAG06699.1; -; Genomic DNA.
 DR SMR: QARY33; 10-105, 452-560.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0005488; F: binding; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOID4.
 DR PRINTS: PR00204; BETAMYLOID.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT NON_TER 1
 FT SEQUENCE 754 AA; 84740 MW; 4A37B051A9FAD77 CRC64;
 SQ
 Query Match 100.0%; Score 155; DB 2; Length 754;
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHQKLVFPAEDVGNKGAIIIGLMVGGVIA 32
 DB 667 VHHQKLVFPAEDVGNKGAIIIGLMVGGVIA 697
 RESULT 28
 A4_CAVPO STANDARD; PRT; 770 AA.
 ID A4_CAVPO
 AC Q60495; Q60496;
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 23-APR-2003, sequence version 2.
 DT 07-FEB-2006, entry version 56.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid beta A4 protein precursor (APP) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN Name=APP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxId=10141;
 OX [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
 RX TISSUE=Brain, and Liver;
 MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.",
 RL Biochim. Biophys. Acta 1351:17-21(1997).

RN INTERACTION OF BETA-APP40 WITH APOE.
 RP MEDLINE:98007700; PubMed:9349544.
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.,
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN (3)
 RP PROCESSING.
 RA MEDLINE:20084499; PubMed:10619481; DOI=10.1016/S0306-4522(99)00390-5;
 RX Beck M., Brunecker M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein.";
 RL Neuroscience 95:243-254(2000).
 RN (4)
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE:20576391; PubMed:1035007; DOI=10.1074/jbc.M005968200;
 RA Pinnix I., Mununu U., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative C-
 RT terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(2+)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Apolipans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MARK3BP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of APP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC ApoB3 appears to be the preferred amyloid binding isoform, while
 CC the apoA4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble

CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC apilicans;
 CC Name=APP770;
 CC IsoId=O60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=O60495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).
 CC -1- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).
 CC -1- PTM: N- and O-glycosylated. O-1-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the apilicans (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.
 CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 CC EMBL: X97631; CAA66230.1; -; mRNA.
 CC EMBL: X99198; CAA67589.1; -; mRNA.
 CC HSSP: P08592; INMJ.
 CC SMR: Q60495; 28-123, 124-189, 287-342, 460-569.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta-APP.

DR InterPro; IPR002223; Prot inh_Kunz-m.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPT1; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAMYLOID.
 DR ProDom; PD000222; Prot inh_Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00331; Kuf_1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
 KM Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KM Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
 KM Metal-binding; Notch signalling pathway; Phosphorylation;
 KM Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KM Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT /FTid=PRO_0000000076.
 FT CHAIN 18 687 Soluble APP-alpha (By similarity).
 FT /FTid=PRO_0000000077.
 FT CHAIN 18 671 Soluble APP-beta (By similarity).
 FT /FTid=PRO_0000000078.
 FT CHAIN 672 770 CTF-alpha (By similarity).
 FT /FTid=PRO_0000000079.

Query Match 100.0%; Score 155; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2,8e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHHQKLVFPAEDVGNKKGALIGLVGVVIA 32
 Db 683 VHHQKLVFPAEDVGNKKGALIGLVGVVIA 713

RESULT 29
 A4_HUMAN STANDARD; PRT; 770 AA.
 ID A4_HUMAN PRT; 770 AA.
 AC P05067; P09000; P78438; Q13764; Q13778; Q13781; Q16011; Q16014;
 AC Q16019; Q16020; Q92738; Q9UCB9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UQ58;
 DT 13-ANG-1987. Integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1991. Sequence version 3.
 DT 07-MAR-2006. Entry version 111.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
 DE nexin-II) (PN-II) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-
 DE alpha) (Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN Name=APP; Synonyms=A4; A01;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207; DOI=10.1038/325733a0;
 RA Kang J., Lemaire H.-G., Unterhaup A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Muelier-Hill B.,
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RL Nature 325:733-736(1987).
 RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.,
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterhaup A., Beyreuther K., Muelier-Hill B.,
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is
 RT encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522 (1989).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;
 RA Yoshikai S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.,
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM.
 RX PubMed=1908403; DOI=10.1016/0378-1119(91)90093-Q;
 RA Yoshikai S., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.,
 RL Gene 102:291-292(1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.,
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sasaki Y.,
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RX DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.,
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA) AND VARIANT LYS-501.
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.,
 RT "NIHES-SNPs, environmental genome project. NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://legp.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBS databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORMS APP305 AND APP751).
 RC TISSUE=Eye, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schein C.M., Schler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toehyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abterson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
 RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-10.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.,
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.",
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP ERRATUM, AND SEQUENCE REVISION.
 RA Schon E.A., Mita S., Sadlock J., Herbert J.,
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 1-75.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Pauci G., Lahiri D.K., Salton S.R., Robakis N.K.,
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.",
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [14]
 RP PROTEIN SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.,
 RT "Purification of protease nexin II from human fibroblasts.",
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [15]
 RP PROTEIN SEQUENCE OF 18-40.
 RC TISSUE=Platelet;
 RX MEDLINE=2260828; PubMed=1265801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.",
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [16]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.,
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.",
 RL Science 245:651-653(1989).
 RN [17]
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.,
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.",
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [18]
 RP NUCLEOTIDE SEQUENCE OF 286-366.
 RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.",

RL Nature 331:528-530(1988).
 RN [19]
 RP NUCLEOTIDE SEQUENCE OF 287-367.
 RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.,
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
 RT inhibitory activity.",
 RL Nature 331:530-532(1988).
 RN [20]
 RP NUCLEOTIDE SEQUENCE OF 507-770.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.,
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.",
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [21]
 RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.,
 Query Match 100.0%; Score 155; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.8e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VHHOKLVFPAEDVGSNKAIIIGLVGVVIA 32
 DB 683 VHHOKLVFPAEDVGSNKAIIIGLVGVVIA 713
 ID A4_MACPA STANDARD; PRT; 770 AA.
 AC P53601; Q60H7; Q95KN7;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 22-FEB-2003, sequence version 3.
 DT 07-FEB-2006, entry version 55.
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease
 DE amyloid protein homology) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta) (C99); Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CRF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CRF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP; ORFNames=QCE-15949;
 OS Macaca fascicularis (Crad eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (MRNA) (ISOFORMS APP695 AND APP770).
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlany M.B., Tolan D.R., Selkoe D.J.,
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease.",
 RL Am. J. Pathol. 138:1423-1435(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 3).
 RC TISSUE=Brain cortex;
 RX Kusuda J., Osada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.,
 RA "Isolation and characterization of cDNA for macaque neurological
 RT disease genes.",
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation

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CC through binding to ABBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ARase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(2+)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC - FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC - FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC - SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APBBP1, IBL, KNS2
CC (via its TPR domains) (By similarity). APBBP2 (via BASS) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC - SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(55) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=PS3601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=PS3601-2; Sequence=VSP_000010, VSP_000011;
CC Name=3;
CC IsoId=PS3601-3; Sequence=VSP_013360, VSP_013361;
CC - DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC - DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC - PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicestrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By

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CC similarity).
CC - PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at App-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC - PTM: N- and O-glycosylated (By similarity).
CC - PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC - MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC - SIMILARITY: Belongs to the APP family.
CC - SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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CC -----
CC EMBL, M58726; AAA36828.1; -; mRNA.
CC EMBL, M58727; AAA36829.1; -; mRNA.
CC EMBL, AB125150; BAD51938.1; -; mRNA.
CC HSSP, P08592; INMU.
CC DR SMR, PS3601; 28-123, 124-189, 287-342, 460-569.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR001255; Beta-APP.
CC InterPro: IPR002223; Prot_inh_Kunz-m.
CC PANTHER, PTHR10083; SRF6; Beta-APP; 6.
CC Pfam, PF02177; A4_EXTRA; 1.
CC Pfam, PR03494; Beta-APP; 1.
CC Pfam, PR00014; Kunitz_BPTI; 1.
CC PRINTS, PR00203; AMYLOID4.
CC PRINTS, PR00759; BASICPTASE.
CC PRINTS, PR00204; BETAMYLOID.
CC PRODOM, PD000222; Prot_inh_Kunz-m; 1.
CC SMART, SM00006; A4_EXTRA; 1.
CC SMART, SM00131; KUF; 1.
CC PROSITE, PS00319; A4_EXTRA; 1.
CC PROSITE, PS00320; A4_INTRA; 1.
CC PROSITE, PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE, PS02279; BPTI_KUNITZ_2; 1.
CC KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
CC Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Membrane;
CC Metal-binding; Notch signaling pathway; Phosphorylation;
CC Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
CC Transmembrane; Zinc.
CC FT SIGNAL 1 17 BY similarity.
CC FT CHAIN 18 770 /FTid=PRO_0000000101.
CC FT CHAIN 18 687 Soluble APP-alpha (Potential).
CC FT CHAIN 18 671 /FTid=PRO_0000000102.
CC FT CHAIN 672 770 Soluble APP-beta (Potential).
CC FT CHAIN 672 770 C99 (Potential).
CC FT CHAIN 672 713 /FTid=PRO_0000000104.
CC FT CHAIN 672 711 /FTid=PRO_0000000105.
CC FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
CC FT CHAIN 688 770 C83 (Potential).
CC FT CHAIN 688 770 /FTid=PRO_0000000106.
CC FT CHAIN 688 770 C99 (Potential).
CC FT CHAIN 688 770 /FTid=PRO_0000000107.
CC FT CHAIN 688 713 P3(42) (Potential).
CC FT CHAIN 688 711 /FTid=PRO_0000000108.
CC FT CHAIN 712 770 P3(40) (Potential).
CC FT CHAIN 712 770 /FTid=PRO_0000000109.
CC FT CHAIN 714 770 Gamma-CTF(59) (Potential).
CC FT CHAIN 714 770 Gamma-CTF(57) (Potential).
CC FT CHAIN 721 770 Gamma-CTF(50) (Potential).

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FT CHAIN 740 770 /FTid=PRO.0000000112.
FT TOPO_DOM 18 699 /C31(Potential).
FT TRANSMEM 700 723 /FTid=PRO.0000000113.
FT TOPO_DOM 724 770 Extracellular (Potential).
FT DOMAIN 291 341 Potential.
FT REGION 96 110 Cytoplasmic (Potential).
FT REGION 181 188 BPRI/Kunitz inhibitor.
FT REGION 391 423 Heparin-binding (By similarity).
FT REGION 491 522 Zinc-binding (By similarity).
FT REGION 523 540 Heparin-binding (By similarity).
FT REGION 732 751 Collagen-binding (By similarity).
FT MOTIF 724 734 Interaction with G(o)-alpha (By
similarity).
Basolateral sorting signal (By
similarity).

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DB 683 VHHQKLVFPADVGSNKGAIIGLMVGVYIA 713

Search completed: September 28, 2006, 06:22:53
JOB time : 109.179 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:23:21 ; Search time 22.5291 Seconds
(without alignments)
124.327 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/PCUTS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	42	1	US-07-744-767A-2
2	155	100.0	42	1	US-08-179-574-1
3	155	100.0	42	1	US-08-347-144-1
4	155	100.0	42	1	US-08-462-859A-19
5	155	100.0	42	1	US-08-123-659A-19
6	155	100.0	42	1	US-08-464-247A-19
7	155	100.0	42	1	US-08-464-248A-19
8	155	100.0	42	1	US-08-476-464A-1
9	155	100.0	42	1	US-08-304-585-2
10	155	100.0	42	1	US-08-302-808-5
11	155	100.0	42	1	US-08-268-348A-1
12	155	100.0	42	1	US-08-433-734-2
13	155	100.0	42	1	US-08-609-090-9
14	155	100.0	42	1	US-07-737-371E-72
15	155	100.0	42	1	US-08-422-333-4
16	155	100.0	42	1	US-08-682-245A-4
17	155	100.0	42	1	US-08-986-948-5
18	155	100.0	42	2	US-08-717-551A-2
19	155	100.0	42	2	US-09-388-890-1
20	155	100.0	42	2	US-09-005-215-20
21	155	100.0	42	2	US-09-242-724-23
22	155	100.0	42	2	US-08-922-930-2
23	155	100.0	42	2	US-09-660-934-1
24	155	100.0	42	2	US-08-923-055-2
25	155	100.0	42	2	US-08-922-889-2
26	155	100.0	42	2	US-09-731-460-1

27	155	100.0	42	2	US-09-133-866-2	Sequence 2, App1
28	155	100.0	42	2	US-09-723-384-1	Sequence 1, App1
29	155	100.0	42	2	US-09-724-961-42	Sequence 42, App1
30	155	100.0	42	2	US-09-724-552-1	Sequence 1, App1
31	155	100.0	42	2	US-09-580-018-42	Sequence 42, App1
32	155	100.0	42	2	US-10-455-218-2	Sequence 2, App1
33	155	100.0	42	2	US-09-723-927-1	Sequence 1, App1
34	155	100.0	42	2	US-09-724-489-1	Sequence 1, App1
35	155	100.0	42	2	US-09-724-477-1	Sequence 1, App1
36	155	100.0	42	2	US-09-723-762-1	Sequence 1, App1
37	155	100.0	42	2	US-09-201-420-1	Sequence 1, App1
38	155	100.0	42	2	US-09-724-551-42	Sequence 42, App1
39	155	100.0	42	2	US-10-815-353-1	Sequence 1, App1
40	155	100.0	42	2	US-10-278-181-1	Sequence 1, App1
41	155	100.0	42	2	US-10-816-529-1	Sequence 1, App1
42	155	100.0	42	2	US-09-623-548A-955	Sequence 955, App
43	155	100.0	42	2	US-09-623-548A-988	Sequence 988, App
44	155	100.0	42	2	US-10-815-391-1	Sequence 1, App1
45	155	100.0	42	2	US-10-816-022-1	Sequence 1, App1
46	155	100.0	42	2	US-09-724-953-34	Sequence 34, App1
47	155	100.0	42	2	US-09-657-276-955	Sequence 955, App
48	155	100.0	42	2	US-09-657-276-988	Sequence 988, App
49	155	100.0	42	2	US-09-724-567-34	Sequence 34, App1
50	155	100.0	42	2	US-09-724-940-42	Sequence 42, App1
51	155	100.0	42	2	US-09-865-294A-65	Sequence 65, App1
52	155	100.0	42	2	US-09-979-952-34	Sequence 34, App1
53	155	100.0	42	2	US-09-585-817-34	Sequence 34, App1
54	155	100.0	42	2	US-09-962-955D-37	Sequence 37, App1
55	155	100.0	42	2	US-09-706-574A-20	Sequence 20, App1
56	155	100.0	42	2	US-10-934-609-1	Sequence 1, App1
57	155	100.0	42	2	US-10-884-892-1	Sequence 1, App1
58	155	100.0	42	2	US-09-848-616-174	Sequence 174, App
59	155	100.0	42	2	US-10-933-559-1	Sequence 1, App1
60	155	100.0	42	2	US-10-816-380-1	Sequence 1, App1
61	155	100.0	42	3	US-10-816-380-1	Sequence 1, App1
62	155	100.0	42	3	US-10-363-082-1	Sequence 1, App1
63	155	100.0	42	5	PCR-US92-06700-2	Sequence 2, App1
64	155	100.0	42	5	PCR-US93-00325-1	Sequence 1, App1
65	155	100.0	42	7	5220013-14	Patent No. 5220013
66	155	100.0	43	1	US-08-235-400-1	Sequence 1, App1
67	155	100.0	43	1	US-08-437-067-1	Sequence 1, App1
68	155	100.0	43	1	US-08-302-808-6	Sequence 6, App1
69	155	100.0	43	1	US-08-079-511-1	Sequence 1, App1
70	155	100.0	43	1	US-08-467-607-1	Sequence 1, App1
71	155	100.0	43	1	US-08-404-831-1	Sequence 1, App1
72	155	100.0	43	1	US-08-602-264A-71	Sequence 3, App1
73	155	100.0	43	1	US-08-469-362-1	Sequence 1, App1
74	155	100.0	43	1	US-08-612-785B-1	Sequence 1, App1
75	155	100.0	43	1	US-08-475-579A-1	Sequence 1, App1
76	155	100.0	43	1	US-08-850-392-1	Sequence 1, App1
77	155	100.0	43	1	US-07-737-371E-70	Sequence 70, App1
78	155	100.0	43	1	US-08-986-948-6	Sequence 6, App1
79	155	100.0	43	1	US-08-975-977-1	Sequence 1, App1
80	155	100.0	43	1	US-08-817-422-1	Sequence 1, App1
81	155	100.0	43	1	US-08-920-162A-1	Sequence 1, App1
82	155	100.0	43	2	US-08-461-018A-3	Sequence 3, App1
83	155	100.0	43	2	US-08-976-191-1	Sequence 1, App1
84	155	100.0	43	2	US-08-976-179-1	Sequence 1, App1
85	155	100.0	43	2	US-09-216-958-3	Sequence 3, App1
86	155	100.0	43	2	US-09-356-931-1	Sequence 1, App1
87	155	100.0	43	2	US-08-733-202-1	Sequence 1, App1
88	155	100.0	43	2	US-08-703-675C-1	Sequence 1, App1
89	155	100.0	43	2	US-09-390-692-1	Sequence 1, App1
90	155	100.0	43	2	US-08-617-267C-1	Sequence 1, App1
91	155	100.0	43	2	US-09-303-635-1	Sequence 1, App1
92	155	100.0	43	2	US-08-294-819-1	Sequence 1, App1
93	155	100.0	43	2	US-09-408-283-1	Sequence 1, App1
94	155	100.0	43	2	US-09-280-966-1	Sequence 1, App1
95	155	100.0	43	2	US-09-032-019-1	Sequence 1, App1
96	155	100.0	43	2	US-09-481-980A-1	Sequence 1, App1
97	155	100.0	43	2	US-09-594-366-1	Sequence 1, App1
98	155	100.0	43	2	US-08-665-649-1	Sequence 1, App1
99	155	100.0	43	2	US-09-519-019A-1	Sequence 1, App1

100 155 100.0 43 2 US-09-915-342-1 Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-07-744-767A-2
; Sequence 2, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Magglio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwesman, Lundberg & Moesner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kuecling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-744-767A-2

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGNKGAIIIGLMVGAVIA 32
DB 12 VHHOKLVFAEDVGNKGAIIIGLMVGAVIA 42

RESULT 2
US-08-179-574-1
; Sequence 1, Application US/08179574
; Patent No. 5506097
; GENERAL INFORMATION:
; APPLICANT: Huntilton Potter
; APPLICANT: Usamah Kayyal
; TITLE OF INVENTION: Compounds and Methods for Inhibiting
; TITLE OF INVENTION: 6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/819,361
; FILING DATE: 13-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU90-03A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-179-574-1

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGNKGAIIIGLMVGAVIA 32
DB 12 VHHOKLVFAEDVGNKGAIIIGLMVGAVIA 42

RESULT 3
US-08-347-144-1
; Sequence 1, Application US/08347144
; Patent No. 5589154
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,144
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
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ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 4
US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5652092

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-462-859A-19
Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 5
US-08-123-659A-19
Sequence 19, Application US/08123659A
Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-123-659A-19

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 6
US-08-464-247A-19
Sequence 19, Application US/08464247A
Patent No. 5693478

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-19

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 32
Db 12 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 42

RESULT 7
US-08-464-248A-19
Sequence 19, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vilek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 32
Db 12 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 42

RESULT 8
US-08-476-464A-1
Sequence 1, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-1

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 32
Db 12 VHHQKLVFFADVGSNKGAIIGLMVGGVIA 42

RESULT 9
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglo, John E.
APPLICANT: Mantyn, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVSNKGAIIIGLMVGCVIA 32
DB 12 VHHQKLVFAEDVSNKGAIIIGLMVGCVIA 42

RESULT 10
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-5

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVSNKGAIIIGLMVGCVIA 32
DB 12 VHHQKLVFAEDVSNKGAIIIGLMVGCVIA 42

RESULT 11
US-08-268-348A-1
Sequence 1, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Dobell, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-1

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred.No.1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 12
US-08-433-734-2
Sequence 2, Application US/08433734

Patent No. 5837473
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muecling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muecling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-433-734-2
Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred.No.1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 13
US-08-609-090-9
Sequence 9, Application US/08609090

Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BRCKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-609-090-9
Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred.No.1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 14
US-07-737-371E-72
Sequence 72, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 15

US-08-422-333-4
Sequence 4, Application US/08422333
Patent No. 5912410

GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 16
US-08-682-245A-4
Sequence 4, Application US/08682245A
Patent No. 5919631

GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-4

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 17

US-08-986-948-5
Sequence 5, Application US/08986948
Patent No. 5955317

GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhito
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-5

Query Match      100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 18
US-08-717-551A-2
; Sequence 2, Application US/08717551A
; Patent No. 6071493
; GENERAL INFORMATION:
; APPLICANT: Dana Guillan
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: 6 No. 6071493 Iris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/717,551A
FILING DATE: Sept-20-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-551A-2

Query Match      100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-09-388-890-1
; Sequence 1, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
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ORGANISM: AMYLOID PEPTIDE
US-09-388-890-1

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 20
US-09-005-215-20
Sequence 20, Application US/09005215

Patent No. 6172043
GENERAL INFORMATION:
APPLICANT: Ingram, Vernon M.
APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0656/7035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-005-215-20

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 21
US-09-242-724-23
Sequence 23, Application US/09242724

Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-242-724-23

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 22
US-08-922-930-2
Sequence 2, Application US/08922930
Patent No. 6451544
GENERAL INFORMATION:
APPLICANT: Dana Giuliani
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 6451544 is LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,930
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-930-2

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 VHQKLVFPAEDVGSNKGAIIGLMVGVIYA 32
      |||||
Db     12 VHQKLVFPAEDVGSNKGAIIGLMVGVIYA 42

```

```

RESULT 23
US-09-660-954-1
: Sequence 1, Application US/09660954
: Patent No. 6471960
: GENERAL INFORMATION:
: APPLICANT: ANDERSON, STEPHEN
: TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWEY & SIMON
: STREET: 1299 PENNSYLVANIA AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: US
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/660,954
: FILING DATE: 13-SEP-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/388,890
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/686,959
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: AUERBACH, JEFFREY I.
: REGISTRATION NUMBER: 32,680
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 383-7451
: TELEFAX: (202) 383-6610
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEITICAL: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: ORGANISM: AMYLOID PEPTIDE
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-660-954-1

Query Match 100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2 VHQKLVFFAEVDGNSKGAIIIGLMTGVVIA 32
| | | | | | | | | | | | | | | | | |
DB 12 VHQKLVFFAEVDGNSKGAIIIGLMTGVVIA 42

RESULT 24
US-08-923-055-2
: Sequence 2, Application US/08923055
: Patent No. 6475742
: GENERAL INFORMATION:
: APPLICANT: Dana Giulian
: TITLE OF INVENTION: Identification of Agents that Protect
: TITLE OF INVENTION: Against Inflammatory Injury to Neurons
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
:

```

```

1 ADDRESS: Woodcock Washburn Kurtz Mackiewicz
2 ADDRESS: & No. 645742x1s LLP
3 STREET: One Liberty Place - 46th Floor
4 CITY: Philadelphia
5 STATE: PA
6 COUNTRY: USA
7 ZIP: 19103
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
11 COMPUTER: IBM PS/2
12 OPERATING SYSTEM: PC-DOS
13 SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
14
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/923.055
17 FILING DATE: Sept-03-97
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:
21
22 FILING DATE:
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Lori Y. Bearde11
26 REGISTRATION NUMBER: 34,293
27 REFERENCE/DOCKET NUMBER: BYLR-0038
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (215) 568-3100
30 TELEFAX: (215) 568-9439
31
32 INFORMATION FOR SEQ ID NO: 2:
33
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 42 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38
39 MOLECULE TYPE: peptide
40
41 US-08-923-055-2

```

```

Query Match      100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,9e-17;
Matches    31; Conservative   0; Mismatches   0; Indels     0; Gaps     0;

OY          2 VH0KLVFPAEDVGSNKGAIITGLWVGGVIA 32
|||||
Db          12 VH0KLVFPAEDVGSNKGAIITGLWVGGVIA 42
|||||

RESULT 25
US-08-922-889-2
; Sequence 2, Application US/08922889
; Patent No. 6475745
; GENERAL INFORMATION:
APPLICANT: Dana Guillan
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESS: & No. 6475745r1s LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,889
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-922-889-2
;
Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 26
US-09-731-460-1
; Sequence 1, Application US/09731460
; Patent No. 6455335
; GENERAL INFORMATION:
; APPLICANT: Chokier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOKIER-04302
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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US-09-731-460-1
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Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 27
US-09-133-866-2
; Sequence 2, Application US/09133866
; Patent No. 6600017
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: 60/055,660
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-09-133-866-2
;
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 28
US-09-723-384-1
; Sequence 1, Application US/09723384
; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
;
US-09-723-384-1
;
Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 29
US-09-724-961-42
; Sequence 42, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-961-42

Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAPEDVGSNKGAIIGLMVGVVIA 32
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Db       12 VHHQKLVFPAPEDVGSNKGAIIGLMVGVVIA 42

RESULT 30
US-09-724-552-1
/ Sequence 1, Application US/09724552
/ Patent No. 6750324
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ APPLICANT: Neuralab Limited
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 15270J-004740US
/ CURRENT APPLICATION NUMBER: US/09/724,552
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US/09/580,019A
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 09/322,289
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-09-724-552-1

Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAPEDVGSNKGAIIGLMVGVVIA 32
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Db       12 VHHQKLVFPAPEDVGSNKGAIIGLMVGVVIA 42

Search completed: September 28, 2006, 06:27:11
Job time : 24.5291 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2006, 06:58:47 ; Search time 73.3274 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
Sequence: 1 XVHHQKLVFADVGSKNGAIGLMVGIVIA 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	155	100.0	42	2	US-08-923-055-2
3	155	100.0	42	3	US-09-867-847-1
4	155	100.0	42	3	US-09-956-625-26
5	155	100.0	42	3	US-09-962-955C-37
6	155	100.0	42	3	US-09-962-955C-37
7	155	100.0	42	3	US-09-848-616-174
8	155	100.0	42	3	US-09-865-294-65
9	155	100.0	42	3	US-09-792-079-13
10	155	100.0	42	3	US-09-825-242-1
11	155	100.0	42	3	US-09-930-915A-293
12	155	100.0	42	4	US-10-051-496-2
13	155	100.0	42	4	US-10-082-804-7
14	155	100.0	42	4	US-10-217-584-2
15	155	100.0	42	4	US-10-169-580-2
16	155	100.0	42	4	US-10-278-181-1
17	155	100.0	42	4	US-10-143-534-2
18	155	100.0	42	4	US-10-190-548A-1
19	155	100.0	42	4	US-10-051-663-2
20	155	100.0	42	4	US-10-159-279-13
21	155	100.0	42	4	US-10-050-902-220
22	155	100.0	42	4	US-10-050-902-220
23	155	100.0	42	4	US-10-082-014-81
24	155	100.0	42	4	US-10-372-076-82
25	155	100.0	42	4	US-10-455-218-2
26	155	100.0	42	4	US-10-231-298B-15
27	155	100.0	42	4	US-10-231-470C-15

28	155	100.0	42	4	US-10-231-063C-15	Sequence 15, Appl
29	155	100.0	42	4	US-10-366-125-28	Sequence 28, Appl
30	155	100.0	42	4	US-10-411-544-2	Sequence 2, Appl
31	155	100.0	42	4	US-10-231-213D-15	Sequence 15, Appl
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33	155	100.0	42	4	US-10-337-261-2	Sequence 15, Appl
34	155	100.0	42	4	US-10-363-082-1	Sequence 1, Appl
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37	155	100.0	42	4	US-10-617-876-7	Sequence 7, Appl
38	155	100.0	42	4	US-10-429-216-1	Sequence 5, Appl
39	155	100.0	42	4	US-10-656-624-5	Sequence 91, Appl
40	155	100.0	42	4	US-10-622-087-91	Sequence 91, Appl
41	155	100.0	42	4	US-10-683-815-11	Sequence 11, Appl
42	155	100.0	42	4	US-10-732-862A-95	Sequence 95, Appl
43	155	100.0	42	4	US-10-806-006-293	Sequence 293, App
44	155	100.0	42	4	US-10-416-262B-6	Sequence 6, Appl
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46	155	100.0	42	4	US-10-805-913-293	Sequence 1, Appl
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49	155	100.0	42	4	US-10-815-353-1	Sequence 1, Appl
50	155	100.0	42	4	US-10-815-391-1	Sequence 55, Appl
51	155	100.0	42	4	US-10-772-656-55	Sequence 3, Appl
52	155	100.0	42	4	US-10-478-308-3	Sequence 1, Appl
53	155	100.0	42	4	US-10-478-307-3	Sequence 3, Appl
54	155	100.0	42	4	US-10-402-420-1	Sequence 1, Appl
55	155	100.0	42	4	US-10-771-174A-1	Sequence 1, Appl
56	155	100.0	42	5	US-10-828-548-1	Sequence 1, Appl
57	155	100.0	42	5	US-10-864-107-2	Sequence 2, Appl
58	155	100.0	42	5	US-10-816-380-1	Sequence 1, Appl
59	155	100.0	42	5	US-10-485-310-19	Sequence 19, Appl
60	155	100.0	42	5	US-10-889-999-42	Sequence 42, Appl
61	155	100.0	42	5	US-10-890-070-42	Sequence 42, Appl
62	155	100.0	42	5	US-10-861-614-65	Sequence 65, Appl
63	155	100.0	42	5	US-10-481-387-2	Sequence 2, Appl
64	155	100.0	42	5	US-10-890-000-42	Sequence 42, Appl
65	155	100.0	42	5	US-10-788-666-1	Sequence 1, Appl
66	155	100.0	42	5	US-10-923-471-1	Sequence 1, Appl
67	155	100.0	42	5	US-10-823-463-42	Sequence 42, Appl
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69	155	100.0	42	5	US-10-933-559-1	Sequence 1, Appl
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73	155	100.0	42	5	US-10-883-150-3	Sequence 3, Appl
74	155	100.0	42	5	US-10-923-474-1	Sequence 1, Appl
75	155	100.0	42	5	US-10-884-892-1	Sequence 1, Appl
76	155	100.0	42	5	US-10-822-968-42	Sequence 42, Appl
77	155	100.0	42	5	US-10-933-206-37	Sequence 37, Appl
78	155	100.0	42	5	US-10-777-792-42	Sequence 42, Appl
79	155	100.0	42	5	US-10-825-958-1	Sequence 1, Appl
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81	155	100.0	42	5	US-10-852-950-1	Sequence 1, Appl
82	155	100.0	42	5	US-10-890-071-42	Sequence 42, Appl
83	155	100.0	42	5	US-10-903-279-1	Sequence 1, Appl
84	155	100.0	42	5	US-10-810-881A-50	Sequence 50, Appl
85	155	100.0	42	5	US-10-890-024-42	Sequence 42, Appl
86	155	100.0	42	5	US-10-934-819-1	Sequence 1, Appl
87	155	100.0	42	5	US-10-508-586-1	Sequence 1, Appl
88	155	100.0	42	5	US-10-505-313-27	Sequence 27, Appl
89	155	100.0	42	5	US-10-770-712-35	Sequence 35, Appl
90	155	100.0	42	5	US-10-923-267-1	Sequence 1, Appl
91	155	100.0	42	5	US-10-928-926-42	Sequence 42, Appl
92	155	100.0	42	5	US-10-923-603-1	Sequence 1, Appl
93	155	100.0	42	5	US-10-934-818-1	Sequence 1, Appl
94	155	100.0	42	5	US-10-945-751-157	Sequence 157, App
95	155	100.0	42	5	US-10-945-133-1	Sequence 1, Appl
96	155	100.0	42	6	US-10-966-919B-3	Sequence 3, Appl
97	155	100.0	42	6	US-11-058-757-42	Sequence 42, Appl
98	155	100.0	42	6	US-11-004-053-37	Sequence 37, Appl
99	155	100.0	42	6	US-11-007-643-37	Sequence 37, Appl
100	155	100.0	42	6	US-11-007-644-37	Sequence 37, Appl

ALIGNMENTS

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RESULT 1
US-08-922-930-2
; Sequence 2, Application US/08922930
; Publication No. US20010016326A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: & No. 645154415 LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,930
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-922-930-2

Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIIGLWGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIIGLWGVVIA 42

RESULT 2
US-08-923-055-2
; Sequence 2, Application US/08923055
; Publication No. US20010016327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: & No. US20010016327A115 LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
```

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; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,055
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-923-055-2

Query Match          100.0%; Score 155; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 VHHQKLVFPAEDVGSNKGAIIIGLWGVVIA 32
Db      12 VHHQKLVFPAEDVGSNKGAIIIGLWGVVIA 42

RESULT 3
US-09-867-847-1
; Sequence 1, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lisa
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCES: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-1

Query Match          100.0%; Score 155; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHQKLVFPAEDVGSNKGAIIIGLWGVVIA 32
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Db 12 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 4

US-09-956-625-26

/ Sequence 26, Application US/09956625

/ Patent No. US20020119926A1

/ GENERAL INFORMATION:

/ APPLICANT: Fraser, Paul

/ TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof

/ FILE REFERENCE: 14445-503

/ CURRENT APPLICATION NUMBER: US/09/956,625

/ CURRENT FILING DATE: 2001-09-19

/ PRIOR APPLICATION NUMBER: 60/233,482

/ PRIOR FILING DATE: 2000-09-19

/ NUMBER OF SEQ ID NOS: 27

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 26

/ LENGTH: 42

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-09-956-625-26

Query Match 100.0%; Score 155; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 32

Db 12 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 5

US-09-731-460-1

/ Sequence 1, Application US/09731460

/ Patent No. US20020137112A1

/ GENERAL INFORMATION:

/ APPLICANT: Chojkier, Mario

/ APPLICANT: Buck, Martina

/ TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's

/ FILE REFERENCE: CHOJKIER-04302

/ CURRENT APPLICATION NUMBER: US/09/731,460

/ CURRENT FILING DATE: 2000-12-07

/ NUMBER OF SEQ ID NOS: 1

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 1

/ LENGTH: 42

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-731-460-1

Query Match 100.0%; Score 155; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 32

Db 12 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 6

US-09-962-955C-37

/ Sequence 37, Application US/09962955C

/ Publication No. US20030013648A1

/ GENERAL INFORMATION:

/ APPLICANT: Gerardo M. Castillo

/ APPLICANT: Alan D. Snow

/ NUMBER OF SEQUENCES: 37

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Patrick M. Dwyer

/ STREET: ProteoTech, Inc, 1818 Westlake Avenue N, Suite 114

/ CITY: Seattle

/ STATE: WA (Washington)

/ COUNTRY: United States of America

/ ZIP: 98109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage

/ COMPUTER: IBM PC

/ OPERATING SYSTEM: Windows 98

/ SOFTWARE: WordPerfect 9

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/962,955C

/ FILING DATE: 24-September-2001

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 09/938,275

/ FILING DATE: 22-August-2001

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Dwyer, Patrick M.

/ REGISTRATION NUMBER: 32,411

/ REFERENCE/DOCKET NUMBER: PROTEO.P03CI

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (206) 343-7074

/ TELEFAX: (206) 343-7085

/ INFORMATION FOR SEQ ID NO: 37:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 42 AMINO ACIDS

/ TYPE: AMINO ACID

/ STRANDEDNESS:

/ TOPOLOGY: LINEAR

/ ORIGINAL SOURCE:

/ ORGANISM: MOUSE

/ FEATURE:

/ OTHER INFORMATION: Also referred to in the specification as "AB 1-42"

US-09-962-955C-37

Query Match 100.0%; Score 155; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 32

Db 12 VHHOKLVFFAEDVGSNKGAIIIGLMVGAVIA 42

RESULT 7

US-09-848-616-174

/ Sequence 174, Application US/09848616

/ Publication No. US20030054010A1

/ GENERAL INFORMATION:

/ APPLICANT: Sebbel, Peter

/ APPLICANT: Dunant, Nicolas

/ APPLICANT: Bachmann, Martin

/ APPLICANT: Tisot, Alain

/ APPLICANT: Lechner, Franziska

/ TITLE OF INVENTION: Molecular Antigen Array

/ FILE REFERENCE: 1700.0180002

/ CURRENT APPLICATION NUMBER: US/09/848,616

/ CURRENT FILING DATE: 2001-05-05

/ NUMBER OF SEQ ID NOS: 186

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 174

/ LENGTH: 42

/ TYPE: PRT

/ ORGANISM: Unknown

/ FEATURE:

/ OTHER INFORMATION: Amyloid Beta Peptide

US-09-848-616-174

Query Match 100.0%; Score 155; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VHQKLVFFAEDVGSNKGAIIGLMVGGVIA 32
 |||||
D6 12 VHQKLVFPAEDVGSNKGAIIGLMVGGVIA 42

RESULT 8
US-09-865-294-65
Sequence 65, Application US/09865294

```

: TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
: TITLE OF INVENTION: Prevention and treatment of Alzheimer's Disease
: FILE REFERENCE: 1151.4167
: CURRENT APPLICATION NUMBER: US/09/865,294
: CURRENT FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 76
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 65
: LENGTH: 42
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-865-294-65

```

Query Match	100.0%	Score 155;	DB 3;	Length 42;
Best Local Similarity	100.0%	Pred. No. 2.3e-15;		
Matches	31;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0
QY	2	VHQQLTVFPAEDVGSNKGATIGLMVG	GVVIA	32
		VHQQLTVFPAEDVGSNKGATIGLMVG	GVVIA	42
DB	12	VHQQLTVFPAEDVGSNKGATIGLMVG	GVVIA	42

RESULT 9
US-09-792-079-13
Sequence 13, Application US/09792079
Publication No. US20030083277A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: Hersch, Louis B.
APPLICANT: Mukherjee, Arish
TITLE OF INVENTION: Use Of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzheimer
TITLE OF INVENTION: Disease Patients
FILE REFERENCE: 050223-0261
CURRENT APPLICATION NUMBER: US/09/792,079
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,826
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-792-079-13

Query Match Similarity	100.0%	Score 155;	DB 3;	Length 42;
Best Local Similarity	100.0%	Pred. No. 2.3e-15;		
Matches	31;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0
Qy	2	VHQQKLVFFPAEDVGSNKGAIIGLMVGGVVIA	32	
Db	12	VHQQKLVFFPAEDVGSNKGAIIGLMVGGVVIA	42	

```

RESULT10
US-09-825-242-1
; Sequence 1, Application US/09835242
; Publication No. US20030092000A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited

```

```

? TITLE REFERENCE: Prevention and Treatment of Amyloidogenic Diseases
? FILE REFERENCE: 15270J-004720US
? CURRENT APPLICATION NUMBER: US/09/825,242
? CURRENT FILING DATE: 2001-04-02
? PRIOR APPLICATION NUMBER: 09/201,430
? PRIOR FILING DATE: 1998-11-30
? PRIOR APPLICATION NUMBER: US 60/080,970
? PRIOR FILING DATE: 1998-04-07
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 42
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: human Abeta42 beta-amyloid peptide
? US-09-825-242-1

```

	Query Match	100.0%;	Score 155;	DB 3;	Length 42;
	Best Local Similarity	100.0%;	Pred. No.	2,3e-15;	
D6	Matches	31;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY		2 VHHOKLVFPADVDSNKGATIIIGLMVGGVIA	32		
D6		12 VHHOKLVFPADVGSNKGAIIIGLWVGGVIA	42		

RESULT 11
 US-09-930-915A-293
 Sequence 293, Application US/09930915A
 Publication No. US20030138765A1
 GENERAL INFORMATION:
 APPLICANT: Birkett, Ashley J.
 TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
 TITLE OF INVENTION: STABILITY
 FILE REFERENCE: 4564/83501 ICC-102.2 PCT
 CURRENT APPLICATION NUMBER: US/09/930,915A
 CURRENT FILING DATE: 2001-08-15
 PRIOR APPLICATION NUMBER: 60/226,867
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 60/225,843
 PRIOR FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 313
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 293
 LENGTH: 42
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-930-915A-293

Query Match	100.0%	Score 155;	DB 3;	Length 42;
Best Local Similarity	100.0%	Prod. No. 2,3e-15;		
Matches	31;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	2	VHOKLIVFAEDVGSNKGAIITGLMWGVVIA	32	
db	12	VHOKLIVFAEDVGSNKGAIITGLMWGVVIA	42	

RESULT 12
 US-10-051-496-2
 Sequence 2, Application US/10051496
 Publication No. US20020182660A1
 GENERAL INFORMATION:
 APPLICANT: Kei-Lai L. Fong
 TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
 Full Length Beta-Amyloid peptide - Abeta(1-40), Abeta(1-39)
 Abeta(1-41), Abeta(1-42) and Abeta(1-43)
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kei-Lai L. Fong
 STREET: 1004 West 8th Avenue
 CITY: King of Prussia

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US20020182660A1epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183,407
FILING DATE: 18-February-2000
ATTORNEY/AGENT INFORMATION:
NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662
REFERENCE/DOCKET NUMBER: PBI-PT001.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1-42
IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-051-496-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
|||
12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

Db 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 13
US-10-082-804-7
Sequence 7, Application US/10082804
Publication No. US20020194632A1
GENERAL INFORMATION:
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Transgenic Knockouts of BACE-1
FILE REFERENCE: MEBB 02-329-A
CURRENT APPLICATION NUMBER: US/10/082,804
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/271,092
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/271,514
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/293,762
PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
|||
12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

Db 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 14
US-10-217-584-2
Sequence 2, Application US/10217584
Publication No. US20030077261A1
GENERAL INFORMATION:
APPLICANT: Paris, Daniel
TITLE OF INVENTION: Modulation of Angiogenesis by A-beta Peptides
FILE REFERENCE: USF-T161XC1
CURRENT APPLICATION NUMBER: US/10/217,584
PRIOR FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,656
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(42)
OTHER INFORMATION: A-beta 1-42 peptide
US-10-217-584-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
|||
12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

Db 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 15
US-10-169-580-2
Sequence 2, Application US/10169580
Publication No. US20030100477A1
GENERAL INFORMATION:
APPLICANT: Yamouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR SUPPRESSING B-AMYLOID PRODUCTION
FILE REFERENCE: Q70898
CURRENT APPLICATION NUMBER: US/10/169,580
PRIOR FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 2000-111037
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: PCT/JP01/03555
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens

US-10-169-580-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 16

US-10-278-181-1
; Sequence 1, Application US/10278181
; Publication No. US20030104488A1
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; TITLE OF INVENTION: Disease
; FILE REFERENCE: CHOJKIER-04302
; CURRENT APPLICATION NUMBER: US/10/278,181
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/731,460
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-278-181-1

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 17
US-10-143-534-2
; Sequence 2, Application US/10143534
; Publication No. US20030105152A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M0656/70078
; CURRENT APPLICATION NUMBER: US/10/143,534
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 10/051,663
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-143-534-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 18
US-10-190-548A-1
; Sequence 1, Application US/10190548A
; Publication No. US20030109435A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Premner, Irene
; APPLICANT: Wright, Sarah
; APPLICANT: Yednock, Theodore
; APPLICANT: Rydel, Russell
; TITLE OF INVENTION: Methods of Inhibiting Amyloid Toxicity
; FILE REFERENCE: 08576.0030-00
; CURRENT APPLICATION NUMBER: US/10/190,548A
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-548A-1

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-10-051-663-2
; Sequence 2, Application US/10051663
; Publication No. US20030114510A1
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; APPLICANT: Stockwell, Brent R.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
; FILE REFERENCE: M0656/7071
; CURRENT APPLICATION NUMBER: US/10/051,663
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/706,574
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-051-663-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 20
US-10-159-279-13
; Sequence 13, Application US/10159279
; Publication No. US20030165481A1

```
/ GENERAL INFORMATION:
/ APPLICANT: University of Kentucky Research Foundation
/ APPLICANT: Hershey, Louis B.
/ APPLICANT: Mukherjee, Atish
/ TITLE OF INVENTION: Use of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzhei
/ FILE REFERENCE: 050229-0298
/ CURRENT APPLICATION NUMBER: US/10/159,279
/ CURRENT FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/184,826
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 09/792,079
/ PRIOR FILING DATE: 2001-02-26
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 13
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-159-279-13
```

```
Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 32
      |||
Db      12 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 42
```

```
RESULT 21
US-10-050-902-220
/ Sequence 220, Application US/10050902
/ GENERAL INFORMATION:
/ APPLICANT: Renner, Wolfgang A.
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Tisot, Alain
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Lechner, Franziska
/ APPLICANT: Seibel, Peter
/ TITLE OF INVENTION: Molecular Antigen Array
/ FILE REFERENCE: 1700.0190004
/ CURRENT APPLICATION NUMBER: US/10/050,902
/ CURRENT FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/262,379
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: US 60/288,549
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/326,998
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 220
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Amyloid Beta Peptide
US-10-050-902-220
```

```
US-10-050-902-220
```

```
Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 32
      |||
Db      12 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 42
```

```
RESULT 22
US-10-050-898-220
```

```
/ Sequence 220, Application US/10050898
/ Publication No. US20030175711A1
/ GENERAL INFORMATION:
/ APPLICANT: Renner, Wolfgang A.
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Tisot, Alain
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Lechner, Franziska
/ APPLICANT: Seibel, Peter
/ APPLICANT: Plosek, Christine
/ APPLICANT: Ortman, Rainer
/ APPLICANT: Luond, Rainer
/ APPLICANT: Staendlel, Mathias
/ APPLICANT: Frey, Peter
/ TITLE OF INVENTION: Molecular Antigen Array
/ FILE REFERENCE: 1700.0190005
/ CURRENT APPLICATION NUMBER: US/10/050,898
/ CURRENT FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/262,379
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: US 60/288,549
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/326,998
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 220
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Amyloid Beta Peptide
US-10-050-898-220
```

```
Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 32
      |||
Db      12 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 42
```

```
RESULT 23
US-10-082-014-81
/ Sequence 81, Application US/10082014
/ Publication No. US20030185858A1
/ GENERAL INFORMATION:
/ APPLICANT: Birkett, Ashley J.
/ TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C
/ FILE REFERENCE: ICC-130.0 4564/85124
/ CURRENT APPLICATION NUMBER: US/10/082,014
/ CURRENT FILING DATE: 2002-02-22
/ PRIOR APPLICATION NUMBER: 09/930,915
/ PRIOR FILING DATE: 2001-08-15
/ NUMBER OF SEQ ID NOS: 290
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 81
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Alzheimer's disease b-Amyloid
US-10-082-014-81
```

```
Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 32
      |||
Db      12 VHHOKLVFAEDVGNKGAIIIGLMVGGVIA 42
```

```
RESULT 24
```

```
US-10-372-076-82
; Sequence 82, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Alzheimer's disease b-Amyloid
US-10-372-076-82

Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 25
US-10-455-218-2
; Sequence 2, Application US/10455218
; Publication No. US20030204051A1
; GENERAL INFORMATION:
; APPLICANT: Glabe, Charles
; APPLICANT: Garzon-Rodriguez, William
; TITLE OF INVENTION: FLUORESCENT AMYLOID ABETA PEPTIDES AND
; FILE REFERENCE: 50016/002002
; CURRENT APPLICATION NUMBER: US/10/455,218
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US/09/133,866
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-455-218-2

Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 26
US-10-231-298B-15
; Sequence 15, Application US/10231298B
; Publication No. US20030219853A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Cross-linking a Compound
; FILE REFERENCE: SAMG/0006
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; CURRENT APPLICATION NUMBER: US/10/231,298B
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-298B-15

Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 27
US-10-231-470C-15
; Sequence 15, Application US/10231470C
; Publication No. US20030219857A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Having Broad Substrate
; FILE REFERENCE: SAMG/0003
; CURRENT APPLICATION NUMBER: US/10/231,470C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-470C-15

Query Match          100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 32
Db 12 VHHOKLVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 28
US-10-231-063C-15
; Sequence 15, Application US/10231063C
; Publication No. US20030224476A1
; GENERAL INFORMATION:
; APPLICANT: Chou, Szu-Yi
; TITLE OF INVENTION: Method of Producing Transglutaminase Reactive Compound
; FILE REFERENCE: SAMG/0004
; CURRENT APPLICATION NUMBER: US/10/231,063C
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/361,166
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/363,445
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 42
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-231-063C-15

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 32
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DB 12 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 42

RESULT 29

US-10-366-125-28
Sequence 28, Application US/10366125
Publication No. US20030228259A1
GENERAL INFORMATION:

APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: EASILY ACCESSIBLE TO DIRECT SAMPLING. NON-INVASIVELY,
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
FILE REFERENCE: 416272003500
CURRENT APPLICATION NUMBER: US/10/366,125

PRIOR FILING DATE: 2003-02-12
PRIORITY FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28

LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-366-125-28

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 32
|||||
DB 12 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 42

RESULT 30

US-10-411-544-2
Sequence 2, Application US/10411544
Publication No. US20030232758A1
GENERAL INFORMATION:

APPLICANT: St. George-Hyslop, Peter
APPLICANT: McLaurin, Joanne
TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzhe
FILE REFERENCE: LI01547
CURRENT APPLICATION NUMBER: US/10/411,544
CURRENT FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-544-2

Query Match 100.0%; Score 155; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 32
|||||
DB 12 VHHOKLVFPAEDVGSNKGAIIGLMVGAVIA 42

Search completed: September 28, 2006, 07:09:23
Job time : 75.494 secs

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OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 / Search time 12.4843 Seconds
(without alignments)
199.069 Million cell updates/sec

Title: US-09-731-899-6
Perfect score: 155
Sequence: 1 XVHHQKLVFADVGSNKGATIGLWGVAVIA 32

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 285145 seqs, 77663843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Published Applications AA.New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	155	100.0	32	1	US-09-731-899-6
2	155	100.0	40	1	US-09-731-899-5
3	155	100.0	40	6	US-10-966-645-38
4	155	100.0	42	1	US-09-731-899-3
5	155	100.0	42	6	US-10-890-071-42
6	155	100.0	42	6	US-10-544-093-1
7	155	100.0	42	6	US-10-546-547-3
8	155	100.0	42	6	US-10-966-645-36
9	155	100.0	42	7	US-11-104-300-2
10	155	100.0	42	7	US-11-297-316-1
11	155	100.0	42	7	US-11-287-157A-49
12	155	100.0	43	1	US-09-731-899-4
13	155	100.0	43	7	US-11-348-091-1
14	155	100.0	56	6	US-10-544-093-16
15	155	100.0	56	6	US-10-544-093-19
16	155	100.0	58	6	US-10-515-919A-30
17	155	100.0	58	6	US-10-544-093-12
18	155	100.0	58	6	US-10-544-093-14
19	155	100.0	58	6	US-10-544-093-27
20	155	100.0	59	1	US-09-731-899-1
21	155	100.0	60	6	US-10-544-093-20
22	155	100.0	64	6	US-10-544-093-13
23	155	100.0	79	6	US-10-544-093-15
24	155	100.0	99	6	US-10-544-093-22
25	155	100.0	99	6	US-10-544-093-24

26	155	100.0	142	6	US-10-544-093-17	Sequence 17, Appl
27	155	100.0	142	6	US-10-544-093-21	Sequence 21, Appl
28	155	100.0	142	6	US-10-544-093-23	Sequence 23, Appl
29	155	100.0	185	6	US-10-544-093-18	Sequence 18, Appl
30	155	100.0	203	6	US-10-544-093-26	Sequence 26, Appl
31	155	100.0	316	6	US-10-544-093-25	Sequence 25, Appl
32	155	100.0	695	6	US-10-515-919A-1	Sequence 1, Appl
33	155	100.0	695	6	US-10-511-269-7	Sequence 7, Appl
34	155	100.0	770	6	US-10-546-547-2	Sequence 2, Appl
35	155	100.0	751	6	US-10-511-269-9	Sequence 9, Appl
36	150	96.8	626	6	US-10-515-919A-13	Sequence 13, Appl
37	150	96.8	626	6	US-10-515-919A-18	Sequence 18, Appl
38	149	96.1	626	6	US-10-515-919A-15	Sequence 15, Appl
39	149	96.1	626	6	US-10-515-919A-20	Sequence 20, Appl
40	148	95.5	42	7	US-11-269-857-5	Sequence 5, Appl
41	148	95.5	626	6	US-10-515-919A-14	Sequence 14, Appl
42	148	95.5	626	6	US-10-515-919A-16	Sequence 16, Appl
43	148	95.5	626	6	US-10-515-919A-19	Sequence 19, Appl
44	148	95.5	626	6	US-10-515-919A-21	Sequence 21, Appl
45	147	94.8	38	6	US-10-966-645-39	Sequence 39, Appl
46	147	94.8	40	1	US-09-731-899-2	Sequence 2, Appl
47	147	94.8	40	6	US-10-966-645-44	Sequence 44, Appl
48	147	94.8	40	6	US-10-966-645-37	Sequence 37, Appl
49	147	94.8	626	6	US-10-515-919A-12	Sequence 12, Appl
50	147	94.8	626	6	US-10-515-919A-17	Sequence 17, Appl
51	147	94.8	695	6	US-10-538-410-96	Sequence 96, Appl
52	147	94.8	770	7	US-11-104-300-1	Sequence 1, Appl
53	142	91.6	42	6	US-10-515-919A-3	Sequence 3, Appl
54	142	91.6	42	6	US-10-515-919A-8	Sequence 8, Appl
55	141	91.0	40	7	US-11-104-300-3	Sequence 3, Appl
56	141	91.0	42	6	US-10-515-919A-5	Sequence 5, Appl
57	141	91.0	42	6	US-10-515-919A-10	Sequence 10, Appl
58	140	90.3	40	7	US-11-269-857-3	Sequence 3, Appl
59	140	90.3	42	6	US-10-515-919A-4	Sequence 4, Appl
60	140	90.3	42	6	US-10-515-919A-6	Sequence 6, Appl
61	140	90.3	42	6	US-10-515-919A-11	Sequence 11, Appl
62	140	90.3	42	6	US-10-515-919A-2	Sequence 2, Appl
63	139	89.7	42	6	US-10-515-919A-7	Sequence 7, Appl
64	139	89.7	42	6	US-10-515-919A-22	Sequence 22, Appl
65	136	87.7	42	6	US-10-515-919A-23	Sequence 23, Appl
66	136	87.7	43	6	US-10-515-919A-23	Sequence 23, Appl
67	125	80.6	26	1	US-09-731-899-7	Sequence 2, Appl
68	90	58.1	28	7	US-11-297-316-2	Sequence 75, Appl
69	84	54.2	19	6	US-10-890-071-75	Sequence 51230, A
70	56.5	35.8	1046	6	US-10-449-902-51230	Sequence 47542, A
71	55.5	35.8	618	6	US-10-449-902-47542	Sequence 21, Appl
72	55	35.2	10	6	US-10-890-071-21	Sequence 87461, A
73	54.5	35.2	826	7	US-11-056-3558-87461	Sequence 87460, A
74	54.5	35.2	826	7	US-11-056-3558-87460	Sequence 87459, A
75	54.5	35.2	1083	7	US-11-056-3558-87459	Sequence 20, Appl
76	54	34.8	19	6	US-10-890-071-20	Sequence 43, Appl
77	54	34.8	19	6	US-10-866-645-43	Sequence 43, Appl
78	54	34.8	19	6	US-10-866-645-45	Sequence 45, Appl
79	54	34.8	21	6	US-10-966-645-42	Sequence 42, Appl
80	53.5	34.5	921	6	US-10-519-135-6	Sequence 6, Appl
81	53	34.2	10	6	US-10-890-071-22	Sequence 22, Appl
82	52	33.5	10	6	US-10-890-071-27	Sequence 27, Appl
83	52	33.5	10	6	US-10-890-071-28	Sequence 28, Appl
84	51	32.9	10	6	US-10-890-071-26	Sequence 26, Appl
85	51	32.9	240	6	US-10-449-902-39653	Sequence 39652, A
86	51	32.9	429	7	US-11-056-3558-53789	Sequence 53788, A
87	51	32.9	556	7	US-11-056-3558-53788	Sequence 53787, A
88	51	32.9	642	7	US-11-056-3558-53787	Sequence 53786, A
89	50.5	32.6	671	6	US-10-449-902-52071	Sequence 52070, A
90	50.5	32.6	883	7	US-11-056-3558-82397	Sequence 82396, A
91	50.5	32.6	896	7	US-11-056-3558-82396	Sequence 82395, A
92	50.5	32.6	927	7	US-11-056-3558-82395	Sequence 82394, A
93	50	32.3	9	7	US-11-434-997-20	Sequence 20, Appl
94	50	32.3	10	6	US-10-890-071-19	Sequence 19, Appl
95	50	32.3	10	6	US-10-890-071-24	Sequence 24, Appl
96	50	32.3	10	6	US-10-890-071-29	Sequence 29, Appl
97	50	32.3	10	6	US-10-890-071-30	Sequence 30, Appl
98	50	32.3	107	7	US-11-434-137-1970	Sequence 1970, Ap

99 50 32.3 107 7 US-11-434-184-1970 Sequence 1970, Ap
100 50 32.3 107 7 US-11-434-199-1970 Sequence 1970, Ap

ALIGNMENTS

RESULT 1
US-09-731-899-6

; Sequence 6, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-6

Query Match 100.0%; Score 155; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32

RESULT 2
US-09-731-899-5
; Sequence 5, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-5

Query Match 100.0%; Score 155; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 10 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 3
US-10-966-645-38

; Sequence 38, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFEMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRÉ JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISSER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 38
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-38

Query Match 100.0%; Score 155; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 10 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 4
US-09-731-899-3
; Sequence 3, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa is L-Asp, D-Asp, or L-Iso Asp
US-09-731-899-3

Query Match 100.0%; Score 155; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 5
US-10-890-071-42
; Sequence 42, Application US/10890071
; Publication No. US20060121038A9

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; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-890-071-42

Query Match          100.0%; Score 155; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 6
US-10-544-093-1
; Sequence 1, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-544-093-1

Query Match          100.0%; Score 155; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 7
US-10-546-547-3
; Sequence 3, Application US/10546547
; Publication No. US20060188951A1
; GENERAL INFORMATION:
; APPLICANT: Mook, In Hee
; APPLICANT: Hur, Ji Yeun
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```

; TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
; TITLE OF INVENTION: Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Sa
; FILE REFERENCE: DE-1646
; CURRENT APPLICATION NUMBER: US/10/546,547
; CURRENT FILING DATE: 2005-08-23
; PRIOR APPLICATION NUMBER: PCT/KR2004/000371
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 1-42 amino acid of amyloid a4 precursor protein (APP)
US-10-546-547-3

Query Match          100.0%; Score 155; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 8
US-10-966-645-36
; Sequence 36, Application US/10966645
; Publication No. US20060189523A1
; GENERAL INFORMATION:
; APPLICANT: SCHILLING, STEPHAN
; APPLICANT: HOFEMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRZEJ JOHANNES
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HEISER, ULRICH
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
; FILE REFERENCE: 20488/59
; CURRENT APPLICATION NUMBER: US/10/966,645
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 36
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-645-36

Query Match          100.0%; Score 155; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB      12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 9
US-11-104-300-2
; Sequence 2, Application US/11104300
; Publication No. US20060099211A1
; GENERAL INFORMATION:
; APPLICANT: Monthe, Carmen
; APPLICANT: Szabo, Paul
; APPLICANT: Weksler, Mark
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treatin
; FILE REFERENCE: 1676.027US1
; CURRENT APPLICATION NUMBER: US/11/104,300
; CURRENT FILING DATE: 2005-04-12
```

PRIOR APPLICATION NUMBER: US 60/561,423
PRIOR FILING DATE: 2004-04-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-104-300-2

Query Match 100.0%; Score 155; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 10
US-11-297-316-1
Sequence 1, Application US/11297316
Publication No. US20060141602A1
GENERAL INFORMATION:
APPLICANT: American Cyanamid Company
TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
FILE REFERENCE: 01142-0200-00304
CURRENT APPLICATION NUMBER: US/11/297,316
PRIOR FILING DATE: 2005-12-08
PRIOR APPLICATION NUMBER: 60/228,906
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-297-316-1

Query Match 100.0%; Score 155; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 11
US-11-287-157A-49
Sequence 49, Application US/11287157A
Publication No. US20060154863A1
GENERAL INFORMATION:
APPLICANT: SKUBATCH, HANNA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
FILE REFERENCE: 32051-701.201
CURRENT APPLICATION NUMBER: US/11/287,157A
PRIOR FILING DATE: 2005-11-25
PRIOR APPLICATION NUMBER: 60/658,859
PRIOR FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 60/652,287
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/630,880
PRIOR FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn version 3.3
SEQ ID NO 49
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-287-157A-49

Query Match 100.0%; Score 155; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 12
US-09-731-899-4
Sequence 4, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-731-899-4

Query Match 100.0%; Score 155; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 13
US-11-348-091-1
Sequence 1, Application US/11348091
Publication No. US20060211679A1
GENERAL INFORMATION:
APPLICANT: Han, Qi
TITLE OF INVENTION: Substituted Lactams as Inhibitors of Abeta Protein Production
FILE REFERENCE: BMS-PH-7164.1(C)
CURRENT APPLICATION NUMBER: US/11/348,091
PRIOR FILING DATE: 2006-02-06
PRIOR APPLICATION NUMBER: US 10/685,031
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 09/832,455
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/196,549
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-11-348-091-1

Query Match 100.0%; Score 155; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 14

US-10-544-093-16
; Sequence 16, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Padre-A-beta fragment fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(56)
; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16
Query Match 100.0%; Score 155; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 32
DB 25 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 55
RESULT 15
US-10-544-093-19
; Sequence 19, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (46)..(46)
; OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-19
Query Match 100.0%; Score 155; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 42
RESULT 16
US-10-515-919A-30
; Sequence 30, Application US/10515919A
; Publication No. US20060160146A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
; FILE REFERENCE: 084952
; CURRENT APPLICATION NUMBER: US/10/515,919A
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: PCT/JP03/06319
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: JP 2002-159472
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-515-919A-30
Query Match 100.0%; Score 155; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 32
DB 28 VHHQKLVFAEDVGSNKGAIIGLMVGVIA 58
RESULT 17
US-10-544-093-12
; Sequence 12, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 15270J-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial

```
/ FEATURE:
/ OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(43)
/ OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
/ OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12

Query Match          100.0%; Score 155; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 18
US-10-544-093-14
/ Sequence 14, Application US/10544093
/ Publication No. US20060188512A1
/ GENERAL INFORMATION:
/ APPLICANT: Vednock, Ted
/ APPLICANT: Vasquez, Nicki
/ APPLICANT: Bard, Frederique
/ APPLICANT: Seubert, Peter A.
/ TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
/ TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
/ FILE REFERENCE: 15270J-009820US
/ CURRENT APPLICATION NUMBER: US/10/544,093
/ PRIOR APPLICATION NUMBER: MO PCT/US2004/002856
/ PRIOR FILING DATE: 2004-01-31
/ PRIOR APPLICATION NUMBER: US 60/444,150
/ PRIOR FILING DATE: 2003-02-01
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 58
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(43)
/ OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
/ OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-14

Query Match          100.0%; Score 155; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-10-544-093-27
/ Sequence 27, Application US/10544093
/ Publication No. US20060188512A1
/ GENERAL INFORMATION:
/ APPLICANT: Vednock, Ted
/ APPLICANT: Vasquez, Nicki
/ APPLICANT: Bard, Frederique
/ APPLICANT: Seubert, Peter A.
/ TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
/ TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
/ FILE REFERENCE: 15270J-009820US
/ CURRENT APPLICATION NUMBER: US/10/544,093
```

```
/ CURRENT FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: MO PCT/US2004/002856
/ PRIOR FILING DATE: 2004-01-31
/ PRIOR APPLICATION NUMBER: US 60/444,150
/ PRIOR FILING DATE: 2003-02-01
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 27
/ LENGTH: 58
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Fusion protein
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(43)
/ OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
/ OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27

Query Match          100.0%; Score 155; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 20
US-09-731-899-1
/ Sequence 1, Application US/09731899
/ Publication No. US20060088548A1
/ GENERAL INFORMATION:
/ APPLICANT: Chain, Benjamin
/ TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
/ TITLE OF INVENTION: FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
/ FILE REFERENCE: 20555/120343-US1
/ CURRENT APPLICATION NUMBER: US/09/731,899
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 60/169,687
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 59
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-731-899-1

Query Match          100.0%; Score 155; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 32
DB 16 VHHQKLVFAEDVGSNKGAIIGLMVGVVIA 46

RESULT 21
US-10-544-093-20
/ Sequence 20, Application US/10544093
/ Publication No. US20060188512A1
/ GENERAL INFORMATION:
/ APPLICANT: Vednock, Ted
/ APPLICANT: Vasquez, Nicki
/ APPLICANT: Bard, Frederique
/ APPLICANT: Seubert, Peter A.
/ TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
/ TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
/ FILE REFERENCE: 15270J-009820US
/ CURRENT APPLICATION NUMBER: US/10/544,093
```



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; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-20
```

```

Query Match          100.0%; Score 155; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
      |||||
Db      12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42
```

```

RESULT 22
US-10-544-093-13
; Sequence 13, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Baird, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 64
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13
```

```

Query Match          100.0%; Score 155; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
      |||||
Db      12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42
```

```

RESULT 23
US-10-544-093-15
; Sequence 15, Application US/10544093
```

```

; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Baird, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-15
```

```

Query Match          100.0%; Score 155; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 7.6e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
      |||||
Db      12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42
```

```

RESULT 24
US-10-544-093-22
; Sequence 22, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Baird, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 99
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (57)..(99)
```

OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-22

Query Match 100.0%; Score 155; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 9, 6e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 25
US-10-544-093-24

Sequence 24, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vasquez, Ted
APPLICANT: Yednock, Ted
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2

SEQ ID NO 24
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-24

Query Match 100.0%; Score 155; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 9, 6e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 26
US-10-544-093-17

Sequence 17, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093

CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444, 150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: A-beta-A-beta-A-beta-Padre fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (87)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (132)..(132)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
US-10-544-093-17

Query Match 100.0%; Score 155; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 1, 4e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 27
US-10-544-093-21

Sequence 21, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444, 150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.

OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-21

Query Match 100.0%; Score 155; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 25 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 55

RESULT 28
US-10-544-093-23
Sequence 23, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 142
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (44)..(86)
OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (87)..(129)
OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-23

Query Match 100.0%; Score 155; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 12 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 29
US-10-544-093-18
Sequence 18, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (143)..(185)
OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-18

Query Match 100.0%; Score 155; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 32
DB 25 VHHOKLVFPAEDVGSNKGAIIGLMVGVVIA 55

RESULT 30
US-10-544-093-26
Sequence 26, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..(3)
OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (14)..(56)
OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (100)..(142)
OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (143)..(185)
OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-26

FILE REFERENCE: 15270J-009820US
CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 26
LENGTH: 203
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (81)..(123)
OTHER INFORMATION: Only a contiguous fragment of residues 81-123 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (161)..(203)
OTHER INFORMATION: Only a contiguous fragment of residues 161-203 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-26

Query Match 100.0%; Score 155; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 32
DB 12 VHHQKLVFFAEDVGSNKGAIIGLMVGSVVIA 42

Search completed: September 28, 2006, 07:10:54
Job time: 12.4843 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:11 ; Search time 69,4888 Seconds
(without alignments)
171.073 Million cell updates/sec

Title: US-09-731-899-7
Perfect score: 125
Sequence: 1 LVFPAEDVGSNKGAITGLMVGCVIA 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	26	4	AA884431 Partial s
2	125	100.0	27	8	ADT66748 Amyloid-b
3	125	100.0	32	4	AA884430 Partial s
4	125	100.0	32	8	ADJ71491 N-termina
5	125	100.0	33	8	ADJ71490 N-termina
6	125	100.0	34	8	ADJ71489 N-termina
7	125	100.0	35	8	ADJ71488 N-termina
8	125	100.0	36	8	ADJ71487 N-termina
9	125	100.0	37	8	ADJ71486 N-termina
10	125	100.0	37	8	ADJ71485 N-termina
11	125	100.0	37	8	ADJ71484 N-termina
12	125	100.0	38	8	ADJ71483 N-termina
13	125	100.0	39	8	ADJ71482 N-termina
14	125	100.0	40	4	AA884429 Partial s
15	125	100.0	40	4	ADJ71482 N-termina
16	125	100.0	40	8	ADJ71482 N-termina
17	125	100.0	40	8	ADJ71482 N-termina
18	125	100.0	40	8	ADJ71482 N-termina
19	125	100.0	40	8	ADJ71482 N-termina
20	125	100.0	40	9	ADJ71482 N-termina
21	125	100.0	40	9	ADJ71482 N-termina
22	125	100.0	40	9	ADJ71482 N-termina
23	125	100.0	41	2	AA845230 Beta amy1

24	125	100.0	41	8	ADJ71481 N-termina
25	125	100.0	42	1	AA883153 Lambda SM
26	125	100.0	42	2	AA810025 Beta-amy1
27	125	100.0	42	2	AA820330 Sequence
28	125	100.0	42	2	AA837867 Beta-amy1
29	125	100.0	42	2	AA860366 Beta-amy1
30	125	100.0	42	2	AA865284 Beta-amy1
31	125	100.0	42	2	AA895248 Beta/A4-a
32	125	100.0	42	2	AA888206 Rat A42 b
33	125	100.0	42	2	AA894591 Alzheimer
34	125	100.0	42	2	AA899536 Murine be
35	125	100.0	42	2	AA812828 Beta A4 p
36	125	100.0	42	2	AA864507 Neurotoxi
37	125	100.0	42	2	AA842989 Full leng
38	125	100.0	42	2	AA847230 Beta-amy1
39	125	100.0	42	2	AA849691 Human bet
40	125	100.0	42	2	AA899585 Mutant ag
41	125	100.0	42	2	AA881474 Synthetic
42	125	100.0	42	2	AA808607 Human bet
43	125	100.0	42	2	AA829093 A-beta-b1
44	125	100.0	42	2	AA825137 Human amy
45	125	100.0	42	2	AA892726 Human tac
46	125	100.0	42	2	AA833407 Human amy
47	125	100.0	42	3	AA869566 Beta-amy1
48	125	100.0	42	4	AA886134 Human Alz
49	125	100.0	42	4	AA835589 Beta/A4-a
50	125	100.0	42	4	AA849098 Human amy
51	125	100.0	42	4	AA884427 Partial s
52	125	100.0	42	4	AA884897 Human amy
53	125	100.0	42	4	AA891785 Amyloid b
54	125	100.0	42	4	AA891818 Amyloid b
55	125	100.0	42	4	AA891779 Amyloid b
56	125	100.0	42	4	AA891812 Amyloid b
57	125	100.0	42	4	AA891791 Amyloid b
58	125	100.0	42	4	AA882622 Amyloid-b
59	125	100.0	42	4	AA849395 Human amy
60	125	100.0	42	4	AA848830 Human amy
61	125	100.0	42	4	AA803425 Mouse amy
62	125	100.0	42	4	AA805484 Human pep
63	125	100.0	42	5	AA881321 Amyloid p
64	125	100.0	42	5	AA880961 Human amy
65	125	100.0	42	5	AA898727 Human amy
66	125	100.0	42	5	AA894281 Amyloid b
67	125	100.0	42	5	AA821438 Human bet
68	125	100.0	42	5	AA876029 Beta amy1
69	125	100.0	42	5	AA825335 Modified
70	125	100.0	42	5	AA815848 Beta-amy1
71	125	100.0	42	5	AA876483 Amino aci
72	125	100.0	42	5	AA826080 Beta amy1
73	125	100.0	42	5	AA868314 Human bet
74	125	100.0	42	5	AA896896 Human Amy
75	125	100.0	42	5	AA893988 Human bet
76	125	100.0	42	5	AA826500 Human bet
77	125	100.0	42	5	AA880593 Human amy
78	125	100.0	42	5	AA851864 Neuronal
79	125	100.0	42	5	AA875433 Amyloid p
80	125	100.0	42	5	AA883306 Amyloid-b
81	125	100.0	42	5	AA877990 Beta-amy1
82	125	100.0	42	6	AA855671 Human bet
83	125	100.0	42	6	AA808711 Amyloid b
84	125	100.0	42	6	AA816344 A-beta pr
85	125	100.0	42	6	AA808506 Human amy
86	125	100.0	42	6	AA833793 Beta-amy1
87	125	100.0	42	6	AA899423 Beta-amy1
88	125	100.0	42	6	AA882633 Beta t1b
89	125	100.0	42	6	AA896144 Human Abe
90	125	100.0	42	6	AA872233 Human bet
91	125	100.0	42	6	AA835428 Human bet
92	125	100.0	42	6	AA833218 Beta amy1
93	125	100.0	42	6	AA893782 Amino aci
94	125	100.0	42	6	AA863707 Rat amy1o
95	125	100.0	42	6	AA874126 Beta-amy1
96	125	100.0	42	6	AA889912 Abeta42 a

97	125	100.0	42	7	ADA37267	Human bet
98	125	100.0	42	7	ADB37652	Human bet
99	125	100.0	42	7	ADB85562	Beta-amy1
100	125	100.0	42	7	ADB75176	Amyloid b

ALIGNMENTS

RESULT 1

AAB84431 standard; peptide; 26 AA.

AAB84431;

22-AUG-2001 (first entry)

Partial sequence of a human beta-amyloid precursor protein.

Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;

Homo sapiens.

WO200142306-A2.

14-JUN-2001.

08-DEC-2000; 2000MO-US033203.

08-DEC-1999; 99US-0169687P.

(MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

Chain B;

WPI; 2001-381648/40.

Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to T cell epitope.

Claim 3; Page 43; 47pp; English.

The present sequence represents a partial sequence of a human beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a N- or C-terminal end-specific B cell epitope from a naturally occurring internal peptide cleavage product of a precursor or mature protein, as a free N- or C-terminus, joined to a T cell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betaAP peptides slow down, reduce or prevent the accumulation of amyloid beta peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They also block the interaction of amyloid beta peptides with other molecules that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide cleavage product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal

Sequence 26 AA:

Query Match 100.0%; Score 125; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 2,4e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LVFPAADVGSNKGAITGLMWGVVIA	26
DB	1	LVFPAADVGSNKGAITGLMWGVVIA	26

RESULT 2	ADT66748	standard; peptide; 27 AA.
ID	ADT66748	
AC	ADT66748;	
DT	30-DEC-2004	(first entry)
DE	Amyloid-beta17-42-CRA3	peptide for raising antibodies.

antitumor; dermatological; immunosuppressive; anti-HIV; hepatotropic; virucide; neurotropic; cytostatic; anticoagulant; antithyroid; antileukemic; antileukemic; uropathic; ophthalmological; vasotropic; catalytic antibody; covalently reactive polypeptide antigen analog; passive immunotherapy; autoimmune disease; systemic lupus erythematosus; HIV-1 infection; hepatitis C virus infection; Alzheimer's disease; cancer; blood coagulation disorder; asthma; rheumatoid arthritis; Reiter's syndrome; Sjogren's disease; bird shot retinopathy; lymphoproliferative disorder; myeloma; leukemia; lymphoma; macroglobulinemia; amyloid-beta.

antitumor; dermatological; immunosuppressive; anti-HIV; hepatotropic; virucide; neurotropic; cytostatic; anticoagulant; antithyroid; antileukemic; antileukemic; uropathic; ophthalmological; vasotropic; catalytic antibody; covalently reactive polypeptide antigen analog; passive immunotherapy; autoimmune disease; systemic lupus erythematosus; HIV-1 infection; hepatitis C virus infection; Alzheimer's disease; cancer; blood coagulation disorder; asthma; rheumatoid arthritis; Reiter's syndrome; Sjogren's disease; bird shot retinopathy; lymphoproliferative disorder; myeloma; leukemia; lymphoma; macroglobulinemia; amyloid-beta.

Homo sapiens.

Key Location/Qualifiers

Modified-site 1 /label= Cys, OTHER

Modified-site 13 /note= "OTHER = biotin"

/note= "side chain amino group conjugated to a suberic acid-(4-amidinophenyl)methylamine-phosphonate diphenyl ester group"

WO2004087735-A2.

14-OCT-2004.

26-MAR-2004; 2004WO-US009398.

26-MAR-2003; 2003US-0458063P.

08-JUN-2004; 2004US-0534689P.

(TEXA) UNIV TEXAS.

Paul S, Nishiyama Y;

WPI; 2004-748030/73.

Preparation of covalent or catalytic antibodies useful for the treatment of autoimmune diseases e.g. systemic lupus erythematosus comprises producing antibodies to a covalently reactive polypeptide antigen analogue.

Example 10; Fig 48; 187pp; English.

The invention relates to a method of preparing covalent or catalytic antibodies by producing antibodies to a covalently reactive polypeptide antigen analog (pcRA) of formula (I): $-(L1-Lx(L'-Y''-Y'-Y)-Lm)- (I)$ where L1 and Lm = components defining antigenic determinants; Lx = a component unit of the antigenic determinant selected from an amino acid residue, sugar residue, a fatty acid residue or a nucleotide; L' = a functional group of Lx; Y'' = atom, covalent bond or linker; Y' = an optional charged or neutral linker; Y = a covalently reactive electrophilic group that reacts specifically with an antibody that binds to the antigenic determinant; n = 1-1000; m = 4-30; Y' and Y'' optionally contain a water-binding group as a terminal or internal component. The method is used for the production of monoclonal and polyclonal antibodies by passive immunotherapy and is useful for the treatment of autoimmune diseases (such as systemic lupus erythematosus), HIV-1 infection, hepatitis C virus infection, Alzheimer's disease, cancer (involving epidermal growth factor receptor), and blood coagulation disorders. It is also useful for stimulating production of prophylactic antibodies having activity specific for an antigen associated with a

CC medical condition (e.g. a microbial disease such as HIV-1 infection); and
 CC for treating autoimmune diseases (e.g. autoimmune thyroiditis, systemic
 CC lupus erythematosus, asthma, rheumatoid arthritis, mixed connective
 CC disease, Reiter's syndrome, Sjogren's disease, vasculitis and bird shot
 CC retinopathy) or lymphoproliferative disorders (such as multiple myeloma,
 CC acute lymphoblastic leukemia, lymphoblastic lymphoma, small lymphocytic
 CC lymphoma, lymphoplasmacytoid lymphoma, Waldenström's macroglobulinemia,
 CC follicular center lymphoma, mucosa-associated lymphoid tissue lymphoma,
 CC hairy cell leukemia, diffuse large B-cell lymphoma, Burkitt's lymphoma
 CC and node based monocytoid lymphoma) by inhibiting the action of a
 CC catalytic antibody. The method provides improved screening,
 CC identification and isolation of monoclonal and polyclonal antibodies
 CC targeted to the specified antigen, compared to the prior art methods. The
 CC binding of antibodies to the polypeptide antigen is resistant to
 CC dissociation by a denaturant that disrupts non-covalent antigen binding,
 CC such as 2% sodium dodecyl sulfate. The antibodies produced are directed
 CC to and capable of catalyzing the cleavage of a peptide bond in a HIV-1
 CC polypeptide antigenic and superantigenic polypeptides, such as in HIV-1
 CC gp120 antigen, hepatitis C virus protein gp 120, factor VIII, CD4, beta-
 CC amyloid peptides 1-40 and 1-42. This sequence corresponds to an antigenic
 CC determinant from the human amyloid beta protein (amino acid residues 17-
 CC 42) which is conjugated to a covalently reactive analog and used to raise
 CC the antibodies of the invention.

CC Sequence 27 AA:

Query Match 100.0%; Score 125; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.5e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVFPAEDVGSNKGAIIIGLWVGGVIA 26
 |||||
 DB 2 LVFPAEDVGSNKGAIIIGLWVGGVIA 27

RESULT 3
 AAB84430
 ID AAB84430 standard; peptide; 32 AA.

AC AAB84430;

DT 22-AUG-2001 (first entry)

DE Partial sequence of a human beta-amyloid precursor protein.

KW Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 vaccine.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note="pyroglutamate"

PN WO200142306-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US033203.

PR 08-DEC-1999; 99US-0169687P.

PA (MIND-) MINDSER BIOPHARMACEUTICALS USA INC.

XX Chain B;

DR WPI; 2001-381648/40.

PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 XX

PS Claim 3; Page 42-43; 47pp; English.

XX The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal

CC Sequence 32 AA:

Query Match 100.0%; Score 125; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVFPAEDVGSNKGAIIIGLWVGGVIA 26
 |||||
 DB 7 LVFPAEDVGSNKGAIIIGLWVGGVIA 32

RESULT 4
 ADJ71491
 ID ADJ71491 standard; peptide; 32 AA.

AC ADJ71491;

DT 06-MAY-2004 (first entry)

DE N-terminal truncated beta-amyloid peptide, SEQ ID 154.

KW Neotropic; Neuroprotective; Vaccine; beta Amyloid;
 amyloid precursor protein; APP; Alzheimer's disease.

OS Homo sapiens.

PN WO2004013172-A2.

PD 12-FEB-2004.

PF 18-JUL-2003; 2003WO-EP007833.

PR 24-JUL-2002; 2002EP-00447147.
 06-AUG-2002; 2002US-0401497P.

PA (INNO-) INNOGENETICS NV.

PI Delacourte A, Sergeant N;

DR WPI; 2004-180423/17.

PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX

XX Claim 4; Page 64; 104pp; English.

CC The present invention relates to preparations (i) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine, or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the

CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 125; DB 8; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 7 LVFFAEDVGSNKGAIIGLMVGVVIA 32

RESULT 5
 ADJ71490

ID ADJ71490 standard; peptide; 33 AA.

XX ADJ71490;

AC ADJ71490;

XX 06-MAY-2004 (first entry)

DE N-terminal truncated beta-amyloid peptide, SEQ ID 153.

XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;

XX amyloid precursor protein; APP; Alzheimer's disease.

OS Homo sapiens.

XX WO2004013172-A2.

XX 12-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007833.

XX 24-JUL-2002; 2002EP-00447147.

XX 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;

XX WPI; 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

PS Claim 4; Page 64; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

XX Sequence 33 AA;

Query Match 100.0%; Score 125; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 8 LVFFAEDVGSNKGAIIGLMVGVVIA 33

RESULT 6
 ADJ71489

ID ADJ71489 standard; peptide; 34 AA.

XX ADJ71489;

XX 06-MAY-2004 (first entry)

DE N-terminal truncated beta-amyloid peptide, SEQ ID 152.

XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;

XX amyloid precursor protein; APP; Alzheimer's disease.

OS Homo sapiens.

XX WO2004013172-A2.

XX 12-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007833.

XX 24-JUL-2002; 2002EP-00447147.

XX 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;

XX WPI; 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

XX Claim 4; Page 64; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

PS Sequence 34 AA;

Query Match 100.0%; Score 125; DB 8; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 9 LVFFAEDVGSNKGAIIGLMVGVVIA 34

RESULT 7
 ADJ71488

ID ADJ71488 standard; peptide; 35 AA.

XX ADJ71488;

XX 06-MAY-2004 (first entry)

DE N-terminal truncated beta-amyloid peptide, SEQ ID 151.

XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;

XX amyloid precursor protein; APP; Alzheimer's disease.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Optionally methylated"

XX WO200403172-A2.
 PN
 XX
 XX 12-FEB-2004.
 PD
 XX 18-JUL-2003; 2003WO-EP007833.
 PF
 XX 24-JUL-2002; 2002EP-00447147.
 PR
 XX 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 XX Delacourte A, Sergeant N;
 PI
 XX WPI; 2004-180423/17.
 DR
 XX
 XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 CC
 XX
 PS Claim 4; Page 64; 104pp; English.
 XX
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 CC
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 125; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.5e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 ||||||||||||||||||
 DB 10 LVFFAEDVGSNKGAIIGLMVGVVIA 35
 ||||||||||||||||||
 RESULT 8
 ADJ71487
 ID ADJ71487 standard; peptide; 36 AA.
 XX
 AC ADJ71487;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 150.
 XX
 XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note="Optionally methylated"
 FT
 FT
 XX
 PN WO200403172-A2.
 XX
 XX 12-FEB-2004.
 PD
 XX 18-JUL-2003; 2003WO-EP007833.
 PF
 XX 24-JUL-2002; 2002EP-00447147.
 PR
 XX 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX

PI Delacourte A, Sergeant N;
 XX
 XX WPI; 2004-180423/17.
 DR
 XX
 XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 CC
 XX
 PS Claim 4; Page 64; 104pp; English.
 XX
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 CC
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 125; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.6e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 ||||||||||||||||||
 DB 11 LVFFAEDVGSNKGAIIGLMVGVVIA 36
 ||||||||||||||||||
 RESULT 9
 ADM97743
 ID ADM97743 standard; peptide; 36 AA.
 XX
 AC ADM97743;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Amyloid beta-derived diffusible ligand peptide #1.
 XX
 KW immunostimulant; neuroprotective; nootropic; Alzheimer's disease;
 KW Down's syndrome; vaccine; amyloid beta; ADDL;
 KW amyloid beta-derived diffusible ligand.
 XX
 OS Unidentified.
 XX
 XX
 XX WO2004031400-A2.
 PN
 XX
 XX 15-APR-2004.
 PD
 XX
 PF 01-OCT-2003; 2003WO-US030930.
 XX
 PR 01-OCT-2002; 2002US-0415074P.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 XX Klein W, Kraft GA, Chang L, Gong Y, Viola K, Lambert M;
 PI Chromy B, Summa D;
 XX
 DR WPI; 2004-330196/30.
 XX
 XX New amyloid beta-derived diffusible ligands, useful in generating an
 PT immune response and in preventing, ameliorating or treating Alzheimer's
 PT disease, memory and learning deficits, degeneration or malfunction of
 PT neurons or Down's syndrome.
 CC
 XX
 PS Claim 32; Page 123; 176pp; English.
 XX
 CC The present invention relates to a new pharmaceutical composition
 CC comprising amyloid beta-derived diffusible ligands (ADDLs) capable of
 CC generating an immune response in a host organism, where the composition
 CC is a vaccine or a component of a vaccine and where the ADDLs are

CC antigenic, immunogenic or act as a binding molecule when the composition
CC is administered to a host organism. The composition, vaccine or
CC antibodies are useful in inducing an immune response. The composition,
CC peptides, molecules and antibodies are useful in preventing or
CC ameliorating Alzheimer's disease, memory and learning deficits,
CC degeneration or malfunction of neurons and in preventing or treating
CC Down's syndrome. The present sequence is a polypeptide of the invention.

XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 125; DB 8; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.7e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGATIGLMVGGVIA 26
Db 11 LVFPAEDVGSNKGATIGLMVGGVIA 36

RESULT 10

ID ADJ71486 standard; peptide; 37 AA.

AC ADJ71486;

DT 06-MAY-2004 (first entry)

DE N-terminal truncated beta-amyloid peptide, SEQ ID 149.

KM Nootropic; Neuroprotective; Vaccine; beta Amyloid;

KW amyloid precursor protein; APP; Alzheimer's disease.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 1 /note="Optionally methylated"

XX MO200403172-A2.

PD 12-FEB-2004.

PF 18-JUL-2003; 2003WO-EP007833.

PR 24-JUL-2002; 2002EP-00447147.

PR 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

PA Delacourte A, Sergeant N;

PI WPI, 2004-180423/17.

DR WPI, 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a
PT prophylactic vaccine or a therapeutic for preventing or treating a
PT disease associated with beta-amyloid formation and/or aggregation, e.g.
PT Alzheimer's disease.

XX Claim 4; Page 64; 104pp; English.

XX The present invention relates to preparations (1) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.

XX Sequence 37 AA;

Query Match 100.0%; Score 125; DB 8; Length 37;

Best Local Similarity 100.0%; Pred. No. 3.7e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGATIGLMVGGVIA 26
Db 12 LVFPAEDVGSNKGATIGLMVGGVIA 37

RESULT 11

ID ADM97744 standard; peptide; 37 AA.

AC ADM97744;

DT 01-JUL-2004 (first entry)

DE Amyloid beta-derived diffusible ligand peptide #2.

KM immunostimulant; neuroprotective; nootropic; Alzheimer's disease;

KW Down's syndrome; vaccine; amyloid beta; ADDL;

KW amyloid beta-derived diffusible ligand.

XX Unidentified.

XX WO2004031400-A2.

PD 15-APR-2004.

PF 01-OCT-2003; 2003WO-US030930.

PR 01-OCT-2002; 2002US-0415074P.

XX (NOUN) UNIV NORTHWESTERN.

PI Klein W, Krafft GA, Chang L, Gong Y, Viola K, Lambert M;

PI Chorny B, Summa D;

DR WPI; 2004-330196/30.

XX New amyloid beta-derived diffusible ligands, useful in generating an
PT immune response and in preventing, ameliorating or treating Alzheimer's
PT disease, memory and learning deficits, degeneration or malfunction of
PT neurons or Down's syndrome.

XX Claim 33; Page 124; 176pp; English.

XX The present invention relates to a new pharmaceutical composition
CC comprising amyloid beta-derived diffusible ligands (ADDLs) capable of
CC generating an immune response in a host organism, where the composition
CC is a vaccine or a component of a vaccine and where the ADDLs are
CC antigenic, immunogenic or act as a binding molecule when the composition
CC is administered to a host organism. The composition, vaccine or
CC antibodies are useful in inducing an immune response. The composition,
CC peptides, molecules and antibodies are useful in preventing or
CC ameliorating Alzheimer's disease, memory and learning deficits,
CC degeneration or malfunction of neurons and in preventing or treating
CC Down's syndrome. The present sequence is a polypeptide of the invention.

XX Sequence 37 AA;

Query Match 100.0%; Score 125; DB 8; Length 37;

Best Local Similarity 100.0%; Pred. No. 3.7e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGATIGLMVGGVIA 26
Db 11 LVFPAEDVGSNKGATIGLMVGGVIA 36

RESULT 12

ID ADM97745 standard; peptide; 37 AA.

AC ADM97745;

XX 01-JUL-2004 (first entry)
 DT Amyloid beta-derived diffusible ligand peptide #3.
 XX
 DE immunostimulant; neuroprotective; nootropic; Alzheimer's disease;
 XX Down's syndrome; vaccine; amyloid beta; ADDL;
 KW amyloid beta-derived diffusible ligand.
 XX
 OS Unidentified.
 XX
 PN WO2004031400-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 01-OCT-2003; 2003WO-US030930.
 XX
 PR 01-OCT-2002; 2002US-0415074P.
 XX
 PA (NOUN) UNITV NORTHWESTERN.
 XX
 PI Klein W, Krafft GA, Chang L, Gong Y, Viola K, Lambert M;
 PI Chromy B, Summa D;
 XX
 DR WPI; 2004-330196/30.
 XX
 PT New amyloid beta-derived diffusible ligands, useful in generating an
 PT immune response and in preventing, ameliorating or treating Alzheimer's
 PT disease, memory and learning deficits, degeneration or malfunction of
 PT neurons or Down's syndrome.
 XX
 PS Claim 34; Page 124; 176pp; English.
 XX
 CC The present invention relates to a new pharmaceutical composition
 CC comprising amyloid beta-derived diffusible ligands (ADDLs) capable of
 CC generating an immune response in a host organism, where the composition
 CC is a vaccine or a component of a vaccine and where the ADDLs are
 CC antigenic, immunogenic or act as a binding molecule when the composition
 CC is administered to a host organism. The composition, vaccine or
 CC antibodies are useful in inducing an immune response. The composition,
 CC peptides, molecules and antibodies are useful in preventing or
 CC ameliorating Alzheimer's disease, memory and learning deficits,
 CC degeneration or malfunction of neurones and in preventing or treating
 CC Down's syndrome. The present sequence is a polypeptide of the invention.
 CC
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 125; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 11 LVFFAEDVGSNKGAIIGLMVGVVIA 36
 RESULT 13
 ADJ71485
 ID ADJ71485 standard; peptide; 38 AA.
 AC ADJ71485;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 148.
 XX
 KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FH Modified-site 1
 FT

FT /note= "Optionally methylated"
 XX
 PN WO2004031372-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007833.
 XX
 PR 24-JUL-2002; 2002EP-00447147.
 PR 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delacourte A, Sergeant N;
 PI
 XX
 DR WPI; 2004-180423/17.
 XX
 PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX
 PS Claim 4; Page 64; 104pp; English.
 XX
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 CC
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 125; DB 8; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.8e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 13 LVFFAEDVGSNKGAIIGLMVGVVIA 38
 RESULT 14
 ADJ71484
 ID ADJ71484 standard; peptide; 39 AA.
 AC ADJ71484;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 147.
 XX
 KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FH Modified-site 1 /note= "Pyroglutamic acid"
 FT
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007833.
 XX
 PR 24-JUL-2002; 2002EP-00447147.
 PR 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;
 PI WPI; 2004-180423/17.
 DR
 XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX
 PS Claim 4; Page 64; 104pp; English.
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 XX
 SQ Sequence 39 AA;
 Query Match 100.0%; Score 125; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 14 LVFFAEDVGSNKGAIIGLMVGVVIA 39
 RESULT 15
 ID ADJ71483 standard; peptide; 39 AA.
 XX
 AC ADJ71483;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 146.
 XX
 KM Neurotropic; Neuroprotective; Vaccine; beta Amyloid;
 KM amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2004013172-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007833.
 XX
 PR 24-JUL-2002; 2002EP-00447147.
 PR 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delacourte A, Sergeant N;
 XX
 DR WPI; 2004-180423/17.
 XX
 PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX
 PS Claim 4; Page 64; 104pp; English.
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for

CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 XX
 SQ Sequence 39 AA;
 Query Match 100.0%; Score 125; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 DB 14 LVFFAEDVGSNKGAIIGLMVGVVIA 39
 RESULT 16
 ID AAB84429 standard; peptide; 40 AA.
 XX
 AC AAB84429;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 XX
 KM Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KM vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200142306-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 08-DEC-2000; 2000WO-US033203.
 XX
 PR 08-DEC-1999; 99US-0169687P.
 XX
 PA (MIND-) BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain B;
 XX
 DR WPI; 2001-381648/40.
 XX
 PT Novel chimeric peptide containing N- or C-terminal end-specific B cell
 PT epitope from naturally occurring internal peptide cleavage product (such
 PT as beta amyloid peptide) of a precursor protein, joined to T cell
 PT epitope.
 XX
 PS Claim 3; Page 42; 47pp; English.
 XX
 CC The present sequence represents a partial sequence of a human beta-
 CC amyloid precursor protein (APP). The peptide is used to create chimeric
 CC peptides of the invention. The chimeric peptides contain a N- or C-
 CC terminal end-specific B cell epitope from a naturally occurring internal
 CC peptide cleavage product of a precursor or mature protein, as a free N-
 CC or C-terminus, joined to a T cell epitope, with or without a spacer amino
 CC acid residue. Chimeric peptides comprising betaAPP peptides slow down,
 CC reduce or prevent the accumulation of amyloid beta peptide in the
 CC extracellular space, interstitial fluid and cerebrospinal fluid of the
 CC brain, and aggregation into senile amyloid deposits or plaques. They also
 CC block the interaction of amyloid beta peptides with other molecules that
 CC contribute the neurotoxicity of amyloid beta. The chimeric peptides are
 CC useful for immunizing humans against the free N- or C-terminus of an
 CC internal self peptide cleavage product (e.g. APP peptide) derived from a
 CC precursor protein or a mature protein. The internal peptide cleavage
 CC product is the self molecule of the mammal

CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
 CC disorders (including depression, seizures including epilepsy, drug
 CC withdrawal and alcoholism), and neurodegenerative disorders (such as
 CC cognitive dysfunction and dementia). The compositions may also be useful
 CC for the treatment of ulcer, gastric cancer, neoplasia, inflammatory host
 CC responses, cancer, melanoma, malignant metastasis, psoriasis, rheumatoid
 CC arthritis, atherosclerosis and leukocyte adhesion and migration processes
 CC in the endothelium. The present sequence is that of a protein which is
 CC related to the treatment method of the invention.

XX Sequence 40 AA;

XX SQ Query Match 100.0%; Score 125; DB 8; Length 40;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVFPAEDVGSNKGAIIIGLMVGVVIA 26
 XX |||||
 DB 15 LVFPAEDVGSNKGAIIIGLMVGVVIA 40

RESULT 19

ADU46709 ADU46709 standard; peptide; 40 AA.

XX ADU46709;

XX 10-FEB-2005 (first entry)

XX Amyloid beta peptide (3-42), substrate of glutaminyl cyclase.

XX Amyloid-beta peptide (3-42); glutaminyl cyclase; neurotropic;

KM neuroprotective; anticonvulsant; antitumor; cytostatic; neuroleptic;
 KM antineurotic; antipsoriatic; antineumatic; antitartaric;
 KM antiarteriosclerotic; Alzheimer's disease; human.

OS Homo sapiens.

XX MO2004098625-A2.

XX 18-NOV-2004.

XX 05-MAY-2004; 2004WO-EP004778.

XX 05-MAY-2003; 2003US-0468014P.

XX 05-MAY-2003; 2003US-0468043P.

XX 15-OCT-2003; 2003US-0512038P.

XX (PROB-) PROBIODRUG AG.

XX Demuth H, Hoffmann T, Niestroj AJ, Schilling S, Heiser U;

XX WPI; 2004-805062/79.

XX Use of effectors of glutaminyl cyclase (QC) for treating diseases and/or
 XX for modulating physiological processes based on the action of pglu-
 XX containing peptides.

XX Disclosure; Page 12; 106pp; English.

XX The present sequence is that of amyloid beta peptide (3-42).

XX Pyroglutamate (pglu)-containing isoforms of amyloid beta peptides in
 XX represent the prominent forms of N-truncated amyloid beta peptides in
 XX senile plaques. The pglu modification exacerbates the toxic properties of
 XX amyloid beta peptides. The invention shows that glutaminyl cyclase (QC,
 XX EC 2.3.2.5) is involved in the cyclisation of glu to pglu, making this
 XX enzyme a target in drug development. The invention relates to the
 XX identification, screening and use of effectors of QC for the preparation
 XX of a medicament for: (a) the treatment of diseases that can be treated by
 XX modulation of QC activity in vivo; and/or (b) the modulation of
 XX physiological processes based on the action of pglu-containing peptides
 XX caused by modulation of QC activity. The QC effectors are used to alter
 XX the conversion of N-terminal Glu or Gln residues to pglu residues in a QC

CC substrate such as amyloid beta1-40/42. They can be used to treat
 CC Alzheimer's disease, Down Syndrome, Huntington's disease, Kennedy's
 CC disease, ulcer disease and gastric cancer with or without Helicobacter
 CC pylori infections, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, melanoma, psoriasis, rheumatoid arthritis, atherosclerosis,
 CC impaired humoral and cell-mediated immune responses, leukocyte adhesion
 CC and migration processes in the endothelium, impaired food intake, sleep-
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids. The effectors of QC are also useful for:
 CC regulating and/or controlling male fertility; stimulating
 CC gastrointestinal tract cell proliferation, preferably proliferation of
 CC gastric mucosal cells, epithelial cells, acute acid secretion and for
 CC differentiating acid-producing parietal cells and histamine-secreting
 CC enterochromaffin-like cells (all claimed). Amyloid beta peptides were
 CC also shown to be substrates of dipeptidyl peptidase IV (DP IV) and DP IV-
 CC like enzymes, and preferred effector compositions additionally comprise
 CC inhibitors of these enzymes.

XX Sequence 40 AA;

XX Query Match 100.0%; Score 125; DB 8; Length 40;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVFPAEDVGSNKGAIIIGLMVGVVIA 26
 XX |||||
 DB 15 LVFPAEDVGSNKGAIIIGLMVGVVIA 40

RESULT 20

ADZ71361 ADZ71361 standard; peptide; 40 AA.

XX ADZ71361;

XX 14-JUL-2005 (first entry)

XX Human beta-amyloid peptide #3.

XX Zollinger-Elison syndrome; gastrointestinal disease; neoplasm;

KM colorectal tumor; gastrointestinal tumor; Helicobacter pylori infection;
 KM antibacterial; infection; beta-amyloid.

XX Homo sapiens.

XX MO2005039548-A2.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011630.

XX 15-OCT-2003; 2003US-0512038P.

XX (PROB-) PROBIODRUG AG.

XX Schilling S, Hoffmann T, Niestroj AJ, Demuth H, Heiser U;

XX WPI; 2005-346574/35.

XX Use of glutaminyl cyclase effectors in the manufacture of a medicament
 XX for modulating conversion of glutamic acid/glutamine residue to
 XX pyroglutamic acid residue at the N-terminus of glutaminyl cyclase
 XX substrate in the treatment e.g. cancer.

XX Disclosure; Page 13; 105pp; English.

XX The invention relates to the use of a glutaminyl cyclase effector (EI)
 XX for modulating conversion of glutamic acid/glutamine residue to
 XX pyroglutamic acid residue at the N-terminus of a glutaminyl cyclase (QC)
 XX substrate. The glutaminyl cyclase effector is useful for treating a
 XX condition mediated by modulation of QC enzyme activity e.g. Familial

CC British Dementia (FBD) and Familial Danish Dementia (FDD), ulcer disease
 CC and duodenal cancer with or without Helicobacter pylori infections,
 CC colorectal cancer, Zollinger-Ellison syndrome, gastric cancer, Alzheimer's
 CC disease, Down's syndrome, pathogenic psychotic conditions, schizophrenia,
 CC infertility, neoplasia, inflammatory host responses, cancer, malign
 CC metastasis, psoriasis, rheumatoid arthritis, atherosclerosis, impaired
 CC humoral and cell-mediated immunity responses, leukocyte adhesion and
 CC migration processes in the endothelium, impaired food intake, sleep
 CC wakefulness, impaired homeostatic regulation of energy metabolism,
 CC impaired autonomic function, impaired hormonal balance and impaired
 CC regulation of body fluids, for the preparation of contraceptive
 CC medicaments for males. The amino acid sequence of the human beta-amyloid
 CC peptide.
 CC
 XX Sequence 40 AA:
 SO
 Query Match 100.0%; Score 125; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
 DB 15 LVFPAEDVGSNKGAIIGLMVGVVIA 40
 RESULT 21
 AEA35394
 ID AEA35394 standard; peptide; 40 AA.
 AC AEA35394;
 XX
 XX 11-AUG-2005 (first entry)
 DT
 XX
 DE Novel QC inhibitor composition-related Abeta(3-42) polypeptide.
 XX
 KW pharmaceutical; nootropic; neuroprotective; antiparkinsonian;
 KW neuroleptic; hypotensive; antipyretic; tranquilizer; antidepressant;
 KW antialcoholic; anticonvulsant; anabolic; eating-disorders-gen.; hypnotic;
 KW amyloid; neurological disease; Alzheimers disease; Down's Syndrome;
 KW Parkinsons disease; Huntingtons chorea; psychotic disorders;
 KW schizophrenia; sleep disorder; hypertension; anorexia nervosa;
 KW anxiety disorder; major depressive disorder; epilepsy; alcoholism;
 KW neurodegenerative disease; cognitive disorder; dementia.
 XX
 OS Unidentified.
 XX
 PN WO2005049027-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 29-OCT-2004; 2004WO-EP012301.
 XX
 PR 03-NOV-2003; 2003US-0516717P.
 XX
 PA (PROB-) PROBIODRUG AG.
 XX
 PI Schulz I, Schilling S, Niestroj AJ, Demuth H, Rosner S;
 XX
 DR WPI; 2005-395979/40.
 XX
 PT Composition used for treating neuronal diseases e.g. Alzheimer's disease,
 PT Down Syndrome, Parkinson disease, Chorea Huntington comprises glutaminyl
 PT cyclase inhibitor.
 XX
 PS Disclosure; Page 15; 123pp; English.
 XX
 CC This invention relates to a novel composition which comprises at least
 CC one glutaminyl cyclase (QC) inhibitor and optionally at least one of
 CC prolyl endopeptidase (PEP) inhibitors, inhibitors of dipeptidyl
 CC aminopeptidases (DP), neuropeptide Y (NPY) receptor ligands, NPY agonists
 CC or antagonists, acetylcholinesterase (ACE) inhibitors, protein
 CC isoenzyme carboxymethyl transferase (PMT) enhancers, inhibitors of
 CC beta or gamma secretases and inhibitors of neutral endopeptidase. The

CC invention may be useful for the development of compounds with a
 CC nootropic, neuroprotective, antiparkinsonian, neuroleptic, hypotensive,
 CC antipyretic, tranquilizer, antidepressant, antialcoholic, anticonvulsant,
 CC anabolic, eating-disorders-gen. or hypnotic activity acting as amyloid
 CC beta-peptide formation inhibitors. The invention may be used for the
 CC treatment of neuronal diseases, particularly Alzheimers disease, Down's
 CC Syndrome, Parkinsons disease, Huntingtons chorea, pathogenic psychotic
 CC conditions, schizophrenia, impaired food intake, sleep-wakefulness,
 CC impaired homeostatic regulation of energy metabolism, impaired autonomic
 CC function, impaired hormonal balance, impaired regulation, body fluids,
 CC hypertension, fever, sleep dysregulation, anorexia, anxiety related
 CC disorders including depression, seizures including epilepsy, drug
 CC withdrawal and alcoholism, neurodegenerative disorders including
 CC cognitive dysfunction and dementia. The QC inhibitors prevent the
 CC aggregation of plaque-forming amyloid-beta-peptides 3-40/42 or amyloid-
 CC beta-peptides 11-40/42, reducing the onset and progression of the
 CC diseases. The present sequence is that of an amyloid beta polypeptide
 CC which is related to the novel compositions of the invention.
 CC
 XX Sequence 40 AA:
 SO
 Query Match 100.0%; Score 125; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
 DB 15 LVFPAEDVGSNKGAIIGLMVGVVIA 40
 RESULT 22
 AEB92567
 ID AEB92567 standard; peptide; 40 AA.
 AC AEB92567;
 XX
 XX 20-OCT-2005 (first entry)
 DT
 XX
 DE Glutaminyl cyclase inhibitor peptide #3.
 XX
 KW Pharmaceutical; enzyme inhibition; neurological disease;
 KW Alzheimers disease; Down syndrome; Parkinsons disease;
 KW Huntingtons chorea; psychotic disorder; schizophrenia; sleep disorder;
 KW metabolic disorder; hypertension; fever; anorexia nervosa;
 KW anxiety disorder; depression; epilepsy; drug dependence; alcoholism;
 KW neurodegenerative disease; cognitive disorder; dementia; neuroprotective;
 KW nootropic; antiparkinsonian; anticonvulsant; neuroleptic; hypnotic;
 KW endocrine-gen.; hypotensive; antipyretic; anabolic;
 KW eating-disorders-gen.; tranquilizer; antidepressant; addictive;
 KW antialcoholic; antileptility; glutaminyl cyclase inhibitor;
 KW glutaminyl-peptide cyclotransferase.
 XX
 OS Synthetic.
 XX
 PN WO2005075436-A2.
 XX
 PD 18-AUG-2005.
 XX
 PF 04-FEB-2005; 2005WO-EP001153.
 XX
 PR 05-FEB-2004; 2004US-0542133P.
 XX
 PR 05-MAY-2004; 2004US-00838993.
 XX
 PR 08-DEC-2004; 2004US-0634364P.
 XX
 PA (PROB-) PROBIODRUG AG.
 XX
 PI Schilling S, Buchholz M, Niestroj AJ, Demuth H, Heiser U;
 XX
 DR WPI; 2005-591611/60.
 XX
 PT New imidazole derivatives are glutaminyl cyclase inhibitors useful to
 PT treat neuronal disorders e.g. Alzheimer's disease, Down syndrome,
 PT Parkinson disease, Chorea Huntington, pathogenic psychotic conditions and

PT schizophrénia.
 XX
 XX Disclosure; Page 20; 122pp; English.
 CC
 CC The invention relates to imidazole derivatives and their salts,
 CC stereoisomers and polymorphs. The invention also relates to a composition
 CC comprising an imidazole optionally in combination with a carrier and/or
 CC excipient. The imidazole derivatives are useful in the manufacture of a
 CC medicament for the treatment of neurological diseases especially
 CC Alzheimer's disease, Down syndrome, Parkinson's disease, Huntington's
 CC chorea, psychotic disorders, schizophrenia, impaired food intake, sleep
 CC disorders, impaired homeostatic regulation of energy metabolism,
 CC hypertension, fever, anorexia nervosa, anxiety disorders, depression,
 CC epilepsy, drug dependence, alcoholism and neurodegenerative diseases
 CC including cognitive disorders and dementia. The imidazole derivatives are
 CC also useful for stimulating the proliferation of myeloid progenitor cells
 CC or to suppress male fertility. This sequence represents a glutamyl
 CC cyclase inhibitor peptide used in the scope of the invention.
 CC
 SQ Sequence 40 AA;
 QY
 DB 1 LVFPADVGSNKGAIIGLMVGVVIA 26
 15 LVFPADVGSNKGAIIGLMVGVVIA 40
 RESULT 23
 AAR45230
 ID AAR45230 standard; protein; 41 AA.
 AC AAR45230;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Beta amyloid protein.
 XX
 KW Amyloid precursor protein; APP; beta amyloid protein; BAP; detection;
 KW Alzheimer's disease; Down's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN AU9338358-A.
 XX
 PD 04-NOV-1993.
 XX
 PF 03-MAY-1993; 93AU-00038358.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PA (AMCY) AMERICAN CYANAMID CO.
 PI Vittek MP, Jacobsen JS;
 XX
 DR WPI; 1993-406194/51.
 PT New mutant forms of amyloid precursor protein - for detecting cpds. that
 PT modify activity of enzymes involved in precursor cleavage, also new
 PT nucleic acid encoding them.
 XX
 PS Disclosure; Page 9; 66pp; English.
 XX
 CC Recombinant polypeptides produced using the coding sequences of mutant
 CC forms of amyloid precursor proteins comprising from the 5' to the 3' end
 CC a sequence encoding a marker and either (1) a sequence encoding the N-
 CC terminus of an amyloid precursor protein (APP) up to, but not including,
 CC the nucleotides encoding the beta amyloid protein (BAP) domain or (2) the
 CC BAP domain, can be used to detect drugs or compounds that inhibit/augment
 CC the activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimer's disease

CC and Down's syndrome)
 XX
 SQ Sequence 41 AA;
 QY
 DB 1 LVFPADVGSNKGAIIGLMVGVVIA 26
 16 LVFPADVGSNKGAIIGLMVGVVIA 41
 RESULT 24
 ADJ71481
 ID ADJ71481 standard; peptide; 41 AA.
 AC ADJ71481;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 144.
 XX
 KW Neurotropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note="Methylated"
 FT
 XX
 PN MO200403172-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007833.
 XX
 PR 24-JUL-2002; 2002EP-00447147.
 PR 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delacourte A, Sergeant N;
 XX
 DR WPI; 2004-180423/17.
 XX
 PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX
 PS Claim 4; Page 64; 104pp; English.
 XX
 CC The present invention relates to preparations (1) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 XX
 SQ Sequence 41 AA;
 QY
 DB 1 LVFPADVGSNKGAIIGLMVGVVIA 26
 16 LVFPADVGSNKGAIIGLMVGVVIA 41
 Query Match 100.0%; Score 125; DB 8; Length 41;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 25
AAP83153
ID AAP83153 standard; protein; 42 AA.
XX
XX
AC AAP83153;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 30-NOV-1990 (first entry)
XX
DE Lambda SMW9 beta-amyloid core protein.
XX
XX Lambda SMW9; beta-amyloid related protein; beta-amyloid core;
KW Alzheimer's disease; ss.
XX
OS Homo sapiens.
OS Unidentified.
XX
XX WO8803951-A.
XX
PD 02-JUN-1988.
XX
PF 12-NOV-1987; 87WO-US002953.
XX
PR 17-NOV-1986; 86US-00932193.
PR 31-DEC-1986; 86US-00948376.
PR 30-JAN-1987; 87US-00008810.
PR 18-AUG-1987; 87US-00087002.
XX
XX (CALD ) CALIFORNIA BIOTECHNOLOGY INC.
PA (GREE) GRENEBERG B D.
XX
PI Greenberg BD, Fuller FH, Ponte P;
XX
DR WPI; 1988-161620/23.
DR N-PSDB; AAN80609.
XX
PT DNA encoding beta-amyloid related proteins - used to identify genomic
PT mutation(s) and produce proteins for prognosis, diagnosis and therapy of
PT Alzheimer's disease.
XX
PS Disclosure; Page ?; 85pp; English.
XX
CC Sequence is a portion of a beta-amyloid related protein which differs
CC from that encoded by AAN80607 by 15 nucleotide differences and by 4 amino
CC acid differences. The sequence is one of 4 covered by the invention which
CC either as fragments or in their entirety are chosen to encode beta-
CC amyloid core protein sequences. See also AAN80604-N80607, AAN82430 and
CC AAP83154. (Updated on 25-MAR-2003 to correct PA field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to sequence location
XX
SQ Sequence 42 AA;

Query Match          100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAITIGLMVGCVIA 26
   |||||
DB 15 LVFFAEDVGSNKGAITIGLMVGCVIA 40

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DE Beta-amyloid-related protein from Lambda SM2W9.
XX
XX Alzheimer's disease; AD; acute pancreatitis.
XX
OS Homo sapiens.
XX
XX WO9014840-A.
XX
XX 13-DEC-1990.
XX
PF 06-JUN-1989; 89US-00361912;
XX
PR 06-JUN-1989; 89US-00361912.
PR 29-MAR-1990; 90US-00502273.
XX
XX (CALD ) CALIFORNIA BIOTECHNOLOGY INC.
XX
XX Schilling JW, Ponte PA, Cordell B;
PI
DR WPI; 1991-006983/01.
DR N-PSDB; AAQ10018.
XX
PT DNA sequences, and protease inhibitors encoded by them and antibodies -
PT for diagnosis and treatment of alzheimers disease.
XX
PS Disclosure; Fig 6; 96pp; English.
XX
CC Sequence may be useful in prognosis and diagnosis of human Alzheimer's
CC disease (AD). Abs may be raised to the gene product, and probes derived
CC from the encoding sequence allowing diagnosis and determination of
CC genetic predisposition. The gene product is a protease inhibitor and may
CC also have utility in treatment of acute pancreatitis. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 42 AA;

Query Match          100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAITIGLMVGCVIA 26
   |||||
DB 15 LVFFAEDVGSNKGAITIGLMVGCVIA 40

RESULT 27
AAR20330
ID AAR20330 standard; peptide; 42 AA.
XX
XX
AC AAR20330;
XX
DT 25-MAR-2003 (revised)
DT 14-APR-1992 (first entry)
XX
DE Sequence of A99 (beta-amyloid core domain).
XX
XX Transgenic mice; Alzheimer's disease; diagnosis; beta-amyloid precursor;
KW plaque core protein.
XX
XX Homo sapiens.
OS
OS WO9119810-A.
XX
XX 26-DEC-1991.
XX
XX 15-JUN-1990; 90US-00538857.
XX
XX 15-JUN-1990; 90US-00538857.
PR 17-JUN-1991; 91US-00716725.
XX
XX (CALD ) CALIFORNIA BIOTECHNOLOGY INC.
PA Cordell B;
PI

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XX DR      MPI; 1992-024426/03.
XX PT      Transgenic mice as models for studying Alzheimer's disease proteins -
XX PT      contg. cells with promoter and beta-amyloid precursor protein
XX PT      deoxyribonucleic acid, useful for testing anti-Alzheimer's drugs.
XX PS      Disclosure; Fig 3; 98bp; English.
XX CC      The inventors specifically claim transgenic mice contg. DNA encoding A42
XX CC      (beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid carboxy
XX CC      tail) (AAR20329), A695 (beta-amyloid precursor protein), A751 (precursor
XX CC      plus inhibitor) or A41 (protease inhibitor) (AAR20328). Human fibroblast
XX CC      cDNA clone lambdaAPCP16814 was deposited at ATCC on July 1, 1987 and has
XX CC      accession No. 40347. The promoter is pref. the NSB promoter with the A751
XX CC      or the A695 sequence. (Updated on 25-MAR-2003 to correct PR field.)
XX CC      (Updated on 25-MAR-2003 to correct PA field.)
SQ      Sequence 42 AA;

Query Match          100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
        |||
Db      17 LVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 28
AAR37867
ID      AAR37867 standard; protein; 42 AA.
XX AC      AAR37867;
XX DT      25-MAR-2003 (revised)
XX DT      27-OCT-1993 (first entry)
XX DE      Beta-amyloid protein residues 3-44 encoded by lambda clone SM2W9.
XX KW      Alzheimer's Disease; Amyloid Plaque Core Protein; APP; neuritic plaque.
XX OS      Homo sapiens.
XX PN      US5220013-A.
XX PD      15-JUN-1993.
XX PF      30-NOV-1989; 89US-00444118.
XX PR      17-NOV-1986; 86US-00933193.
XX PR      31-DEC-1986; 86US-00948376.
XX PR      30-JAN-1987; 87US-00008810.
XX PR      18-AUG-1987; 87US-00087002.
XX PA      (SCIO-) SCIOS NOVA INC.
XX PT      Ponte PA, Cordell B;
XX DR      MPI; 1993-205383/25.
XX DR      N-PSDB; AAQ42666.
XX PT      DNA sequence useful for detection of Alzheimer's disease - for encoding
XX PT      beta amyloid core protein.
XX PS      Disclosure; Fig 6; 40bp; English.
XX CC      A clone was obtained from the genomic library described in Lawn et al.,
XX CC      Cell, 15:1157-1174 (1978) which included a 57 base pair segment which
XX CC      encoded amino acids 1-18 of the beta-amyloid protein, immediately
XX CC      preceded by a Methionine. A HindIII/NotI fragment derived from the
XX CC      genomic clone and containing the 57bp segment was used to isolate cDNA
XX CC      fragments from a library prepared from temporal and parietal cortical

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CC      tissue from a normal human brain. AAQ42666 is the sequence of lambda
CC      clone SM2W9 which differs from lambda clone SM2W3 (see AAQ42664) by 15
CC      nucleotides (see Features table) and by several amino acid in the region
CC      covering residues 3-44 of the beta-amyloid protein. (Updated on 25-MAR-
CC      2003 to correct PF field.)
XX CC      2003 to correct PF field.)
SQ      Sequence 42 AA;

Query Match          100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
        |||
Db      15 LVFFAEDVGSNKGAIIGLMVGVVIA 40

RESULT 29
AAR60366
ID      AAR60366 standard; peptide; 42 AA.
XX AC      AAR60366;
XX DT      25-MAR-2003 (revised)
XX DT      15-MAR-1995 (first entry)
XX DE      Beta-amyloid (1-42).
XX KW      Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
XX KW      anti-beta-amyloid antibody; diagnosis.
XX OS      Homo sapiens.
XX PN      WO9417197-A1.
XX PD      04-AUG-1994.
XX PF      24-JAN-1994; 94WO-UP000089.
XX PR      25-JAN-1993; 93JP-00010132.
XX PR      05-FEB-1993; 93JP-00019035.
XX PR      16-NOV-1993; 93JP-00286985.
XX PR      28-DEC-1993; 93JP-00334773.
XX PA      (TAKE ) TAKEDA CHEM IND LTD.
XX PT      Suzuki N, Odaka A, Kitada C;
XX DR      MPI; 1994-264110/32.
XX PT      Antibodies recognising specific parts of beta-amyloid - can be used for
XX PT      diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
XX PT      disease.
XX PS      Disclosure; Page 83; 116pp; Japanese.
XX CC      Antibodies which recognise specific subfragments of the beta-amyloid
XX CC      protein are claimed. Specifically, the antibodies (which are pref.
XX CC      monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
XX CC      portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
XX CC      the C-terminal portion. The antibodies are useful for assaying beta-
XX CC      amyloid and its derivatives for diagnosis of Alzheimer's disease.
XX CC      (Updated on 25-MAR-2003 to correct PN field.)
SQ      Sequence 42 AA;

Query Match          100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
        |||
Db      17 LVFFAEDVGSNKGAIIGLMVGVVIA 42

```

RESULT 30

AAR65284

ID AAR65284 standard; peptide; 42 AA.

AC AAR65284;

DT 24-OCT-1995 (first entry)

DE Beta amyloid peptide (ba4-peptide).

XX Beta amyloid peptide; fusion protein; hydrophobic; hydrophilic;
 KW surface antigen; lymphokine; receptor; HIV; hepatitis; screening;
 KW treatment; diagnosis; drug; Alzheimer's disease.

XX Rattus rattus.

OS AU9466122-A.

PN 27-JAN-1995.

PF 01-JUL-1994; 94AU-00066122.

PR 06-JUL-1993; 93EP-00110755.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Dobeli H, Draeger N, Trottmann GH, Jakob P, Stuber D;

DR WPI; 1995-082537/12.

PT New fusion protein of bulky hydrophilic peptide and hydrophobic component
 PT containing specific cleavage site - for prodn. and purificn. of
 PT hydrophobic peptide(s), esp. new monomeric beta-amyloid peptide.

PS Claim 4; Page 21; 49pp; English.

XX Fusion proteins of formula A-B-C where A is a bulky hydrophilic peptide;
 CC B is a selective cleavage site and C is a desired hydrophobic
 CC polypeptide, protein or peptide, may be used for the production of the
 CC hydrophobic polypeptide, protein or peptide. Proteins which can be
 CC produced include surface antigens, lymphokine receptors, and HIV or
 CC hepatitis proteins. The proteins can be used in the screening of drugs
 CC and in diagnostic procedures. This hydrophobic peptide is a beta amyloid
 CC peptide and can be used for the screening of drugs and treatment of
 CC Alzheimer's disease

SQ Sequence 42 AA;

Query Match 100.0%; Score 125; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 4.3e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGATIGLMVGIVIA 26

DB 17 LVFPAEDVGSNKGATIGLMVGIVIA 42

Search completed: September 28, 2006, 06:10:43
 Job time : 70.488 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:11:16 ; Search time 10.7265 Seconds
(without alignments)
233.221 Million cell updates/sec

Title: US-09-731-899-7
Perfect score: 125
Sequence: 1 LVFFADVSNKGAITGLMGVIA 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	42	2 PNO512	beta-amyloid prote
2	125	100.0	57	2 A60045	Alzheimer's diseas
3	125	100.0	57	2 F60045	Alzheimer's diseas
4	125	100.0	57	2 D60045	Alzheimer's diseas
5	125	100.0	57	2 E60045	Alzheimer's diseas
6	125	100.0	57	2 G60045	Alzheimer's diseas
7	125	100.0	57	2 B60045	Alzheimer's diseas
8	125	100.0	82	2 PQ0438	Alzheimer's diseas
9	125	100.0	695	1 A49795	Alzheimer's diseas
10	125	100.0	695	1 A27485	Alzheimer's diseas
11	125	100.0	695	2 S00550	Alzheimer's diseas
12	125	100.0	770	1 ORH044	Alzheimer's diseas
13	121	96.8	747	2 JH0773	Alzheimer's diseas
14	60	48.0	33	2 S23094	beta-amyloid prote
15	59	47.2	755	2 A13228	tryptophan 2-mono
16	58	46.4	755	1 QQA64T	tryptophan 2-mono
17	57	45.6	503	2 S73843	general amino acid
18	57	45.6	755	1 DA6GWT	tryptophan 2-mono
19	53	42.4	390	2 C75103	na+/h+ antiporter
20	52	41.6	327	2 T18232	conserved hypotet
21	52	41.6	678	2 G71526	3-methyl-2-oxobuta
22	52	41.6	678	2 C81683	conserved hypotet
23	52	41.6	738	2 C95936	sugc protein - Del
24	51	40.8	103	2 D75449	hypothetical glyci
25	50	40.0	234	2 G95989	polysugar degradin
26	50	40.0	296	2 A69856	probable Na+/H+-ex
27	50	40.0	390	2 H71083	hypothetical prote
28	50	40.0	487	2 T49424	SLG1 protein - yea
29	49	39.2	378	2 S61992	

30	49	39.2	403	2 T36019	phosphoglycerate k
31	49	39.2	469	2 C90446	permease, multidu
32	49	39.2	674	2 C39476	kinase-like trans
33	48.5	38.8	459	2 I64224	aromatic amino aci
34	48	38.4	337	2 E95288	probable zinc-bind
35	48	38.4	415	2 G72335	hypothetical prote
36	48	38.4	656	2 B86289	probable serine/th
37	48	38.4	728	2 D86278	hypothetical prote
38	47.5	38.0	159	1 I83299	sigma-E factor reg
39	47	37.6	119	2 C70027	multidrug-efflux t
40	47	37.6	135	2 G87686	hypothetical prote
41	47	37.6	303	2 D69114	conserved hypotet
42	47	37.6	330	2 AD0305	probable sugar tra
43	47	37.6	406	2 T23496	hypothetical prote
44	47	37.6	492	1 E69114	fumurate reductase
45	47	37.6	771	2 AB2160	hypothetical prote
46	46.5	37.2	159	2 B85903	sigma-E factor, ne
47	46.5	37.2	159	2 D91058	sigma-E factor reg
48	46.5	37.2	311	2 G86324	hypothetical prote
49	46.5	37.2	375	2 A49336	hemolysin B1, precu
50	46.5	37.2	464	2 D71219	probable L-asparta
51	46.5	37.2	1215	2 S50428	probable Ca2+-tran
52	46	36.8	144	2 AC2572	hypothetical prote
53	46	36.8	254	2 P90107	60S ribosomal prot
54	46	36.8	317	2 G64408	hypothetical prote
55	46	36.8	331	2 A71365	probable Lambda CI
56	46	36.8	417	2 F97789	ampc protein (limp
57	46	36.8	448	2 T41145	probable amine tra
58	46	36.8	471	2 E90269	multidrug resistan
59	46	36.8	543	2 B97092	ABC-type transport
60	46	36.8	589	2 H83199	phosphotransferase
61	46	36.8	601	2 H82039	GTP-binding protei
62	46	36.8	678	2 C86495	hypothetical prote
63	46	36.8	678	2 H72128	3-methyl-2-oxobuta
64	46	36.8	769	1 UC1121	leukocyte adhesion
65	46	36.8	827	1 S66094	stage II sporulati
66	46	36.8	976	2 B84659	probable receptor-
67	46	36.8	1286	2 T02187	probable ABC trans
68	46	36.8	1292	2 T48007	P-glycoprotein hom
69	46	36.8	1364	2 T51920	probable xanthine
70	45.5	36.4	245	2 AH1098	a probable phospho
71	45.5	36.4	245	2 AG1461	probable phospho-b
72	45.5	36.4	311	2 H75411	conserved hypotet
73	45.5	36.4	409	2 S29124	membrane glycoprot
74	45.5	36.4	523	2 JC7556	linoleoyl-CoA desa
75	45	36.0	54	2 F70249	hypothetical prote
76	45	36.0	79	2 F82647	hypothetical prote
77	45	36.0	193	2 E95340	hypothetical prote
78	45	36.0	232	2 AD3350	outer membrane pro
79	45	36.0	249	1 A61087	myelin P0 glycopro
80	45	36.0	257	2 AC1024	probable dimethyl
81	45	36.0	344	2 T40167	hypothetical prote
82	45	36.0	374	2 C83078	still frameshift t
83	45	36.0	385	2 AF2427	hypothetical prote
84	45	36.0	386	2 AD0098	probable sugar tra
85	45	36.0	401	1 A35691	pilin biogenesis p
86	45	36.0	406	1 B35384	pilC protein - Pse
87	45	36.0	461	2 S74414	Na+/H+-exchanging
88	45	36.0	467	2 E91112	hypothetical prote
89	45	36.0	467	2 G85957	unknown protein en
90	45	36.0	479	2 F87474	major facilitator
91	45	36.0	522	2 D96602	nucleolar protein
92	45	36.0	546	2 S48313	hexose transport p
93	45	36.0	553	1 A46329	cell fusion glycop
94	45	36.0	553	1 B46329	cell fusion glycop
95	45	36.0	553	1 B46329	cell fusion glycop
96	45	36.0	553	1 E46329	cell fusion glycop
97	45	36.0	578	2 B37852	phosphotransferase
98	45	36.0	601	2 T02581	nodulin-like prote
99	45	36.0	737	2 C84232	kinase anchor prot
100	45	36.0	768	2 JC6564	cellobiose oxidase

ALIGNMENTS

RESULT 1

PN0512
 beta-amyloid protein - guinea pig (fragment)
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: PN0512
 R/Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993
 A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
 A/Reference number: PN0512; MUID:93290653; PMID:7685598
 C/Accession: PN0512
 A/Molecule type: protein
 A/Residues: 1-42 <JOH>
 A/Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031588
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C/Keywords: alternative splicing; amyloid

Query Match

Best Local Similarity 100.0%; Score 125; DB 2; Length 42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LVFPADVGSNKGAIIGLMVGVVIA 26
 |||
 17 LVFPADVGSNKGAIIGLMVGVVIA 42

RESULT 2

A60045
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C/Species: Canis lupus familiaris (dog)
 C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C/Accession: A60045
 R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A/Reference number: A60045; MUID:92017079; PMID:1656157
 C/Accession: A60045
 A/Molecule type: mRNA
 A/Residues: 1-57 <JOH>
 A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 125; DB 2; Length 57;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LVFPADVGSNKGAIIGLMVGVVIA 26
 |||
 22 LVFPADVGSNKGAIIGLMVGVVIA 47

RESULT 3

F60045
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C/Accession: F60045
 R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A/Reference number: A60045; MUID:92017079; PMID:1656157
 C/Accession: F60045
 A/Molecule type: mRNA
 A/Residues: 1-57 <JOH>
 A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIRN:CA39592.1; PID:
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 125; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LVFPADVGSNKGAIIGLMVGVVIA 26
 |||
 22 LVFPADVGSNKGAIIGLMVGVVIA 47

RESULT 4

D60045
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C/Accession: D60045
 R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A/Reference number: A60045; MUID:92017079; PMID:1656157
 C/Accession: D60045
 A/Molecule type: mRNA
 A/Residues: 1-57 <JOH>
 A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 125; DB 2; Length 57;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LVFPADVGSNKGAIIGLMVGVVIA 26
 |||
 22 LVFPADVGSNKGAIIGLMVGVVIA 47

RESULT 5

A60045
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C/Species: Ovis sp. (sheep)
 C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C/Accession: E60045
 R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A/Reference number: A60045; MUID:92017079; PMID:1656157
 C/Accession: E60045
 A/Molecule type: mRNA
 A/Residues: 1-57 <JOH>
 A/Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 125; DB 2; Length 57;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LVFPADVGSNKGAIIGLMVGVVIA 26
 |||
 22 LVFPADVGSNKGAIIGLMVGVVIA 47

RESULT 6

G60045
 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C/Accession: G60045
 R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A/Reference number: A60045; MUID:92017079; PMID:1656157
 C/Accession: G60045
 A/Molecule type: mRNA
 A/Residues: 1-57 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 125; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGATIGLMVGAVIA 26
 DB 22 LVFFADVGSNKGATIGLMVGAVIA 47

RESULT 7

B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: Ursus maritimus (polar bear)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #ext_change 09-Jul-2004
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; PMID:92017079; PMID:1656157
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56128; NID:92165; PIDN:
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 125; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGATIGLMVGAVIA 26
 DB 22 LVFFADVGSNKGATIGLMVGAVIA 47

RESULT 8

P00438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #ext_change 19-Oct-1995
 C:Accession: P00438; C60045
 R:Davidson, J.S.; West, R.U.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A:Reference number: P00438; PMID:93075180; PMID:1445331
 A:Accession: P00438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; PMID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 125; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGATIGLMVGAVIA 26
 DB 33 LVFFADVGSNKGATIGLMVGAVIA 58

RESULT 9

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999
 C:Accession: A49795
 R:Podlasky, M.B.; Tolian, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; PMID:91273117; PMID:1905108
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: UNIPARC:UPI000002A2P2; GB:M58727; NID:9342062; PIDN:AAA36829.1; PID
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 125; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGATIGLMVGAVIA 26
 DB 613 LVFFADVGSNKGATIGLMVGAVIA 638

RESULT 10

A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #ext_change 09-Jul-2004
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec
 A:Reference number: A27485; PMID:88106489; PMID:3322280
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YMA>
 A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:9191566; PIDN
 A:Experimental source: brain
 R:de Strooper, B.; Van Leuven, F.; Van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; PMID:92096458; PMID:1756177
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: UNIPARC:UPI000002A2P9; EMBL:X59379
 R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; PMID:92209998; PMID:1555768
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: UNIPARC:UPI0000003B7; GB:D10603; NID:9220328; PIDN:BA01456.1; PID
 C:Genetics:
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 125; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGATIGLMVGAVIA 26
 DB 613 LVFFADVGSNKGATIGLMVGAVIA 638

RESULT 11
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 09-Jul-2004
A:Accession: S00550; A41245; A39820; S46251
R:Shivver, B.D.; Hlilbich C.; Malthaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SH1>
A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2B2; EMBL:X07648; NID:G55616; PIDN:
R.Schubert, D.; Schroeder, R.; LaCordiere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Cross-references: UNIPARC:UPI0000177FD
A:Note: evidence for heparan sulfate attachment
R.Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R.Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Moller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Cross-references: UNIPARC:UPI00001777FE
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C:Keyword: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
P:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 125; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNGAIGLVGVVIA 26
DB 613 LVFPAEDVGSNGAIGLVGVVIA 638

RESULT 12
QSHUMA
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
A:Accession: S02260; A32277; A33260; A35466; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R.Lemstra, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: UNIPARC:UPI000002A2P2; EMBL:X13466

A:Note: alternative splice form APP(695)
R.Lemstra, H.G.
Submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: UNIPARC:UPI000016A5FC; EMBL:X13466; NID:G55599; PIDN:CAA31830.1; PID
A:Note: alternative splice form APP(695)
R.Lemstra, H.G.; Lemstra, D.K.; Salton, S.R.; Robak, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AA313
R.Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <QOH>
A:Cross-references: UNIPARC:UPI000016A551; GB:M23270; NID:G17863; PIDN:AA51768.1; PID:
R.Prelli, F.; Levy, E.; van Duinen, S.G.; Bote, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Cross-references: UNIPARC:UPI0000148176
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
R.Joshikali, S.I.; Sasaki, H.; Don-ura, K.; Futuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: UNIPARC:UPI000002DB1C; GB:M3112; NID:G178613; PIDN:AA59502.1; PID
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QMLMPVTPAEKAVGR' <YOS2>
A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AA59501.1; PID:
R.Joshikali, S.I.; Sasaki, H.; Don-ura, K.; Futuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R.Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:211584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEF>
A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AA51727.1; PID:
R.Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: UNIPARC:UPI000011FTFA; GB:S57665; NID:G236720; PIDN:AA319991.1; PID
R.Kamano, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonso, M.E.; Pulic, S.M.; Anderson,

arakle, S.E.; Korenberg, J.R.; Sharma, V.; Kukulj, W.; Larson, E.; Heaton, L.L.; Martin, Am. J. Hum. Genet. 51, 998-1014, 1992

A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the

A:Reference number: A44017; MUID:93035397; PMID:1415269

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692, 'G', 694-718 <KAN1>

A:Cross-references: UNIPARC:UPI000011F7B; GB:S45135; NID:q257377; PIDN:AA23645.1; PID:

A:Experimental source: familial Alzheimer disease family SB

A>Note: sequence extracted from NCBI backbone (NCBIP:115374)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <KAN2>

A:Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:q257379; PIDN:AA23646.1; PID:

A:Experimental source: familial Alzheimer disease family LT

A>Note: sequence extracted from NCBI backbone (NCBIP:115376)

A>Note: this sequence has a silent mutation

R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface

A:Reference number: A03134; MUID:87144572; PMID:2881207

A:Accession: A03134

A:Molecule type: mRNA

A:Residues: 1-288, 'V', 365-770 <KAN>

A:Cross-references: UNIPARC:UPI00002A2F2; GB:Y00264; NID:q28525; PIDN:CAA68374.1; PID:9

A>Note: alternative splice form APP(695)

R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular

A:Reference number: A29030; MUID:87231971; PMID:3035574

A:Accession: A29030

A:Molecule type: mRNA

A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>

A:Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:q178339; PIDN:AAA51722.1; PID:

A>Note: the authors translated the codon GAG for residue 647 as Asp

R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C. Science 235, 877-880, 1987

A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid

A:Reference number: A47584; MUID:87120328; PMID:3810169

A:Accession: A47584

A:Molecule type: mRNA

A:Residues: 674-756, 'S', 758-770 <GOL>

A:Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:

A:Experimental source: brain

R:Ranzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke Science 235, 880-884, 1987

A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th

A:Reference number: A47585; MUID:87120329; PMID:2949367

A:Accession: A47585

A:Molecule type: mRNA

A:Residues: 674-703 <TAN1>

A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:

R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle EMO J. 7, 949-957, 1988

A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec

A:Reference number: S02638; MUID:88266437; PMID:2800137

A:Accession: S02638

A:Molecule type: mRNA

A:Residues: 672-678 <DYR>

A:Cross-references: UNIPARC:UPI0000035AB0

R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve Nature 331, 528-530, 1988

A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat

A:Reference number: S00707; MUID:88122640; PMID:2893230

A:Accession: S00707

A:Molecule type: mRNA

A:Residues: 286-344, 'I', 365-366 <TAN2>

A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:

A:Experimental source: promyelocytic leukemia cell line HL60

A>Note: alternative splice form APP(751)

R:Ponte, P.; Gonzalez-Demuth, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da Nature 331, 525-527, 1988

A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi

A:Reference number: S00925; MUID:88122639; PMID:2893289

A:Accession: S00925

A:Molecule type: mRNA

A:Residues: 1-344, 'I', 365-770 <PO2>

A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:X00297; NID:q28720; PIDN:CAA3

A>Note: alternative splice form APP(751)

R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988

A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor

A:Reference number: A38949; MUID:88122641; PMID:2893291

A:Accession: A38949

A:Molecule type: mRNA

A:Residues: 287-367 <KIT>

A:Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:9

A:Experimental source: glioblastoma cell line

A>Note: alternative splice form APP(770)

R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton Brain Res. Mol. Brain Res. 4, 121-131, 1988

A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p

A:Reference number: A30320

A:Accession: A30320

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 284-288, 'V', 365-770 <VIT1>

A:Cross-references: UNIPARC:UPI0000174094

A:Accession: B30320

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 122-288, 'V', 365-770 <VIT2>

A:Cross-references: UNIPARC:UPI0000174094

A:Accession: C30320

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 606-770 <VIT3>

A:Cross-references: UNIPARC:UPI0000174094

R:Rai, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulowska, E.M.; Majocha, R.E.; Marotta, C.A. Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988

A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br

A:Reference number: A31087; MUID:88124954; PMID:2893379

A:Accession: A31087

A:Molecule type: mRNA

Query Match 100.0%; Score 125; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITGLMGVGVTA 26
|||||
Db 688 LVFPAEDVGSNKGAITGLMGVGVTA 713

RESULT 13

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #ext_change 13-Aug-1999

C:Accession: JH0773

R:Okado, H.; Okamoto, H. Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A>Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental

A:Reference number: JH0773; MUID:93129227; PMID:1282805

A:Accession: JH0773

A:Molecule type: mRNA

A:Residues: 1-747 <OKA>

A:Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:q263150; PIDN:AA24853.1; PID

A:Experimental source: larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; amyloid

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 96.8%; Score 121; DB 2; Length 747;
Best Local Similarity 96.2%; Pred. No. 5.4e-09;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A:Genetic code: SGC3

Query Match 45.6%; Score 57; DB 2; Length 503;
Best Local Similarity 61.1%; Pred. No. 3;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 VGSNKGAIIGLMVGVI 25
DB 131 VQDNNGALIGLVGFLV 148

RESULT 18

DAGWT

tryptophan-2-monooxygenase (EC 1.13.12.3) TA - Agrobacterium tumefaciens plasmid pTm4

C:Species: Agrobacterium tumefaciens

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C:Accession: S15002; S15450

R:Bonnard, G.; Vincent, F.; Octen, L.

Plant Mol. Biol. 16, 733-738, 1991

A:Title: Sequence of Agrobacterium tumefaciens biotype III auxin genes.

A:Reference number: S15001; MUID:91329707; PMID:1868204

A:Accession: S15002

A:Molecule type: DNA

A:Residues: 1-755 <BO2>

A:Cross-references: UNIPARC:UP100001372B1; EMBL:X56185; NID:G39133; PIDN:CAA39646.1; PID

A:Experimental source: strain Tm4; strain octopine

C:Genetics:

A:Gene: taam

A:Genome: plasmid pTm4

C:Function:

A:Pathway: tryptophan metabolism; auxin biosynthesis

A:Note: catalyzes the first step in the biosynthesis of auxins from tryptophan

C:Superfamily: tryptophan-2-monooxygenase

C:Keywords: monooxygenase; oxidoreductase

Query Match 45.6%; Score 57; DB 1; Length 755;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 FPAEDVGSNKGAIIGLMVGVI 26
DB 229 FPEEDVPRPKVAVTIGISGLVVA 252

RESULT 19

C75103

na+/h+ antiporter (napa-4) PAB0809 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: C75103

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: C75103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-350 <KAM>

A:Cross-references: UNIPROT:Q9U2D1; UNIPARC:UP10000034520; GB:AJ248286; GB:AL096836; NID

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: napa-4; PAB0809

C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napa1

Query Match 42.4%; Score 53; DB 2; Length 390;
Best Local Similarity 46.2%; Pred. No. 8.5;
Matches 12; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 1 LVFPAEDVGSNKGAIIGLMVGVI 26
DB 225 LVFPAEDVGSNKGAIIGLMVGVI 248

RESULT 20

T18232

conserved hypothetical protein - yeast (Candida albicans)

C:Species: Candida albicans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18232

R:Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z18831

A:Accession: T18232

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-527 <BAR>

A:Cross-references: UNIPROT:Q94040; UNIPARC:UP1000006A885; EMBL:AL033501; NID:e1341022;

C:Genetics:

A:Note: CA41C10.06c

Query Match 41.6%; Score 52; DB 2; Length 527;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 FPAEDVGSNKGAIIGLMVGVI 24
DB 56 VYCAVSXKSGSPIGIVGVI 77

RESULT 21

G71526

3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain pdhA,

N:Alternate names: oxoisovalerate dehydrogenase

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: G71526

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: G71526

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-678 <ARN>

A:Cross-references: UNIPROT:O84344; UNIPARC:UP100000D7604; GB:AE001307; GB:AE001273; NIT

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: pdhA/B

C:Keywords: oxidoreductase

Query Match 41.6%; Score 52; DB 2; Length 678;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGL 18
DB 371 VVVFGEVDVAGNKGVGIV 388

RESULT 22

C81683

3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC061

N:Alternate names: oxoisovalerate dehydrogenase

C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: C81683

R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: C81683

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-678 <TR>

A:Cross-references: UNIPROT:Q9PK54; UNIPARC:UP100000579G3; GB:AE002330; GB:AE002160; NIT

A:Experimental source: strain NigG (MOPn)
C:Genetics:
A:Gene: TC0618
C:Keywords: oxidoreductase

Query Match 41.6%; Score 52; DB 2; Length 678;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITGL 18
DB 371 VVVFGEDEVAGNKGVFGV 388

RESULT 23

C95936 conserved hypothetical membrane protein, similar to Y1058 Smb21251 [imported] - Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: C95936
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95936
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-738 <KUR>
A:Cross-references: UNIPROT:Q92VFL; UNIPARC:UPI00000CB649; GB:AL591985; PIDN:CAC49155.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiet, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeJaure, hebaull, P.; Vandenhof, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21251
A:Genome: plasmid

Query Match 41.6%; Score 52; DB 2; Length 738;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 FAEDVGSNKGAITGLMVGVVI 25
DB 300 FPEDEVNLGAVGLVGLAI 321

RESULT 24

D75449 sngE protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: D75449
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamthekavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75449
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-103 <WHI>
A:Cross-references: UNIPROT:Q9RVM3; UNIPARC:UPI0000003DA8; GB:AE001952; GB:AE000513; NTD
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1004
A:Map position: 1

C:Superfamily: sngE protein

Query Match 40.8%; Score 51; DB 2; Length 103;
Best Local Similarity 39.1%; Pred. No. 42; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 VFPAEDVGSNKGAITGLMVGVV 24
DB 75 VFGEQLGGKRLALLVAVVAAIL 97

RESULT 25

G95989 hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) mega
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: G95989
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95989
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-234 <KUR>
A:Cross-references: UNIPROT:Q92UE8; UNIPARC:UPI00000CB79E; GB:AL591985; PIDN:CAC49583.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiet, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeJaure, hebaull, P.; Vandenhof, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20889
A:Genome: plasmid

Query Match 40.0%; Score 50; DB 2; Length 234;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 FAEDVGSNKGAITGLMVGV 22
DB 25 FAOSVGSNGGLNVGSLGG 43

RESULT 26

A69856 polysugar degrading enzyme homolog ykfc - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: A69856
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bester C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho Nature 390, 249-256, 1997
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69856
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-234 <WHI>
A:Cross-references: UNIPROT:Q9RVM3; UNIPARC:UPI0000003DA8; GB:AE001952; GB:AE000513; NTD
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1004
A:Map position: 1

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69856
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

Qy 2 VFFAD-VGSNKGATII-GIMGCVVI 25
| | | | | : | | | | :
Db 89 VAFABDTVGSSAEAVVTGLADGGVAV 114

Search completed: September 28, 2006, 06:24:32
Job time : 11.7265 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:00:51; Search time 84.6457 Seconds
(without alignments)
284.130 Million cell updates/sec

Title: US-09-731-899-7
Perfect score: 125
Sequence: 1 LVFFADVSNKGAIIGLVGAVIA 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	42	Q56J16 GRAGR	Q56J16 girampus gri
2	125	100.0	42	Q56J17 TURTR	Q56J17 turrops tr
3	125	100.0	42	Q7M088 CAYPO	Q7M088 cavia porce
4	125	100.0	52	Q8W299 HUVAN	Q8W299 homo sapien
5	125	100.0	57	A4_URSPA	Q29149 u amyloid b
6	125	100.0	58	A4_CANFA	Q28280 c amyloid b
7	125	100.0	58	A4_RABIT	Q28748 o amyloid b
8	125	100.0	58	A4_SHEEP	Q28757 o amyloid b
9	125	100.0	59	A4_BOVIN	Q28053 b amyloid b
10	125	100.0	79	Q35463 CRIGR	Q35463 cricetulus
11	125	100.0	113	Q8JH58 CHBSE	Q8JH58 chelydra se
12	125	100.0	218	Q8BPV5 MOUSE	Q8BPV5 mus musculu
13	125	100.0	384	Q8BPC7 MOUSE	Q8BPC7 mus musculu
14	125	100.0	534	Q93296 CHICK	Q93296 gallus gall
15	125	100.0	569	Q9PYL1 CHICK	Q9PYL1 gallus gall
16	125	100.0	695	Q2XQAO PIG	Q2XQAO sus scrofa
17	125	100.0	695	Q56JK3 CANFA	Q56JK3 canis faml
18	125	100.0	695	Q5R477 PONY	Q5R477 pongo pygma
19	125	100.0	695	Q6RH29 CANFA	Q6RH29 canis faml
20	125	100.0	695	Q6GR78 MOUSE	Q6GR78 mus musculu
21	125	100.0	695	Q9DSJ8 CHICK	Q9DSJ8 gallus gall
22	125	100.0	714	Q56JK4 CANFA	Q56JK4 canis faml
23	125	100.0	733	Q6PE05 RAT	Q6PE05 rattus norv
24	125	100.0	749	Q56JK2 STECO	Q56JK2 stenella co
25	125	100.0	751	A4_SAIIC	Q95241 s amyloid b
26	125	100.0	751	Q6GSGO HUMAN	Q6GSGO homo sapien
27	125	100.0	751	Q4R4R8 MACFA	Q4R4R8 macaca fasc
28	125	100.0	751	Q56JK5 CANFA	Q56JK5 canis faml
29	125	100.0	751	Q6RH28 CANFA	Q6RH28 canis faml
30	125	100.0	751	Q2XQ99 PIG	Q2XQ99 sus scrofa
31	125	100.0	751	Q9DGJ7 CHICK	Q9DGJ7 gallus gall

32	125	100.0	752	Q3TW33 MOUSE	Q3TW33 mus musculu
33	125	100.0	752	Q3TX19 MOUSE	Q3TX19 mus musculu
34	125	100.0	754	Q4RY33 TETROD	Q4RY33 tetradon n
35	125	100.0	759	Q4S0J4 TETNG	Q4S0J4 tetradon n
36	125	100.0	770	A4_CAVPO	Q60495 c amyloid b
37	125	100.0	770	A4_HUMAN	P05067 h amyloid b
38	125	100.0	770	A4_MACFA	P53601 m amyloid b
39	125	100.0	770	A4_MOUSE	P12023 m amyloid b
40	125	100.0	770	A4_PANTR	Q5180 p amyloid b
41	125	100.0	770	A4_PIG	P79307 s amyloid b
42	125	100.0	770	A4_RAT	P08592 r amyloid b
43	125	100.0	770	Q56JK6 CANFA	Q56JK6 canis faml
44	125	100.0	770	Q6RH30 CANFA	Q6RH30 canis faml
45	125	100.0	770	Q53ZT3 MOUSE	Q53ZT3 mus musculu
46	125	100.0	770	Q547B7 RAT	Q547B7 rattus norv
47	125	100.0	780	A4_TENFL	Q73683 tetradon f
48	122	97.6	737	A4_FUGRU	Q93279 fuga rubrip
49	121	96.8	49	Q97917 BOVIN	Q97917 bos taurus
50	121	96.8	49	Q2XQ98 PIG	Q2XQ98 sus scrofa
51	121	96.8	693	Q98SGO XENLA	Q98SGO xenopus lae
52	121	96.8	747	Q91963 PEPI	Q91963 xenopus ap
53	121	96.8	749	Q6NRJ1 XENLA	Q6NRJ1 xenopus lae
54	121	96.8	750	Q6DJB6 XENTR	Q6DJB6 xenopus tro
55	119	95.2	357	Q8U018 BRARE	Q8U018 brachydanio
56	119	95.2	472	Q8U050 BRARE	Q8U050 brachydanio
57	119	95.2	612	Q919E7 BRARE	Q919E7 brachydanio
58	119	95.2	678	Q7ZET1 BRARE	Q7ZET1 brachydanio
59	119	95.2	738	Q6RUZ1 BRARE	Q6RUZ1 brachydanio
60	119	95.2	738	Q90W28 BRARE	Q90W28 brachydanio
61	118	94.4	695	Q7ZXQ0 XENLA	Q7ZXQ0 xenopus lae
62	118	94.4	695	Q98SF9 XENLA	Q98SF9 xenopus lae
63	116	92.8	699	Q57394 NARJA	Q57394 narke japon
64	115	92.0	64	Q3M025 ANRST	Q3M025 anechinus
65	113	90.4	239	Q8UT17 BRARE	Q8UT17 brachydanio
66	113	90.4	362	Q5X1Y5 BRARE	Q5X1Y5 brachydanio
67	113	90.4	694	Q8U0R9 BRARE	Q8U0R9 brachydanio
68	113	90.4	33	Q9UC33 HUMAN	Q9UC33 homo sapien
69	84	67.2	33	Q9R472 GRHIZ	Q9R472 agrobacteri
70	59	47.2	755	Q9R694 GRHIZ	Q9R694 agrobacteri
71	59	47.2	755	Q9R717 GRHIZ	Q9R717 agrobacteri
72	59	47.2	755	Q9WMA1 GRHIZ	Q9WMA1 agrobacteri
73	59	47.2	755	Q8U6A3 AGRT5	Q8U6A3 agrobacteri
74	58	46.4	252	Q6LJ99 PHOPR	Q6LJ99 photobacter
75	58	46.4	755	Q44388 GRHIZ	Q44388 agrobacteri
76	58	46.4	755	Q44388 GRHIZ	Q44388 agrobacteri
77	58	46.4	755	Q44388 GRHIZ	Q44388 agrobacteri
78	57	45.6	328	Q9RPS4 ENTFA	Q9RPS4 enterococcu
79	57	45.6	503	Y319 MYCPN	P75462 mycoplasma
80	57	45.6	755	Y319 MYCPN	P25017 agrobacteri
81	56	44.8	361	Q6BML2 DEBHA	Q6BML2 debaryomyce
82	56	44.8	915	Q6BML2 DEBHA	Q6BML2 candida gla
83	56	44.8	969	Q4C795 CROWT	Q4C795 croceophaer
84	55	44.0	344	Q41SK2 PERCA	Q41SK2 ferropiasma
85	55	44.0	602	Q2SROS MYSCA	Q2SROS mycoplasma
86	54	43.2	550	Q41914 GIBZE	Q41914 gibberella
87	54	43.2	602	Q6WTK8 MYCWS	Q6WTK8 mycoplasma
88	53	42.4	108	Q2WMC8 CLOBE	Q2WMC8 clostridium
89	53	42.4	360	Q91UX1 92Z2Z	Q91UX1 plasmid pip
90	53	42.4	390	Q9U2D1 PYRAB	Q9U2D1 pyrococcus
91	53	42.4	469	Q3EMX8 BACTI	Q3EMX8 bacillus th
92	53	42.4	608	Q2KGN7 MAGGR	Q2KGN7 magnaporthe
93	53	42.4	903	Q41ZDS AZOVI	Q41ZDS azotobacter
94	52.5	42.0	451	Q40MM2 DBSAC	Q40MM2 desulfurono
95	52.5	42.0	597	Q6AKC6 DBSPS	Q6AKC6 desulfotale
96	52	41.6	170	Q8ZYVO PYRAB	Q8ZYVO pyrobacterium
97	52	41.6	351	Q7NJF2 GLOVI	Q7NJF2 gloeobacter
98	52	41.6	365	Q5UMG5 HALMA	Q5UMG5 haloarcula
99	52	41.6	431	Q6NIR1 CORDI	Q6NIR1 corynebacte
100	52	41.6	444	Q21E29 9DELTA	Q21E29 anaeromyxob

ALIGNMENTS

RESULT 1
 OS6J06 GRAGR PRELIMINARY; PRT; 42 AA.
 AC OS6J06;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DE Amyloid beta protein (Fragment).
 OS Grampus griseus (Risso's dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Grampus.
 OX NCBI_TaxID=83653;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarasa M.;
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AY926589; AAX81918.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PRO0204; BETAMYL0ID.
 FT NON_TER 1
 FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
 SQ

Query Match 100.0%; Score 125; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 17 LVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 2
 OS6J07 TURTR PRELIMINARY; PRT; 42 AA.
 AC OS6J07;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DE Amyloid beta protein (Fragment).
 OS Grampus griseus (Risso's dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Tursiops.
 OX NCBI_TaxID=9739;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarasa M.;
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AY926588; AAX81917.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PRO0204; BETAMYL0ID.
 FT NON_TER 1
 FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
 SQ

FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
 Query Match 100.0%; Score 125; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 17 LVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 3
 OTM088 CAVPO PRELIMINARY; PRT; 42 AA.
 AC OTM088;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DE Beta-amyloid protein (Fragment).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystericognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93290653; PubMed=7685598;
 RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
 RA Kamuya H., Ohno M.;
 RT "Receptor-mediated specific biological activity of a beta-amyloid
 RT protein fragment for NK-1 substance P receptors.";
 RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
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 CC PIR; P05012; P05012.
 DR HSSP; Q16019; 11YF.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083.SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PRO0204; BETAMYL0ID.
 FT NON_TER 1
 FT SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
 SQ

Query Match 100.0%; Score 125; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
 17 LVFFAEDVGSNKGAIIGLMVGVVIA 42

RESULT 4
 O8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
 ID O8WZ99; HUMAN
 AC O8WZ99;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 2.
 DE Amyloid protein (Fragment).
 OS Homo sapiens (Human).
 GN Name=APP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo
 OX NCBI_TaxID=9606;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
 RA Makitani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
 RA Niimiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.,
 RT "Novel amyloid precursor protein gene missense mutation (D678H) in
 RT probable familial Alzheimer's disease.";
 RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
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 CC -----
 CC EMBL, AB066441, BAB71958.2; -, mRNA.
 CC Ensembl, ENSG00000142192; Homo sapiens.
 CC GO, GO:0016021; C:integral to membrane, IEA.
 CC GO, GO:0005486; F:binding, IEA.
 CC InterPro, IPR001255; Beta-APP.
 CC PANTHER, PTHR10083:SF6; Beta-APP; 1.
 CC Pfam, PF03494; Beta-APP; 1.
 CC NON_TER 1 1
 CC FT 52 52
 CC FT SEQUENCE 52 AA; 5597 MW; 3F0EB9EC18011AD CRC64;
 SQ
 Query Match 100.0%; Score 125; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFADVGSNKGAIIGLVGGVIA 26
 DB 17 LVFFADVGSNKGAIIGLVGGVIA 42
 RESULT 5
 A4_URSMA STANDARD; PRT; 57 AA.
 ID A4_URSMA
 AC Q29149;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) (Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)) (Fragment).
 GN Name=APP;
 OS Ursus maritimus (Polar bear) (Thalassos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
 OC Ursus.
 CC NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.,
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 CC EMBL, X56128; CAA39593.1; -, mRNA.
 CC FJR, B60045; B60045.
 CC HSSP, P08592; INMJ.
 CC InterPro, IPR008155; A4_APP.
 CC InterPro, IPR001255; Beta-APP.

DR PANTHER, PTHR10083:SF6; Beta-APP; 1.
 DR Pfam, PF03494; Beta-APP; 1.
 DR PRINTS, PR00204; BETAMYLOID.
 DR PROSITE, PS00319; A4-EXTRA; PARTIAL.
 DR PROSITE, PS00320; A4-INTRA; PARTIAL.
 KW Amyloid; Membrane; Transmembrane.
 FT CHAIN <1 57
 FT /FTID=PRO_0000226244.
 FT /FTID=PRO_0000000191.
 FT /FTID=PRO_0000000191.
 FT CHAIN 6 >57
 FT /FTID=PRO_0000000192.
 FT CHAIN 6 47
 FT /FTID=PRO_0000000193.
 FT CHAIN 6 45
 FT /FTID=PRO_0000000194.
 FT CHAIN 46 >57
 FT /FTID=PRO_0000000195.
 FT CHAIN 48 >57
 FT /FTID=PRO_0000000196.
 FT CHAIN 34 57
 FT /FTID=PRO_0000000196.
 FT NON_TER 1 1
 FT NON_TER 57 57
 FT SEQUENCE 57 AA; 6172 MW; 84209D8E8BA82DFA CRC64;
 SQ
 Query Match 100.0%; Score 125; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFADVGSNKGAIIGLVGGVIA 26
 DB 22 LVFFADVGSNKGAIIGLVGGVIA 47
 RESULT 6
 A4_CANFA STANDARD; PRT; 58 AA.
 ID A4_CANFA
 AC Q28280;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 1.
 DT 07-MAR-2006, entry version 37.
 DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
 DE protein homolog) (Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
 DE Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
 DE APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57)) (Fragment).
 GN Name=APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 CC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.,
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 CC EMBL, X56125; CAA39590.1; -, mRNA.


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CC -I- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -I- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
CC
CC EMBL: X56130; CAA39595.1; -, mRNA.
CC
CC DR HSSP; P08592; 1NMJ.
CC DR InterPro; IPR008155; A4_APP.
CC DR InterPro; IPR001255; Beta-APP.
CC DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC DR Pfam; PF03494; Beta-APP; 1.
CC DR PRINTS; PR00204; BETAAMYL0ID.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC DR Amyloid; Membrane; Transmembrane.
CC KW CHAIN <1 >58
CC Amyloid beta A4 protein.
CC FT FTid=PRO 0000226243.
CC FT Soluble APP-beta (By similarity).
CC FT FTid=PRO 0000000185.
CC FT CHAIN 6 >58
CC CTF-alpha (By similarity).
CC FT FTid=PRO 0000000186.
CC FT Beta-amyloid protein 42 (By similarity).
CC FT FTid=PRO 0000000187.
CC FT Beta-amyloid protein 40 (By similarity).
CC FT FTid=PRO 0000000188.
CC FT Gamma-CTF(59) (By similarity).
CC FT FTid=PRO 0000000189.
CC FT CHAIN 46 >58
CC Gamma-CTF(57) (By similarity).
CC FT FTid=PRO 0000000190.
CC FT CHAIN 48 >58
CC Gamma-CTF(57) (By similarity).
CC FT FTid=PRO 0000000190.
CC FT Extracellular (Potential).
CC FT Cytoplasmic (Potential).
CC FT NON_TER 1 1
CC FT NON_TER 58 58
CC SQ SEQUENCE 58 AA; 6300 MW; FA34209D88EBA82D CRC64;
CC
CC Query Match 100.0%; Score 125; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 1.8e-09;
CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LVFFAEDVGSNKGATIGMGCVVTA 26
CC |||||
CC DB 22 LVFFAEDVGSNKGATIGMGCVVTA 47
CC
CC RESULT 9
CC A4_BOVIN
CC ID A4_BOVIN STANDARD; PRT; 59 AA.
CC AC Q28053;
CC DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
CC DT 01-NOV-1997, sequence version 1.
CC DT 07-FEB-2006, entry version 36.
CC DE Amyloid beta A4 protein (APP) (ABPP) (Alzheimer disease amyloid A4
CC protein homolog) [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha;
CC Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-
CC APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
CC CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).
CC OS Bos taurus (Bovine) .
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
CC Pecora; Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
CC [1]
CC NUCLEOTIDE SEQUENCE [MRNA] .
CC RP TISSUE=Brain;
CC RA MEDLINE=99010709; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC peptide in dog, polar bear and five other mammals by cross-species
CC polypeptide chain reaction analysis.";
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CC	Brain Res.	MOL.	Brain Res.	10:299-305(1991).
CC	-I-	FUNCTION:	Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).	
CC	-I-	SUBCELLULAR LOCATION:	Membrane; single-pass type I membrane protein.	
CC	-I-	SIMILARITY:	Belongs to the APP family.	
CC	-----			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	-----			
DR	EMBL;	X56124;	CAA39589.1;	-; mRNA.
DR	EMBL;	X56126;	CAA39591.1;	-; mRNA.
DR	HSSP;	P08592;	INMJ	
DR	InterPro;	IPR008155;	A4_APP.	
DR	InterPro;	IPR012551;	Beta-APP.	
DR	PANTHER;	PTHR10083:SF6;	Beta-APP; 1.	
DR	Pfam;	PF03494;	Beta-APP; 1.	
DR	PRINTS;	PR00204;	BETAAMYLROID.	
DR	PROSITE;	PS00319;	A4_EXTRA; PARTIAL.	
DR	PROSITE;	PS00320;	A4_INTRA; PARTIAL.	
DR	AmYloid;	Membrane;	Transmembrane.	
FT	CHAIN	<1	6	/Soluble APP-beta (By similarity).
FT	CHAIN	7	>59	/Frid=PRO_0000000064.
FT	CHAIN	7	>59	/Ctf-alpha (By similarity).
FT	CHAIN	7	48	/Frid=PRO_0000000065.
FT	CHAIN	7	46	/Beta-amyloid protein 42 (By similarity).
FT	CHAIN	7	46	/Frid=PRO_0000000066.
FT	CHAIN	47	>59	/Beta-amyloid protein 40 (By similarity).
FT	CHAIN	47	>59	/Frid=PRO_0000000067.
FT	CHAIN	49	>59	/Gamma-CTF(59) (By similarity).
FT	CHAIN	49	>59	/Frid=PRO_0000000068.
FT	TOPO_DOM	<1	34	/Gamma-CTF(57) (By similarity).
FT	TRANSEM	35	58	/Frid=PRO_0000000069.
FT	TOPO_DOM	59	>59	/Extracellular (Potential).
FT	NON_TER	1	1	/Potential.
FT	NON_TER	59	59	/Cytoplasmic (Potential).
SQ	SEQUENCE	59 AA;	6414 MW;	F43469D488A2E12D CRC64;
Query Match 100.0%; Score 125; DB 1; Length 59;				
Best Local Similarity 100.0%; Prod. NO. 1.8e-09;				
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1	LVFPAEDVGSNKGAIIGLMWGVVIA	26	
Db	23	LVFPAEDVGSNKGAIIGLMWGVVIA	48	
RESULT 10				
ID	035463_CRIGR	PRELIMINARY;	PRT;	79 AA.
AC	035463;			
DT	01-JAN-1998,	integrated into UniProtKB/TrEMBL.		
DT	01-JAN-1998,	sequence version 1.		
DT	07-FEB-2006,	entry version 20.		
DE	Alzheimer's amyloid beta protein (Fragment).			
CN	Name-beta App;			
OS	Cricetus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridea; Cricetidae; Cricetinae; Cricetus.			
OX	NCBI_TaxID=10029;			
RX	[1]			
RP	NOCLEOTIDE SEQUENCE.			
RP	Sambamurti K., Pinnix I., Gandhi S.;			
RL	Submitted (OCT-1997)	to the EMBL/GenBank/DBJ databases.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	-----			
DR	EMBL;	AF030413;	AAB86608.1;	-; mRNA.

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DR HSP; P08592; INM.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:Sf6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMAMLOID.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BF3F597 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPADVGSNKGATIGLWVGIVIA 26
Db 37 LVFPADVGSNKGATIGLWVGIVIA 62

RESULT 11
Q8UH58 CHESE PRELIMINARY; PRT; 113 AA.
AC Q8UH58;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OX NCBI_Taxid=134619;
RN [1]_Taxid=134619;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RA "Ocy1phenol (OP) alters the expression of members of the amyloid
RA protein family in the hypothalamus of the snapping turtle, Chelydra
RA serpentina serpentina."
RL Environ. Health Perspect. 110:269-275(2002).
CC -----
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CC -----
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSP; Q16019; IYT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:Sf6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAMAMLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
FT NON_TER 113 AA; 12750 MW; 72515C930496B053 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPADVGSNKGATIGLWVGIVIA 26
Db 31 LVFPADVGSNKGATIGLWVGIVIA 56

RESULT 12
Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
AC Q8BPV5;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.

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DT 07-FEB-2006, entry version 18.
DE 13 days embryo lung cDNA, RIKEN full-length enriched library,
DE clone: D430025b14 product: amyloid beta (A $\beta$ ) protein, full insert
DE sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmong L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Atturliya R.N., Bailey T.L.,
RA Banael M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matveeva H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mortazavi-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.U., Pavoni G., Peesle G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sander A.A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugizaki K., Sultana R., Takenawa Y., Taki K.,
RA Tamajoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang J.,
RA Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Hilde M., Bult C.,
RA Grimmond S.M., Tesardale R.D., Liu E.T., Brusic V., Queckenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki Y., Aikawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiyu N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT "Antisense Transcription in the Mammalian Transcriptome."
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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RA Nikaido I., Oseato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin S., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chottha C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmerond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
 RA Matsushima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynchuk-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiroki T., Waki K., Kawai J., Aizawa K., Arkawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuelpi L., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann C., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbarteis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wynchuk-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Taehiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hara A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hironaka K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Oseato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiroki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takada Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK052448; BAC34997.1; -; mRNA.
 DR HSSP: P08592; INMO.
 DR Ensembl: ENSMUSG0000022892; Mus musculus.
 DR MGI: MGI:88059; App.
 DR GO: GO:0045177; C:apical part of cell; IDA.
 DR GO: GO:0030424; C:axon; IDA.
 DR GO: GO:0031410; C:cytoplasmic vesicle; IDA.
 DR GO: GO:0016021; C:integral to membrane; IDA.
 DR GO: GO:0016020; C:membrane; TAS.
 DR GO: GO:0005624; C:membrane fraction; IDA.
 DR GO: GO:0031594; C:neuromuscular junction; IDA.
 DR GO: GO:0048471; C:perinuclear region; IDA.
 DR GO: GO:0051233; C:spindle midzone; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0008344; F:adult locomotory behavior; IMP.
 DR GO: GO:0008086; P:axon cargo transport; IMP.
 DR GO: GO:0016199; P:axon midline choice point recognition; IMP.
 DR GO: GO:0007409; P:axonogenesis; IMP.
 DR GO: GO:0048669; P:collateral sprouting in the absence of injury; IGI.
 DR GO: GO:0006878; P:copper ion homeostasis; IGI.
 DR GO: GO:0006878; P:copper ion homeostasis; IMP.
 DR GO: GO:0016358; P:dendrite morphogenesis; IGI.
 DR GO: GO:0016358; P:dendrite morphogenesis; IMP.
 DR GO: GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
 DR GO: GO:0030900; P:forebrain development; IMP.
 DR GO: GO:0000085; P:G2 phase of mitotic cell cycle; IMP.
 DR GO: GO:0007617; P:mating behavior; IGI.
 DR GO: GO:0016322; P:neuron remodeling; IMP.
 Query Match 100.0%; Score 125; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 5.8e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFPADVGSNKGATITGLWGVVIA 26
 DB 136 LVFPADVGSNKGATITGLWGVVIA 161
 RESULT 13
 Q8BPC7 MOUSE PRELIMINARY; PRT; 384 AA.
 AC Q8BPC7; integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE 0 day neonate head cDNA. RIKEN full-length enriched library,
 DE clone:4833432109 product:amyloid beta (A4) protein, full insert
 DE sequence. (Fragment).
 GN Name=App;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

- OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Methods Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilm M.L., Aldins V., Allen J.E.,
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Banerji M., Baxter L., Beiselt K.W., Bergsma T., Bono H., Chalk A.M.,
Chiu K.P., Chowdhury V., Christoffels A., Clutterbuck D.R.,
Cioe W.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
Flecher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Harcup J., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Kitano H., Kiyohara G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matada H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mortrud T., Muzier N., Nakano N., Nakachi H., Ng P.,
Nelson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki K., Ohtsuka Y., Pang K.C., Pavan W.J., Pavoni G., Pebole G.,
Petkovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Roos B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugtara K., Sultana R., Takenawa Y., Taki K.,
Takeda H.R., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Walstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki Y., Aizawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome";
RL Science 309:1559-1563(2005).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141073; DOI=10.1126/science.1112809;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RC (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the mammalian transcriptome";
RL Science 309:1564-1566(2005).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nakada I., Oosato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beiselt K.W.,
Blake J.A., Bird D., Brysac V., Ciothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.D., Petrea G., Pebole G.,
Petkovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
Sultana R., Takenawa Y., Taylor M.S., Tesdale R.D., Tomita M.,
Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
Wilm M.L., Wymshew-Boris A., Yanagisawa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
Shiraki T., Maki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imocani K., Iehli Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
Yasunishi A., Yoshino Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kaubawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
Blake J., Bottelli D., Bojunga N., Carninci P., de Bono B., F.,
Brownstein M.D., Bult C., Fletcher C., Fujita A., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarte P.,
Nordine P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Siorch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilm M.,
Wymshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Kono H., Akiyama Y., Nishi K., Katsunari T., Teshitoh H., Itoh M.,
Sumi N., Iehli Y., Nakamura S., Hazama M., Nishino T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Keshiwa K.,
Fujisaki S., Inoue K., Togawa K., Izawa M., Ohara E., Watanabe K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141073; PubMed=12466851; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishii K., Nomura K., Numazaki R., Ono M., Ono N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AK076506; BAC36369.1; -; mRNA.
DR HSSP: P08592; 1NMJ.
DR SMR: Q8BPC7; 74-183.
DR Ensembl: ENSMUSG00000022892; Mus musculus.
DR MGI: MGI:88059; App.
DR GO: GO:0045177; C:apical part of cell; IDA.
DR GO: GO:0030424; C:axon; IDA.
DR GO: GO:0031410; C:cytoplasmic vesicle; IDA.
DR GO: GO:0016021; C:integral to membrane; IDA.
DR GO: GO:0016020; C:membrane; IDA.
DR GO: GO:0005624; C:membrane fraction; IDA.
DR GO: GO:0031594; C:neuromuscular junction; IDA.
DR GO: GO:0048471; C:perinuclear region; IDA.
DR GO: GO:0051233; C:spindle midzone; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0008344; P:adult locomotory behavior; IMP.
DR GO: GO:0008088; P:axon cargo transport; IMP.
DR GO: GO:0016199; P:axon midline choice point recognition; IMP.
DR GO: GO:0007409; P:axonogenesis; IMP.
DR GO: GO:0004669; P:collateral sprouting in the absence of injury; IGI.
DR GO: GO:0006878; P:copper ion homeostasis; IGI.
DR GO: GO:0006878; P:copper ion homeostasis; IMP.
DR GO: GO:0016358; P:dendrite morphogenesis; IMP.
DR GO: GO:0016358; P:dendrite morphogenesis; IGI.
DR GO: GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
DR GO: GO:0030900; P:forebrain development; IMP.
DR GO: GO:0000085; P:G2 phase of mitotic cell cycle; IMP.
DR GO: GO:0007617; P:mating behavior; IGI.

Query Match 100.0%; Score 125; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAIIGLMVGVVIA 26
DB 302 LVFPADVGSNKGAIIGLMVGVVIA 327

RESULT 14
093296 CHICK PRELIMINARY; PRT; 534 AA.
AC 093296;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";

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RL J. Neurosci. 18:5869-5880 (1998).
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CC -----
DR EMBL: AF042098; AAC25052.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR SMR: Q93296; 224-333.
DR Ensembl: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; F853ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAIIGLMVGVVIA 26
DB 452 LVFPADVGSNKGAIIGLMVGVVIA 477

RESULT 15
09PVL1 CHICK PRELIMINARY; PRT; 569 AA.
AC 09PVL1;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Amyloid protein (Fragment).
DE Name=APP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0 (2000).
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CC -----
DR EMBL: AF030341; AAF12698.1; -; mRNA.
DR HSSP: Q16019; 11YT.
DR SMR: Q9PVL1; 1-64; 260-369.
DR Ensembl: ENSGALG00000015770; Gallus gallus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00204; BETAMYLOID.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.

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DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB85163A19D CRC64;

Query Match
Best Local Similarity 100.0%; Score 125; DB 2; Length 569;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 488 LVFPAEDVGSNKGAIIGLMVGVVIA 513

RESULT 16
Q2XQAO_PIG PRELIMINARY; PRT; 695 AA.
AC Q2XQAO;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Amyloid protein variant 1.
GN NameAPP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_Taxid=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oerum M.A., Larsen K., Bendixen C.;
RT "Porcine amyloid precursor protein, APP: Cloning and characterization
RT of cDNA."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; DQ267684; AB82033.1; -; mRNA.
SQ SEQUENCE 695 AA; 78615 MW; 825A7EAC10E8F0B CRC64;

Query Match
Best Local Similarity 100.0%; Score 125; DB 2; Length 695;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 613 LVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 17
Q56UK3_CANFA PRELIMINARY; PRT; 695 AA.
AC Q56UK3;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_Taxid=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY926582; AAX81911.1; -; mRNA.
DR SMR; Q56UK3; 28-123, 124-189, 385-494.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome C R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00019; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78627 MW; 0BF5DD9BA221B49 CRC64;

Query Match
Best Local Similarity 100.0%; Score 125; DB 2; Length 695;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 613 LVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 18
Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
AC Q5R477;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein DKFZp459D212.
GN Name=DKFZp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE-Cortex;
RG The German cDNA Consortium;
RA Mamult R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Subolt G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; CR861380; CAH93439.1; -; mRNA.
DR SMR; Q5R477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome C R.
DR PANTHER; PTHR10083:SF6; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00019; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78627 MW; 0BF5DD9BA221B49 CRC64;

Query Match
Best Local Similarity 100.0%; Score 125; DB 2; Length 695;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVFPAEDVGSNKGAIIGLWVGAVIA 26
DB 613 LVFPAEDVGSNKGAIIGLWVGAVIA 638

RESULT 19
O6RH29_CANFA PRELIMINARY; PRT; 695 AA.
AC O6RH29;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Beta amyloid protein isoform APP695.
GN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY98707; AAR9727.1; -; mRNA.
DR HSSP; O16019; 1BA4.
DR SMR; O6RH29; 28-123, 124-189, 385-494.
DR Ensembl; ENSCARG0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083; SFE; Beta-APP; 5.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0203; AMYLOID4.
DR PRINTS; PRO0204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9EC10 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVFPAEDVGSNKGAIIGLWVGAVIA 26
DB 613 LVFPAEDVGSNKGAIIGLWVGAVIA 638

RESULT 20
O6GR78_MOUSE PRELIMINARY; PRT; 695 AA.
AC O6GR78;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Amyloid beta (A4) protein (CDNA, RIKEN full-length enriched library,
DE clone:MGC1069M13 product:amyloid beta (A4) protein, full insert
DE sequence).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Heaton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
RN (3)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN (4)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; DOI=10.1126/science.1112014;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Atturaliya R.N., Balley T.L.,
RA Bamsel M., Baxter L., Betsel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matuszewska S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Payan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sincclair B.,
RA Sperling S., Stupka E., Sugiyara K., Sultana R., Takenaka Y., Taki K.,
RA Tamojia K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hilde W., Bult C.,
RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,

RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirm L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Choitha C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond D., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziarski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltse L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa T., Okido T., Pavani M., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Koshikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=11217851; DOI=10.1038/35055500;
 RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirm L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaez P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [8]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiyosawa H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [10]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kasugawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakezume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Wataniki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: BC070409; AAH70409.1; -; mRNA.
 DR EMBL: AK147543; BAE27986.1; -; mRNA.
 DR SRR: 06GR78; 28-123, 124-189, 385-494.
 DR Ensembl: ENSMUSG0000022892; Mus musculus.
 DR MGI: 88059; App.
 Query Match 100.0%; Score 125; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFPAEDVGSNGAIIIGLMVGGVIA 26
 DB 613 LVFPAEDVGSNGAIIIGLMVGGVIA 638
 RESULT 21
 O99CJ8 CHICK PRELIMINARY; PRT; 695 AA.
 AC O99CJ8;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Beta-amyloid protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16039787; DOI=10.1016/j.neuroscience.2005.05.020;
 RA Cardenas J.A., Rodolose A., Garza M.V., Sans-Clemente A.,
 RA Perez-Pe R., Lacosta A.M., Dominguez L., Montleon I., Sanchez-Diaz R.,
 RA Sorribes V., Sarasa M.;
 RT "The chick embryo appears as a natural model for research in beta-
 RT amyloid precursor protein processing";
 RL Neuroscience 134:1285-1300(2005).
 [8]

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DR EMBL: AF289218; AAG00593.1; -; mRNA.
DR HSP: Q16019; 1177.
DR SMR: Q9DGR8; 28-123, 124-189, 385-494.
DR Ensembl: ENSGALG0000015770; Gallus gallus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMAMLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR SEQUENCE 695 AA; 78566 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
Db 613 LVFPAEDVGSNKGAIIGLMVGVVIA 638

RESULT 22
OS6UK4 CANFA PRELIMINARY; PRT; 714 AA.
AC Q56UK4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxId=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.,
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AY926581; AAX81910.1; -; mRNA.
DR SMR: Q56UK4; 28-123, 124-189, 404-513.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR012282; Cytochrome C_R.
DR PANTHER: PTHR10083:SF6; Beta-APP; 5.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00204; BETAMAMLOID.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR SEQUENCE 714 AA; 80827 MW; 50DDE51F9B9E0EC5 CRC64;

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Query Match 100.0%; Score 125; DB 2; Length 714;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
Db 632 LVFPAEDVGSNKGAIIGLMVGVVIA 657

RESULT 23
OS6605 RAT PRELIMINARY; PRT; 733 AA.
AC Q6P6Q5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE App protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Bouffard G.G.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Mizny K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC062082; AAH62082.1; -; mRNA.
DR SMR: Q6P6Q5; 28-123, 124-189, 287-342, 441-550.
DR Ensembl: ENSRNORG0000006997; Rattus norvegicus.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Prot inh. Kunz-m.
DR PANTHER: PTHR10083:SF6; Beta-APP; 4.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz-BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICTYASE.

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AC Q6GSC0; integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 10-MAY-2005, entry version 1.
 DT 07-FEB-2006, entry version 7.
 DE Amyloid beta A4 protein,, isoform b.
 GN Name=APP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RC TISSUE=Eye;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 CC -----
 CC EMBL: BC065529, AAH65529.1, -, mRNA.
 DR SMR: Q6GSC0; 28-123, 124-189, 287-342, 441-550.
 DR Ensembl: ENSG00000142192; Homo sapiens.
 DR GO: GO:0016021, C:integral to membrane; IEA.
 DR GO: GO:0005488, F:binding; IEA.
 DR GO: GO:0020037, F:heme binding; IEA.
 DR GO: GO:0004867, F:serine-type endopeptidase inhibitor activity; IEA.
 DR GO: GO:0006118, P:electron transport; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR012282; Cytochrome c_R.
 DR InterPro: IPR012223; Prot inh Kunitz-m.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz BPTI; 1.
 DR PRINTS: PRO0203; AMYLOIDA4.
 DR PRINTS: PRO0759; BASICPTASE.
 DR PRINTS: PRO0204; BETAMYLOID.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW PROTEASE.
 SQ SEQUENCE 751 AA; 84819 MW; C987C557CA3714E CRC64;

Query Match 100.0%; Score 125; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVFFADVGNKGAITGLWGVVIA 26
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 DB 669 LVFFADVGNKGAITGLWGVVIA 694
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 AC Q4R48;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Brain cDNA, clone: Q1A-13524, similar to human amyloid beta (A4)
 DE protein (protease nexin-II, Alzheimer disease) (APP), transcript
 DE variant 2'.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 RX PubMed=15944441; DOI=10.1093/molbev/m187;
 RA Oseada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gotohori T., Shen C.-K.J., Wu C.I., Hashimoto K.,
 RT "Substitution Rate and Structural Divergence of 5' UTR Evolution:
 RT Comparative Analysis between Human and Cynomolgus Monkey cDNAs";
 RL Mol. Biol. Evol. 22:1976-1982(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG International consortium for macaque cDNA sequencing and analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 CC -----
 CC EMBL: AB169826; BAB01907.1, -, mRNA.
 DR SMR: Q4R48; 28-123, 124-189, 287-342, 441-550.
 DR GO: GO:0016021, C:integral to membrane; IEA.
 DR GO: GO:0005488, F:binding; IEA.
 DR GO: GO:0020037, F:heme binding; IEA.
 DR GO: GO:0004867, F:peptidase activity; IEA.
 DR GO: GO:0006118, P:electron transport; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR012282; Cytochrome c_R.
 DR InterPro: IPR012223; Prot inh Kunitz-m.
 DR PANTHER: PTHR10083; SF6; Beta-APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz BPTI; 1.
 DR PRINTS: PRO0203; AMYLOIDA4.
 DR PRINTS: PRO0759; BASICPTASE.
 DR PRODOM: PD000222; Prot inh Kunitz-m; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW PROTEASE.
 SQ SEQUENCE 751 AA; 84817 MW; 83C1C096AD355158 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAITGLMWGVVIA 26
 DB 669 LVFFAEDVGSNKGAITGLMWGVVIA 694

RESULT 28
 Q56JK5 CANFA PRELIMINARY; PRT; 751 AA.
 AC Q56JK5;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Beta-amyloid protein 751.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.*
 NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
 RT "Relationship between canine dementia and Alzheimer's disease."
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: AY926580; AAX81909.1; -; mRNA.
 DR SMR: Q56JK5; 28-123, 124-189, 287-342, 441-550.
 DR GO; GO:0016021, C:integral to membrane, IEA.
 DR GO; GO:0005488, F:binding, IEA.
 DR GO; GO:0020037, F:heme binding, IEA.
 DR GO; GO:0004867, F:serine-type endopeptidase inhibitor activity, IEA.
 DR GO; GO:0006118, P:electron transport, IEA.
 DR InterPro: IPR008155, A4_APP.
 DR InterPro: IPR008154, A4_extra.
 DR InterPro: IPR001255, Beta_APP.
 DR InterPro: IPR012282, Cytochrome_C_R.
 DR InterPro: IPR002223, Prot_inh_Kunz-m.
 DR PANTHER: PTHR10083:SF6; Beta_APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00204; BETAMYLOID.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
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Query Match 100.0%; Score 125; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAITGLMWGVVIA 26
 DB 669 LVFFAEDVGSNKGAITGLMWGVVIA 694

RESULT 29
 Q6RH28 CANFA PRELIMINARY; PRT; 751 AA.
 AC Q6RH28;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 13.

DE Beta amyloid protein isoform APP751.
 GN Name=Beta APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nakata M.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 CC -----
 CC EMBL: AY96708; AAR97728.1; -; mRNA.
 DR HSSP: Q16019; IAP.
 DR SMR: Q6RH28; 28-123, 124-189, 287-342, 441-550.
 DR Ensembl: ENSCAFG0000008557; Canis familiaris.
 DR GO; GO:0016021, C:integral to membrane, IEA.
 DR GO; GO:0005488, F:binding, IEA.
 DR GO; GO:0004867, F:serine-type endopeptidase inhibitor activity, IEA.
 DR InterPro: IPR008155, A4_APP.
 DR InterPro: IPR008154, A4_extra.
 DR InterPro: IPR001255, Beta_APP.
 DR InterPro: IPR002223, Prot_inh_Kunz-m.
 DR PANTHER: PTHR10083:SF6; Beta_APP; 5.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00204; BETAMYLOID.
 DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 SO SEQUENCE 751 AA; 84833 MW; 7541A947B46DA5A4 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAITGLMWGVVIA 26
 DB 669 LVFFAEDVGSNKGAITGLMWGVVIA 694

RESULT 30
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 AC Q2XO99;
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 07-MAR-2006, sequence version 1.
 DT 07-MAR-2006, entry version 4.
 DE Amyloid protein variant 2.
 GN Name=APP;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
 OC Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Oerum M.A., Larsen K., Bendixen C.;
 RT "Porcine amyloid precursor protein, APP: Cloning and characterization of cDNA".
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 DR EMBL; DQ267685; ABB82034.1; -; mRNA.
 SQ SEQUENCE 751 AA; 84799 MW; 37868743880C369F CRC64;

Query Match 100.0%; Score 125; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
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Qy 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26
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 Db 669 LVFFAEDVGSNKGAIIGLMVGVVIA 694

Search completed: September 28, 2006, 06:22:56
 Job time : 85.6457 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:23:21 ; Search time 18.1049 Seconds
(without alignments)
124.327 Million cell updates/sec

Title: US-09-731-899-7
Perfect score: 125
Sequence: 1 LVFAEDVGSNKGAITGLMVGAVIA 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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2: /EMC_Celerra_SIDS3/Ptodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/Ptodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/Ptodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/Ptodata/2/1aa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/Ptodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/Ptodata/2/1aa/backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	42	1	US-07-744-767A-2
2	125	100.0	42	1	US-08-179-574-1
3	125	100.0	42	1	US-08-371-162-5
4	125	100.0	42	1	US-08-347-144-1
5	125	100.0	42	1	US-08-462-859A-19
6	125	100.0	42	1	US-08-123-659A-19
7	125	100.0	42	1	US-08-464-247A-19
8	125	100.0	42	1	US-08-464-248A-19
9	125	100.0	42	1	US-08-476-464A-1
10	125	100.0	42	1	US-08-304-585-2
11	125	100.0	42	1	US-08-302-808-5
12	125	100.0	42	1	US-08-268-348A-1
13	125	100.0	42	1	US-08-268-348A-2
14	125	100.0	42	1	US-08-433-734-2
15	125	100.0	42	1	US-08-609-090-9
16	125	100.0	42	1	US-07-737-371E-72
17	125	100.0	42	1	US-08-422-333-4
18	125	100.0	42	1	US-08-682-245A-4
19	125	100.0	42	1	US-08-986-948-5
20	125	100.0	42	2	US-08-717-551A-2
21	125	100.0	42	2	US-09-388-890-1
22	125	100.0	42	2	US-09-005-215-20
23	125	100.0	42	2	US-09-242-724-23
24	125	100.0	42	2	US-08-922-930-2
25	125	100.0	42	2	US-09-660-954-1
26	125	100.0	42	2	US-08-923-055-2

27	125	100.0	42	2	US-08-922-889-2	Sequence 2, Appl1
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29	125	100.0	42	2	US-09-133-866-2	Sequence 2, Appl1
30	125	100.0	42	2	US-09-723-384-1	Sequence 1, Appl1
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39	125	100.0	42	2	US-09-724-551-42	Sequence 42, Appl1
40	125	100.0	42	2	US-10-815-353-1	Sequence 1, Appl1
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43	125	100.0	42	2	US-09-623-548A-955	Sequence 955, App
44	125	100.0	42	2	US-09-623-548A-961	Sequence 961, App
45	125	100.0	42	2	US-09-623-548A-967	Sequence 967, App
46	125	100.0	42	2	US-09-623-548A-987	Sequence 987, App
47	125	100.0	42	2	US-09-623-548A-988	Sequence 988, App
48	125	100.0	42	2	US-09-623-548A-994	Sequence 994, App
49	125	100.0	42	2	US-10-815-391-1	Sequence 1, Appl1
50	125	100.0	42	2	US-10-816-022-1	Sequence 1, Appl1
51	125	100.0	42	2	US-09-724-953-34	Sequence 34, Appl1
52	125	100.0	42	2	US-09-657-276-955	Sequence 955, App
53	125	100.0	42	2	US-09-657-276-961	Sequence 961, App
54	125	100.0	42	2	US-09-657-276-967	Sequence 967, App
55	125	100.0	42	2	US-09-657-276-988	Sequence 988, App
56	125	100.0	42	2	US-09-657-276-994	Sequence 994, App
57	125	100.0	42	2	US-09-724-940-42	Sequence 42, Appl1
58	125	100.0	42	2	US-09-865-294A-65	Sequence 65, Appl1
59	125	100.0	42	2	US-09-979-952-34	Sequence 34, Appl1
60	125	100.0	42	2	US-09-585-817-34	Sequence 34, Appl1
61	125	100.0	42	2	US-09-962-955D-20	Sequence 20, Appl1
62	125	100.0	42	2	US-09-706-574A-20	Sequence 1, Appl1
63	125	100.0	42	2	US-10-934-609-1	Sequence 1, Appl1
64	125	100.0	42	2	US-10-884-892-1	Sequence 1, Appl1
65	125	100.0	42	2	US-09-848-616-174	Sequence 174, App
66	125	100.0	42	2	US-10-933-553-1	Sequence 1, Appl1
67	125	100.0	42	2	US-10-815-404-1	Sequence 1, Appl1
68	125	100.0	42	3	US-10-816-380-1	Sequence 1, Appl1
69	125	100.0	42	3	US-10-363-082-1	Sequence 1, Appl1
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71	125	100.0	42	5	PCT-US93-00325-1	Sequence 1, Appl1
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76	125	100.0	43	1	US-08-437-067-1	Sequence 1, Appl1
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81	125	100.0	43	1	US-08-602-264A-3	Sequence 3, Appl1
82	125	100.0	43	1	US-08-469-362-1	Sequence 1, Appl1
83	125	100.0	43	1	US-08-612-785B-1	Sequence 1, Appl1
84	125	100.0	43	1	US-08-475-579A-1	Sequence 1, Appl1
85	125	100.0	43	1	US-08-850-392-1	Sequence 1, Appl1
86	125	100.0	43	1	US-07-737-371E-70	Sequence 70, Appl1
87	125	100.0	43	1	US-08-986-948-6	Sequence 6, Appl1
88	125	100.0	43	1	US-08-975-977-1	Sequence 1, Appl1
89	125	100.0	43	1	US-08-817-423-1	Sequence 1, Appl1
90	125	100.0	43	1	US-08-920-162A-1	Sequence 1, Appl1
91	125	100.0	43	1	US-08-461-018A-3	Sequence 3, Appl1
92	125	100.0	43	2	US-08-976-191-1	Sequence 1, Appl1
93	125	100.0	43	2	US-08-976-179-1	Sequence 1, Appl1
94	125	100.0	43	2	US-09-216-958-3	Sequence 3, Appl1
95	125	100.0	43	2	US-09-356-931-1	Sequence 1, Appl1
96	125	100.0	43	2	US-08-733-202-1	Sequence 1, Appl1
97	125	100.0	43	2	US-08-703-675C-1	Sequence 1, Appl1
98	125	100.0	43	2		
99	125	100.0	43	2		

100 125 100.0 43 2 US-09-390-692-1

Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-744-767A-2

Sequence 2, Application US/07744767A

Patent No. 5434050

GENERAL INFORMATION:

APPLICANT: Magglio, John E.

APPLICANT: Mantyla, Patrick W.

TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods

TITLE OF INVENTION: for use in Detecting Alzheimer's Disease

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwesman, Lundberg & Woessner, P.A.

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07744,767A

FILING DATE: 13-AUG-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Maeting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 600.226-US-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-0311

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-744-767A-2

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITIGLMVGVVIA 26

Db 17 LVFFADVGSNKGAITIGLMVGVVIA 42

RESULT 2

US-08-179-574-1

Sequence 1, Application US/08179574

Patent No. 5506097

GENERAL INFORMATION:

APPLICANT: Huntington Potter

APPLICANT: Usamah Kayyal

TITLE OF INVENTION: Compounds and Methods for Inhibiting

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08179,574

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/819,361

FILING DATE: 13-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: HU90-03A3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-179-574-1

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITIGLMVGVVIA 26

Db 17 LVFFADVGSNKGAITIGLMVGVVIA 42

RESULT 3

US-08-271-162-5

Sequence 5, Application US/08271162

Patent No. 5523295

GENERAL INFORMATION:

APPLICANT: Fasman, Gerald D.

TITLE OF INVENTION: METHOD FOR TREATING AND PREVENTING

TITLE OF INVENTION: ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/271,162

FILING DATE: July, 1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Greer, Helen A.

REGISTRATION NUMBER: 36,816

REFERENCE/DOCKET NUMBER: F0437/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-271-162-5

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 4

US-08-347-144-1
Sequence 1, Application US/08347144
Patent No. 5589154
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOMREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,144
FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 5

US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-19

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 6

US-08-123-659A-19
Sequence 19, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518) 475-0611

TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-19

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 7
US-08-464-247A-19
Sequence 19, Application US/08464247A
PATENT No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-19

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 8
US-08-464-248A-19
Sequence 19, Application US/08464248A

PATENT No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-19

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 9
US-08-476-464A-1
Sequence 1, Application US/08476464A
PATENT No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A

QY 1 LVFPADVSNKGAITGLMWGVVIA 26
Db 17 LVFPADVSNKGAITGLMWGVVIA 42

RESULT 10
US-08-304-585-2
Sequence 2, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggic, John E.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 561415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-2

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVSNKGAITGLMWGVVIA 26
Db 17 LVFPADVSNKGAITGLMWGVVIA 42

RESULT 11
US-08-302-808-5
Sequence 5, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
Prior Application Data:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-5

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVSNKGAITGLMWGVVIA 26
Db 17 LVFPADVSNKGAITGLMWGVVIA 42

```
RESULT 12
US-08-268-348A-1
; Sequence 1, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobell, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotterman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-268-348A-1

Query Match          100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVFPAADVGSNKGAIIIGLMVGGVIA 26
DB      17 LVFPAADVGSNKGAIIIGLMVGGVIA 42

RESULT 13
US-08-268-348A-2
; Sequence 2, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobell, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotterman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

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ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-268-348A-2

Query Match          100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVFPAADVGSNKGAIIIGLMVGGVIA 26
DB      17 LVFPAADVGSNKGAIIIGLMVGGVIA 42

RESULT 14
US-08-433-734-2
; Sequence 2, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Magglio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muehling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110,00010102
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-2

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 15

US-08-609-090-9
Sequence 9, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: ASENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-9

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 16
US-07-737-371E-72
Sequence 72, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 07/559,172
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-72

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 17
US-08-422-333-4
Sequence 4, Application US/08422333
Patent No. 5912410
GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITGLMVGGVIA 42

RESULT 18
US-08-682-245A-4
Sequence 4, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214330
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-4

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITGLMVGGVIA 42

RESULT 19
US-08-986-948-5
Sequence 5, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317unhiro
APPLICANT: ODAKA, Aaano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
TOPOLOGY: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-5

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITGLMWGVVIA 26
|||||
Db 17 LVFPAEDVGSNKGAITGLMWGVVIA 42

RESULT 20

US-08-717-551A-2
; Sequence 2, Application US/08717551A
; Patent No. 6071493
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESS: 6 No. 60714931st LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,551A
; FILING DATE: Sept-20-96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-717-551A-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITGLMWGVVIA 26
|||||
Db 17 LVFPAEDVGSNKGAITGLMWGVVIA 42

RESULT 21

US-09-388-890-1
; Sequence 1, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

ORGANISM: AMYLOID PEPTIDE
US-09-388-890-1

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITGLMWGVVIA 26
|||||
Db 17 LVFPAEDVGSNKGAITGLMWGVVIA 42

RESULT 22

US-09-005-215-20
; Sequence 20, Application US/09005215
; Patent No. 6172043
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
; TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,215
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/035,847

FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0656/7035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-005-215-20

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 17 LVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 23
US-09-242-724-23
Sequence 23, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 23
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-242-724-23

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 17 LVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 24
US-08-922-930-2
Sequence 2, Application US/08922930
Patent No. 6451544
GENERAL INFORMATION:
APPLICANT: Dana Glauian
TITLE OF INVENTION: Identification of Agents that Protect
AGAINST INFLAMMATORY INJURY TO NEURONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz MacLewicz
ADDRESSEE: & No. 6451544 is LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,930
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYDR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-930-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 17 LVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 25
US-09-660-954-1
Sequence 1, Application US/09660954
Patent No. 6471960
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/660,954
FILING DATE: 13-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/686,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: AUBERACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451

TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-660-954-1

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAIIIGLWVGAVIA 26
DB 17 LVFFAEDVGSNKGAIIIGLWVGAVIA 42

RESULT 26
US-08-923-055-2
Sequence 2, Application US/08923055
Patent No. 6475742
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 6475742irs LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,055
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-923-055-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVFFAEDVGSNKGAIIIGLWVGAVIA 26
DB 17 LVFFAEDVGSNKGAIIIGLWVGAVIA 42

DB 17 LVFFAEDVGSNKGAIIIGLWVGAVIA 42

RESULT 27
US-08-922-889-2
Sequence 2, Application US/08922889
Patent No. 6475745
GENERAL INFORMATION:
APPLICANT: Dana Giullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 6475745irs LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,889
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-889-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 9, 4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFAEDVGSNKGAIIIGLWVGAVIA 26
DB 17 LVFFAEDVGSNKGAIIIGLWVGAVIA 42

RESULT 28
US-09-731-460-1
Sequence 1, Application US/09731460
Patent No. 6495335
GENERAL INFORMATION:
APPLICANT: Choikier, Mario
TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
TITLE OF INVENTION: Disease
FILE REFERENCE: CHOIKIER-04302
CURRENT APPLICATION NUMBER: US/09/731,460
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 42
TYPE: PRT

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 06:58:47 ; Search time 59.5785 Seconds
(without alignments)
202.147 Million cell updates/sec

Title: US-09-731-899-7

Perfect score: 125
Sequence: 1 LVFPAEDVGSNKGAIIGLMVGVIA 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	32	5	US-10-625-854-154
2	125	100.0	33	5	US-10-625-854-153
3	125	100.0	34	5	US-10-625-854-152
4	125	100.0	35	5	US-10-625-854-151
5	125	100.0	36	5	US-10-625-854-150
6	125	100.0	37	5	US-10-625-854-149
7	125	100.0	38	5	US-10-625-854-148
8	125	100.0	39	5	US-10-625-854-147
9	125	100.0	40	5	US-10-625-854-146
10	125	100.0	41	5	US-10-625-854-145
11	125	100.0	41	5	US-10-625-854-144
12	125	100.0	42	2	US-08-922-930-2
13	125	100.0	42	2	US-08-923-055-2
14	125	100.0	42	3	US-09-867-847-1
15	125	100.0	42	3	US-09-956-625-26
16	125	100.0	42	3	US-09-731-460-1
17	125	100.0	42	3	US-09-962-955C-37
18	125	100.0	42	3	US-09-848-616-174
19	125	100.0	42	3	US-09-865-294-65
20	125	100.0	42	3	US-09-792-079-13
21	125	100.0	42	3	US-09-825-242-1
22	125	100.0	42	3	US-09-930-915A-293
23	125	100.0	42	4	US-10-051-496-2
24	125	100.0	42	4	US-10-082-804-7
25	125	100.0	42	4	US-10-217-584-2
26	125	100.0	42	4	US-10-169-580-2
27	125	100.0	42	4	US-10-278-181-1

28	125	100.0	42	4	US-10-143-534-2	Sequence 2, App1
29	125	100.0	42	4	US-10-190-548A-1	Sequence 1, App1
30	125	100.0	42	4	US-10-051-663-2	Sequence 2, App1
31	125	100.0	42	4	US-10-159-279-13	Sequence 13, App1
32	125	100.0	42	4	US-10-050-902-220	Sequence 220, App
33	125	100.0	42	4	US-10-050-898-220	Sequence 220, App
34	125	100.0	42	4	US-10-082-014-81	Sequence 81, App1
35	125	100.0	42	4	US-10-372-076-82	Sequence 82, App1
36	125	100.0	42	4	US-10-455-218-2	Sequence 2, App1
37	125	100.0	42	4	US-10-231-298B-15	Sequence 15, App1
38	125	100.0	42	4	US-10-231-470C-15	Sequence 15, App1
39	125	100.0	42	4	US-10-231-063C-15	Sequence 15, App1
40	125	100.0	42	4	US-10-366-125-28	Sequence 28, App1
41	125	100.0	42	4	US-10-411-544-2	Sequence 2, App1
42	125	100.0	42	4	US-10-231-213D-15	Sequence 15, App1
43	125	100.0	42	4	US-10-231-114C-15	Sequence 15, App1
44	125	100.0	42	4	US-10-337-261-2	Sequence 2, App1
45	125	100.0	42	4	US-10-363-082-1	Sequence 1, App1
46	125	100.0	42	4	US-10-433-385-6	Sequence 6, App1
47	125	100.0	42	4	US-10-423-047-1	Sequence 1, App1
48	125	100.0	42	4	US-10-617-876-7	Sequence 7, App1
49	125	100.0	42	4	US-10-429-216-1	Sequence 1, App1
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51	125	100.0	42	4	US-10-656-624-6	Sequence 6, App1
52	125	100.0	42	4	US-10-622-087-91	Sequence 91, App1
53	125	100.0	42	4	US-10-683-815-11	Sequence 11, App1
54	125	100.0	42	4	US-10-732-862A-95	Sequence 95, App1
55	125	100.0	42	4	US-10-806-006-293	Sequence 293, App
56	125	100.0	42	4	US-10-416-262B-6	Sequence 6, App1
57	125	100.0	42	4	US-10-677-074-82	Sequence 82, App1
58	125	100.0	42	4	US-10-805-913-293	Sequence 293, App
59	125	100.0	42	4	US-10-816-022-1	Sequence 1, App1
60	125	100.0	42	4	US-10-816-529-1	Sequence 1, App1
61	125	100.0	42	4	US-10-815-353-1	Sequence 1, App1
62	125	100.0	42	4	US-10-815-391-1	Sequence 1, App1
63	125	100.0	42	4	US-10-772-656-55	Sequence 55, App1
64	125	100.0	42	4	US-10-478-308-3	Sequence 3, App1
65	125	100.0	42	4	US-10-478-307-3	Sequence 3, App1
66	125	100.0	42	4	US-10-402-420-1	Sequence 1, App1
67	125	100.0	42	4	US-10-771-174A-1	Sequence 1, App1
68	125	100.0	42	5	US-10-828-548-1	Sequence 1, App1
69	125	100.0	42	5	US-10-864-107-2	Sequence 2, App1
70	125	100.0	42	5	US-10-816-380-1	Sequence 1, App1
71	125	100.0	42	5	US-10-485-310-19	Sequence 19, App1
72	125	100.0	42	5	US-10-889-999-42	Sequence 42, App1
73	125	100.0	42	5	US-10-890-070-42	Sequence 42, App1
74	125	100.0	42	5	US-10-861-614-65	Sequence 65, App1
75	125	100.0	42	5	US-10-481-387-2	Sequence 2, App1
76	125	100.0	42	5	US-10-890-000-42	Sequence 42, App1
77	125	100.0	42	5	US-10-788-666-1	Sequence 1, App1
78	125	100.0	42	5	US-10-923-471-1	Sequence 1, App1
79	125	100.0	42	5	US-10-823-463-42	Sequence 42, App1
80	125	100.0	42	5	US-10-923-469-1	Sequence 1, App1
81	125	100.0	42	5	US-10-933-559-1	Sequence 1, App1
82	125	100.0	42	5	US-10-815-404-1	Sequence 1, App1
83	125	100.0	42	5	US-10-934-609-1	Sequence 1, App1
84	125	100.0	42	5	US-10-950-018-1	Sequence 1, App1
85	125	100.0	42	5	US-10-883-150-3	Sequence 3, App1
86	125	100.0	42	5	US-10-923-474-1	Sequence 1, App1
87	125	100.0	42	5	US-10-884-892-1	Sequence 1, App1
88	125	100.0	42	5	US-10-822-968-42	Sequence 42, App1
89	125	100.0	42	5	US-10-933-206-37	Sequence 37, App1
90	125	100.0	42	5	US-10-777-792-42	Sequence 42, App1
91	125	100.0	42	5	US-10-825-958-1	Sequence 1, App1
92	125	100.0	42	5	US-10-775-562-1	Sequence 1, App1
93	125	100.0	42	5	US-10-852-950-1	Sequence 1, App1
94	125	100.0	42	5	US-10-890-071-42	Sequence 42, App1
95	125	100.0	42	5	US-10-903-279-1	Sequence 1, App1
96	125	100.0	42	5	US-10-810-881A-50	Sequence 50, App1
97	125	100.0	42	5	US-10-890-024-42	Sequence 42, App1
98	125	100.0	42	5	US-10-934-819-1	Sequence 1, App1
99	125	100.0	42	5	US-10-508-586-1	Sequence 1, App1
100	125	100.0	42	5	US-10-505-313-27	Sequence 27, App1


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/ FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
/ CURRENT APPLICATION NUMBER: US/10/625,854
/ CURRENT FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/401,497
/ PRIOR FILING DATE: 2002-08-06
/ NUMBER OF SEQ ID NOS: 261
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 150
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-625-854-150

Query Match          100.0%; Score 125; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.7e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGVVIA 26
Db 11 LVFPAEDVGSNKGAITIGLMVGVVIA 36

RESULT 6
US-10-625-854-149
/ Sequence 149, Application US/10625854
/ Publication No. US20050175626A1
/ GENERAL INFORMATION:
/ APPLICANT: Delacourte, Andr
/ APPLICANT: Sergeant, Nicolas
/ TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
/ FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
/ CURRENT APPLICATION NUMBER: US/10/625,854
/ CURRENT FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/401,497
/ PRIOR FILING DATE: 2002-08-06
/ NUMBER OF SEQ ID NOS: 261
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 149
/ LENGTH: 37
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-625-854-149

Query Match          100.0%; Score 125; DB 5; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGVVIA 26
Db 12 LVFPAEDVGSNKGAITIGLMVGVVIA 37

RESULT 7
US-10-625-854-148
/ Sequence 148, Application US/10625854
/ Publication No. US20050175626A1
/ GENERAL INFORMATION:
/ APPLICANT: Delacourte, Andr
/ APPLICANT: Sergeant, Nicolas
/ TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
/ FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
/ CURRENT APPLICATION NUMBER: US/10/625,854
/ CURRENT FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/401,497
/ PRIOR FILING DATE: 2002-08-06
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/ NUMBER OF SEQ ID NOS: 261
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 148
/ LENGTH: 38
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-625-854-148

Query Match          100.0%; Score 125; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGVVIA 26
Db 13 LVFPAEDVGSNKGAITIGLMVGVVIA 38

RESULT 8
US-10-625-854-146
/ Sequence 146, Application US/10625854
/ Publication No. US20050175626A1
/ GENERAL INFORMATION:
/ APPLICANT: Delacourte, Andr
/ APPLICANT: Sergeant, Nicolas
/ TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
/ FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
/ CURRENT APPLICATION NUMBER: US/10/625,854
/ CURRENT FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/401,497
/ PRIOR FILING DATE: 2002-08-06
/ NUMBER OF SEQ ID NOS: 261
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 146
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-625-854-146

Query Match          100.0%; Score 125; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGVVIA 26
Db 14 LVFPAEDVGSNKGAITIGLMVGVVIA 39

RESULT 9
US-10-625-854-147
/ Sequence 147, Application US/10625854
/ Publication No. US20050175626A1
/ GENERAL INFORMATION:
/ APPLICANT: Delacourte, Andr
/ APPLICANT: Sergeant, Nicolas
/ TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
/ FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
/ CURRENT APPLICATION NUMBER: US/10/625,854
/ CURRENT FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/401,497
/ PRIOR FILING DATE: 2002-08-06
/ NUMBER OF SEQ ID NOS: 261
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 147
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ FEATURE:
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NAME/KEY: MISC FEATURE
LOCATION: (1)-(1)
OTHER INFORMATION: Xaa represents pyroglutamate
US-10-625-854-147

Query Match 100.0%; Score 125; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 6,3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAADVGSNKGAIIIGLWVGAVIA 26
DB 14 LVFPAADVGSNKGAIIIGLWVGAVIA 39

RESULT 10
US-10-625-854-145
Sequence 145, Application US/10625854
Publication No. US20050175626A1
GENERAL INFORMATION:
APPLICANT: Delacourte, Andr
APPLICANT: Sergeant, Nicolas
TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
CURRENT APPLICATION NUMBER: US/10/625,854
PRIOR FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/401,497
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 261
SOFTWARE: Patentin version 3.2
SEQ ID NO 145
LENGTH: 40
TYPE: PRT
ORGANISM: homo sapiens
US-10-625-854-145

Query Match 100.0%; Score 125; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 6,4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAADVGSNKGAIIIGLWVGAVIA 26
DB 15 LVFPAADVGSNKGAIIIGLWVGAVIA 40

RESULT 11
US-10-625-854-144
Sequence 144, Application US/10625854
Publication No. US20050175626A1
GENERAL INFORMATION:
APPLICANT: Delacourte, Andr
APPLICANT: Sergeant, Nicolas
TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
CURRENT APPLICATION NUMBER: US/10/625,854
PRIOR FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/401,497
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 261
SOFTWARE: Patentin version 3.2
SEQ ID NO 144
LENGTH: 41
TYPE: PRT
ORGANISM: homo sapiens
US-10-625-854-144

Query Match 100.0%; Score 125; DB 5; Length 41;
Best Local Similarity 100.0%; Pred. No. 6,6e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVFPAADVGSNKGAIIIGLWVGAVIA 26
DB 16 LVFPAADVGSNKGAIIIGLWVGAVIA 41

RESULT 12
US-08-922-930-2
Sequence 2, Application US/08922930
Publication No. US20010016327A1
GENERAL INFORMATION:
APPLICANT: Dana Giuliani
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 645154418 LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,930
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-922-930-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAADVGSNKGAIIIGLWVGAVIA 26
DB 17 LVFPAADVGSNKGAIIIGLWVGAVIA 42

RESULT 13
US-08-923-055-2
Sequence 2, Application US/08923055
Publication No. US20010016327A1
GENERAL INFORMATION:
APPLICANT: Dana Giuliani
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. US20010016327A118 LLP
STREET: One Liberty Place - 46th Floor

CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,055
FILING DATE: Sept-03-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0038
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-923-055-2

Query Match 100.0%; Score 125; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFFAEDVGSNKGAIIIGLMVGVVIA 26
Db 17 LVFFAEDVGSNKGAIIIGLMVGVVIA 42

RESULT 14
US-09-867-847-1
Sequence 1, Application US/09867847
Patent No. US20020094335A1
GENERAL INFORMATION:
APPLICANT: Chaillout, Robert
APPLICANT: Hebert, Lise
APPLICANT: Kong, Xiangi
APPLICANT: Gervais, Francine
TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
FILE REFERENCE: 14445-501 CIP
CURRENT APPLICATION NUMBER: US/09/867,847
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/168,594
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-1

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFFAEDVGSNKGAIIIGLMVGVVIA 26
Db 17 LVFFAEDVGSNKGAIIIGLMVGVVIA 42

RESULT 15
US-09-956-625-26
Sequence 26, Application US/09956625
Patent No. US20020119926A1
GENERAL INFORMATION:
APPLICANT: Fraser, Paul
TITLE OF INVENTION: Inhibitors of TADP Fibril Formation and Uses Thereof
FILE REFERENCE: 14445-503
CURRENT APPLICATION NUMBER: US/09/956,625
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,482
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-956-625-26

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFFAEDVGSNKGAIIIGLMVGVVIA 26
Db 17 LVFFAEDVGSNKGAIIIGLMVGVVIA 42

RESULT 16
US-09-731-460-1
Sequence 1, Application US/09731460
Patent No. US20020137112A1
GENERAL INFORMATION:
APPLICANT: Chojkier, Mario
APPLICANT: Buck, Martina
TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
FILE REFERENCE: CHOJKIER-04302
CURRENT APPLICATION NUMBER: US/09/731,460
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-731-460-1

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFFAEDVGSNKGAIIIGLMVGVVIA 26
Db 17 LVFFAEDVGSNKGAIIIGLMVGVVIA 42

RESULT 17
US-09-962-955C-37
Sequence 37, Application US/09962955C
Publication No. US20030013648A1
GENERAL INFORMATION:
APPLICANT: Gerardo M. Castillo
APPLICANT: Alan D. Snow
NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: Proteotech, Inc, 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Wordperfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,955C
; FILING DATE: 24-September-2001
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/938,275
; FILING DATE: 22-August-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; REFERENCE/DOCKET NUMBER: PROTEO.P03CI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: Also referred to in the specification as "AB 1-42"
; US-09-962-955C-37

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
DB 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 18
US-09-848-616-174
; Sequence 174, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tiseet, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
; US-09-848-616-174

Query Match 100.0%; Score 125; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
DB 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 19
US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-865-294-65

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
DB 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 20
US-09-792-079-13
; Sequence 13, Application US/09792079
; Publication No. US20030083277A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Herish, Louis B.
; APPLICANT: Mukherjee, Atish
; TITLE OF INVENTION: Use of Insulin Degrading Enzyme (IDE) For The Treatment Of Alzheimer
; FILE REFERENCE: 050229-0261
; CURRENT APPLICATION NUMBER: US/09/792,079
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,826
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-792-079-13

Query Match 100.0%; Score 125; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
DB 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 21
US-09-825-242-1
; Sequence 1, Application US/09825242
; Publication No. US20030092000A1
; GENERAL INFORMATION:

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1  APPLICANT: Schenck, Dale B.
2  APPLICANT: Neurulab Limited
3  TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
4  FILE REFERENCE: 15270J-004720US
5  CURRENT APPLICATION NUMBER: US/09/825,242
6  CURRENT FILING DATE: 2001-04-02
7  PRIOR APPLICATION NUMBER: 09/201,430
8  PRIOR FILING DATE: 1998-11-30
9  PRIOR APPLICATION NUMBER: US 60/080,970
10 PRIOR FILING DATE: 1998-04-07
11 NUMBER OF SEQ ID NOS: 5
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 1
14     LENGTH: 42
15     TYPE: PRT
16     ORGANISM: Homo sapiens
17     FEATURE:
18 OTHER INFORMATION: human Abeta42 beta-amyloid peptide
19 US-09-825-242-1

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Query Match	100.0%	Score 125; DB 3;	Length 42;
Best Local Similarity	100.0%	Pred. No. 6.8e-11;	
Matches	26;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;

OY 1 LVFFAEDVGSNKGAIIGLMVGGVIA 26
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Db 17 LVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 22
US-09-930-915A-293

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? Sequence 293, Application US/09930915A
? Publication No. US20030138769A1
? GENERAL INFORMATION:
? APPLICANT: Bickert, Ashley J.
? TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
? TITLE OF INVENTION: STABILITY
? FILE REFERENCE: 4564/83501 ICC-102.2 PCT
? CURRENT APPLICATION NUMBER: US/09/930,915A
? CURRENT FILING DATE: 2001-08-15
? PRIOR APPLICATION NUMBER: 60/226,867
? PRIOR FILING DATE: 2000-08-22
? PRIOR APPLICATION NUMBER: 60/225,943
? PRIOR FILING DATE: 2000-08-16
? NUMBER OF SEQ ID NOS: 313
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 293
? LENGTH: 42
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-930-915A-293

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Query Match	100.0%	Score 125;	DB 3;	Length 42;
Best Local Similarly	100.0%	Pred. No. 6.8e-11;		
Matches 26; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 LVFFAEDVGSNKGAIIGLMVGWVIA 26
|||
Db 17 LVFFAEDVGSNKGAIIGLMVGWVIA 42

RESULT 23
US-10-051

US-10-051-496-2
; Sequence 2, Application US/10051496
; Publication No. US20020182660A1

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; GENERAL INFORMATION:
;
; APPLICANT: Kei-Lai L. Fong
;
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
;

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TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39) Abeta(1-41), Abeta(1-42) and Abeta(1-43)

Adelta(1-41)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Kai-lai T. FONG

STREET: 1004 West 8th Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
STD: 18405

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 50 inch 1 44MB storage

COMPUTER: IBM PC Compatib
OPERATING SYSTEM: Windows

SOFTWARE: MS No. US20020182660A1epad
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US/09/184,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183 407

ATTORNEY/AGENT INFORMATION:
FILING DATE: 18-February-2000
APPLICATION NUMBER: 80/103,400

NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662

REFERENCE/DOCKET NUMBER: PBI-PT001.1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 42 Amino Acid
TYPE: Amino Acid
TOPOLOGY: 11902

MOLECULE TYPE: Protein
FEATURE:

NAME/KEY:	Signal Sequence
LOCATION:	1-42

IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
OTHER INFORMATION:

PUBLICATION INFORMATION
AUTHORS:

TITLE: _____
JOURNAL: _____
VOLUME: _____

VOLUME:
ISSUE:
PAGES:

DATE: _____
RELEVANT

SEQUENCE DESCRIPTION:	SEQ ID NO: 2:
US-10-051-496-2	

Query Match 100.0%; Score 125; DB 4; Length 42;

Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 LVFFAEDVGSNKGAIIGLMVGVVIA 26

Db 17 LVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 24
US-10-082-804-7
Sequence 7 Amplification HS/10082804

Publication No. US20020194633

APPLICANT: McConlogue, Lisa
APPLICANT: Gurney, Mark E.

FILE REFERENCE: MBHB 02-329-A

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; CURRENT APPLICATION NUMBER: US/10/082,804  
; CURRENT FILING DATE: 2002-02-22
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PRIOR APPLICATION NUMBER: 60/271 514
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/271 514

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/293,762
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7

Query Match 100.0%; Score 125; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 25
US-10-217-584-2
Sequence 2, Application US/10217584
Publication No. US2003007261A1
GENERAL INFORMATION:
APPLICANT: Paris, Daniel
APPLICANT: Mullen, Michael
TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
FILE REFERENCE: USF-T161XCI
CURRENT APPLICATION NUMBER: US/10/217,584
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,656
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(42)
OTHER INFORMATION: A-beta 1-42 peptide
US-10-217-584-2

Query Match 100.0%; Score 125; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 26
US-10-169-580-2
Sequence 2, Application US/10169580
Publication No. US20030100477A1
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR SUPPRESSING B-AMYLOID PRODUCTION
FILE REFERENCE: 070898
CURRENT APPLICATION NUMBER: US/10/169,580
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 2000-131037
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: PCT/JP01/03555
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 42

TYPE: PRT
ORGANISM: Homo sapiens
US-10-169-580-2

Query Match 100.0%; Score 125; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 27
US-10-278-181-1
Sequence 1, Application US/10278181
Publication No. US20030104488A1
GENERAL INFORMATION:
APPLICANT: Choikier, Mario
APPLICANT: Buck, Martina
TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
FILE REFERENCE: CHOKIER-04302
CURRENT APPLICATION NUMBER: US/10/278,181
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/731,460
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-278-181-1

Query Match 100.0%; Score 125; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6,8e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVFPAEDVGSNKGAITIGLMVGGVIA 26
Db 17 LVFPAEDVGSNKGAITIGLMVGGVIA 42

RESULT 28
US-10-143-534-2
Sequence 2, Application US/10143534
Publication No. US20030105152A1
GENERAL INFORMATION:
APPLICANT: Ingram, Vernon M.
APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE
FILE REFERENCE: M00656/70078
CURRENT APPLICATION NUMBER: US/10/143,534
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 10/051,663
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/706,574
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 2
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-143-534-2

Query Match 100.0%; Score 125; DB 4; Length 42;

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2006, 07:01:12 ; Search time 10.1435 Seconds
(without alignments)
199.069 Million cell updates/sec

Title: US-09-731-899-7
Perfect score: 125
Sequence: 1 LVFPAEDVSNKGAITGLMGVAVIA 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 285145 seqs, 77663843 residues

Total number of hits satisfying chosen parameters: 285145

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEM_PUB pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEM_PUB pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEM_PUB pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	125	100.0	26	1	US-09-731-899-7
2	125	100.0	32	1	US-09-731-899-6
3	125	100.0	40	1	US-09-731-899-5
4	125	100.0	40	6	US-10-966-645-38
5	125	100.0	42	1	US-09-731-899-3
6	125	100.0	42	6	US-10-890-071-42
7	125	100.0	42	6	US-10-544-093-1
8	125	100.0	42	6	US-10-546-547-3
9	125	100.0	42	6	US-10-966-645-36
10	125	100.0	42	7	US-11-104-300-2
11	125	100.0	42	7	US-11-297-316-1
12	125	100.0	42	7	US-11-287-157A-49
13	125	100.0	43	1	US-09-731-899-4
14	125	100.0	43	7	US-11-348-091-1
15	125	100.0	56	6	US-10-544-093-16
16	125	100.0	56	6	US-10-544-093-19
17	125	100.0	58	6	US-10-515-919A-30
18	125	100.0	58	6	US-10-544-093-12
19	125	100.0	58	6	US-10-544-093-14
20	125	100.0	58	6	US-10-544-093-27
21	125	100.0	59	1	US-09-731-899-1
22	125	100.0	60	6	US-10-544-093-20
23	125	100.0	64	6	US-10-544-093-13
24	125	100.0	79	6	US-10-544-093-15
25	125	100.0	99	6	US-10-544-093-22

26	125	100.0	99	6	US-10-544-093-24	Sequence 24, Appl
27	125	100.0	142	6	US-10-544-093-17	Sequence 17, Appl
28	125	100.0	142	6	US-10-544-093-21	Sequence 21, Appl
29	125	100.0	142	6	US-10-544-093-23	Sequence 23, Appl
30	125	100.0	185	6	US-10-544-093-18	Sequence 18, Appl
31	125	100.0	203	6	US-10-544-093-26	Sequence 26, Appl
32	125	100.0	316	6	US-10-544-093-25	Sequence 25, Appl
33	125	100.0	626	6	US-10-515-919A-12	Sequence 12, Appl
34	125	100.0	626	6	US-10-515-919A-17	Sequence 17, Appl
35	125	100.0	695	6	US-10-515-919A-1	Sequence 1, Appl
36	125	100.0	695	6	US-10-515-919A-10	Sequence 10, Appl
37	125	100.0	751	6	US-10-515-919A-2	Sequence 2, Appl
38	125	100.0	770	6	US-10-515-919A-9	Sequence 9, Appl
39	125	100.0	770	7	US-11-104-300-1	Sequence 1, Appl
40	125	100.0	626	6	US-10-515-919A-13	Sequence 13, Appl
41	121	96.8	626	6	US-10-515-919A-15	Sequence 15, Appl
42	121	96.8	626	6	US-10-515-919A-16	Sequence 16, Appl
43	121	96.8	626	6	US-10-515-919A-18	Sequence 18, Appl
44	121	96.8	626	6	US-10-515-919A-19	Sequence 19, Appl
45	121	96.8	626	6	US-10-515-919A-20	Sequence 20, Appl
46	121	96.8	626	6	US-10-515-919A-21	Sequence 21, Appl
47	121	96.8	626	6	US-11-269-857-5	Sequence 5, Appl
48	121	96.8	42	7	US-11-269-857-3	Sequence 3, Appl
49	117	93.6	38	6	US-10-966-645-44	Sequence 44, Appl
50	117	93.6	38	6	US-09-731-899-2	Sequence 2, Appl
51	117	93.6	40	1	US-10-966-645-37	Sequence 37, Appl
52	117	93.6	40	6	US-10-515-919A-2	Sequence 2, Appl
53	117	93.6	42	6	US-10-515-919A-7	Sequence 7, Appl
54	117	93.6	42	6	US-10-515-919A-3	Sequence 3, Appl
55	117	93.6	42	6	US-10-515-919A-4	Sequence 4, Appl
56	113	90.4	42	6	US-10-515-919A-5	Sequence 5, Appl
57	113	90.4	42	6	US-10-515-919A-6	Sequence 6, Appl
58	113	90.4	42	6	US-10-515-919A-8	Sequence 8, Appl
59	113	90.4	42	6	US-10-515-919A-9	Sequence 9, Appl
60	113	90.4	42	6	US-10-515-919A-10	Sequence 10, Appl
61	113	90.4	42	6	US-10-515-919A-11	Sequence 11, Appl
62	113	90.4	42	6	US-10-515-919A-22	Sequence 22, Appl
63	113	90.4	43	6	US-11-104-300-3	Sequence 3, Appl
64	113	90.4	40	7	US-11-269-857-3	Sequence 3, Appl
65	113	88.8	40	7	US-11-269-857-3	Sequence 3, Appl
66	111	88.0	28	7	US-11-297-316-2	Sequence 2, Appl
67	110	88.0	28	7	US-11-297-316-2	Sequence 2, Appl
68	66	52.8	19	6	US-10-890-071-75	Sequence 75, Appl
69	60	48.0	19	6	US-10-890-071-28	Sequence 28, Appl
70	52	41.6	10	6	US-10-890-071-28	Sequence 28, Appl
71	52	41.6	10	6	US-10-890-071-28	Sequence 28, Appl
72	51	40.8	10	6	US-10-890-071-26	Sequence 26, Appl
73	51	40.8	240	6	US-10-449-902-39853	Sequence 39853, A
74	51	40.8	429	7	US-11-056-355B-53789	Sequence 53789, A
75	51	40.8	556	7	US-11-056-355B-53788	Sequence 53788, A
76	51	40.8	642	7	US-11-056-355B-53787	Sequence 53787, A
77	50	40.0	10	6	US-10-890-071-29	Sequence 29, Appl
78	50	40.0	10	6	US-10-890-071-30	Sequence 30, Appl
79	50	40.0	469	7	US-11-330-403-1463	Sequence 1463, Ap
80	50	40.0	469	7	US-11-330-403-12796	Sequence 12796, A
81	49	39.2	10	6	US-10-890-071-25	Sequence 25, Appl
82	49	39.2	10	6	US-10-890-071-31	Sequence 31, Appl
83	49	39.2	10	6	US-10-890-071-32	Sequence 32, Appl
84	49	39.2	10	6	US-10-890-071-33	Sequence 33, Appl
85	49	39.2	10	6	US-10-890-071-37	Sequence 37, Appl
86	49	39.2	26	6	US-10-533-266-11	Sequence 11, Appl
87	49	39.2	403	7	US-11-330-403-13296	Sequence 13296, A
88	49	39.2	675	6	US-10-519-135-45	Sequence 45, Appl
89	49	39.2	870	6	US-10-953-349-1268	Sequence 1268, Ap
90	49	39.2	921	6	US-10-519-135-6	Sequence 6, Appl
91	48	38.4	10	6	US-10-890-071-34	Sequence 34, Appl
92	48	38.4	10	6	US-10-890-071-35	Sequence 35, Appl
93	48	38.4	10	6	US-10-890-071-36	Sequence 36, Appl
94	48	38.4	407	7	US-11-056-355B-95913	Sequence 95913, A
95	48	38.4	458	7	US-11-056-355B-95912	Sequence 95912, A
96	48	38.4	656	7	US-11-056-355B-95911	Sequence 95911, A
97	48	38.4	671	6	US-10-449-902-52071	Sequence 52071, A
98	47.5	38.0	356	7	US-11-056-355B-51389	Sequence 51389, A

99 47.5 38.0 480 7 US-11-056-355B-51388 Sequence 51388, A
100 47.5 38.0 504 7 US-11-056-355B-51387 Sequence 51387, A

ALIGNMENTS

RESULT 1
US-09-731-899-7

Sequence 7, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 7
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-09-731-899-7

Query Match 100.0%; Score 125; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 1 LVFFADVGSNKGAIIGLMVGVVIA 26

RESULT 2
US-09-731-899-6

Sequence 6, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1)
OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-6

Query Match 100.0%; Score 125; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 7 LVFFADVGSNKGAIIGLMVGVVIA 32

RESULT 3
US-09-731-899-5

Sequence 5, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 5
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1)
OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-5

Query Match 100.0%; Score 125; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 15 LVFFADVGSNKGAIIGLMVGVVIA 40

RESULT 4
US-10-966-645-38

Sequence 38, Application US/10966645
Publication No. US20060189523A1
GENERAL INFORMATION:
APPLICANT: SCHILLING, STEPHAN
APPLICANT: HOFFMANN, TORSTEN
APPLICANT: NIESTROU, ANDRE JOHANNES
APPLICANT: DEMUTH, HANS-ULRICH
APPLICANT: HEISER, ULRICH
TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
FILE REFERENCE: 20488/59
CURRENT APPLICATION NUMBER: US/10/966,645
PRIOR FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: 60/512,038
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 38
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-10-966-645-38

Query Match 100.0%; Score 125; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAIIGLMVGVVIA 26
DB 15 LVFFADVGSNKGAIIGLMVGVVIA 40

RESULT 5
US-09-731-899-3

Sequence 3, Application US/09731899
Publication No. US20060088548A1
GENERAL INFORMATION:
APPLICANT: Chain, Benjamin
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREO, AND METHODS
FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1)
OTHER INFORMATION: Xaa is pyroglutamate
US-09-731-899-3

FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa is L-Asp, D-Asp, or L-Iso Asp
US-09-731-899-3

Query Match 100.0%; Score 125; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 6
US-10-890-071-42
Sequence 42, Application US/10890071
Publication No. US20060121038A9
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Bard, Frederique
APPLICANT: Yednock, Ted
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
FILE REFERENCE: 15270J-004760US
CURRENT APPLICATION NUMBER: US/10/890,071
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US/09/580,018
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/322,289
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-890-071-42

Query Match 100.0%; Score 125; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 7
US-10-544-093-1
Sequence 1, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
PREVENTION AND TREATMENT OF AMYLOIDGENIC DISEASE
FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544,093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-544-093-1

Query Match 100.0%; Score 125; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 8
US-10-546-547-3
Sequence 3, Application US/10546547
Publication No. US20060188951A1
GENERAL INFORMATION:
APPLICANT: Mook, In Hee
APPLICANT: Hur, Ji Yeun
TITLE OF INVENTION: Method for Measuring the Level of Anti-beta-amyloid Antibody in
Body Fluids and Diagnostic Kit for Alzheimer's Disease Using Sa
FILE REFERENCE: DE-1646
CURRENT APPLICATION NUMBER: US/10/546,547
CURRENT FILING DATE: 2005-08-23
PRIOR APPLICATION NUMBER: PCT/KR2004/000371
PRIOR FILING DATE: 2004-02-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: 1-42 amino acid of amyloid a4 precursor protein (APP)
US-10-546-547-3

Query Match 100.0%; Score 125; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPADVGSNKGAITGLMWGVVIA 26
DB 17 LVFPADVGSNKGAITGLMWGVVIA 42

RESULT 9
US-10-966-645-36
Sequence 36, Application US/10966645
Publication No. US20060189523A1
GENERAL INFORMATION:
APPLICANT: SCHILLING, STEPHAN
APPLICANT: HOFFMANN, TORSTEN
APPLICANT: NIESTROJ, ANDRZ JOHANNES
APPLICANT: DEMUTH, HANS-ULRICH
APPLICANT: HEISER, ULRICH
TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL AND GLUTAMATE CYCLASES
FILE REFERENCE: 20488/59
CURRENT APPLICATION NUMBER: US/10/966,645
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: 60/512,038
PRIOR FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 53

```

; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-966-645-36

```

Query Match	100.0%;	Score 125;	DB 6;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 2.3e-11;		
Matches	26;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY		1	LVFPAEDVGSNKGAIIIGLMVG	26
Db		17	LVFPAEDVGSNKGAIIIGLMVG	42

```

RESULT 10
US-11-104-300-2
; Sequence 2, Application US/11104300
; Publication No. US20060099211A1
; GENERAL INFORMATION:
; APPLICANT: Monche, Carmen
; APPLICANT: Szabo, Paul
; APPLICANT: Weksler, Mark
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Safer, More Potent Human Immunoglobulin Preparations for Treating
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 1676.027US1
; CURRENT APPLICATION NUMBER: US/11/104,300
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US 60/561,423
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
;
; LENGTH: 42
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-11-104-300-2

```

Query Match	100.0%;	Score 125;	DB 7;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 2.3e-11;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 LVFFAEDVGSNKGATIGLMVGWVIA 26
 |||||
Db 17 LVFFAEDVGSNKGATIGLMVGWVIA 42

```

RESULT 11
US-11-297-316-1
; Sequence 1, Application US/11297316
; Publication No. US20060141602A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; TITLE OF INVENTION: particles
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-1

```

Query Match	100.0%	Score 125;	DB 7;	Length 42;
Best Local Similarity	100.0%	Pred. No. 2.3e-11;		
Matches 26; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible]

RESULT 12
US-11-287-157A-49
; Sequence 49, Application US/11287157A
; Publication No. US20060154863A1

```

APPLICANT: SKIBATCH, HANNA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CONDITIONS
FILE REFERENCE: 32051-701.201
CURRENT APPLICATION NUMBER: US/11/287,157A
CURRENT FILING DATE: 2005-11-25
PRIOR APPLICATION NUMBER: 60/658,859
PRIOR FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 60/652,287
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/630,880
PRIOR FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn version 3.3
SEQ ID NO 49
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-11-287-157A-49

```

Query Match	100.0%;	Score 125;	DB 7;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 2.3e-11;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 LVFFAEDVGSNKGALITGLMVGAVIA 26
|||
Db 17 LVFFAEDVGSNKGALITGLMVGAVIA 42

```

RESULT 13
US-09-731-899-4
; Sequence 4, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chai, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; TITLE OF INVENTION: FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
; FILE REFERENCE: 20555/1203433-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; PRIORITY FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIORITY FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-899-4

```

Query Match	100.0%	Score 125;	DB 1;	Length 43;
Best Local Similarity	100.0%	Pred. No. 2.3e-11;		
Matches	26;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps	0

Dy 1 LVFFAEDVGSNKGALITGLMVGGVIA 26
|||
Db 17 LVFFAEDVGSNKGALITGLMVGGVIA 42

RESULT 14
US-11-348-091-1
; Sequence 1, Application US/11348091
; Publication No. US20060211679A1

US-11-348-091-1
; Sequence 1, Application US/11348091
; Publication No. US20060211679A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Han, Qi
/ TITLE OF INVENTION: Substituted Lactams as Inhibitors of Abeta Protein Production
/ FILE REFERENCE: BMS-PH-7164.1(C)
/ CURRENT APPLICATION NUMBER: US/11/348,091
/ CURRENT FILING DATE: 2006-02-06
/ PRIOR APPLICATION NUMBER: US 10/685,031
/ PRIOR FILING DATE: 2003-10-14
/ PRIOR APPLICATION NUMBER: US 09/832,455
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: US 60/196,549
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-348-091-1
```

```
Query Match          100.0%; Score 125; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 2,3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 LVFPAEDVGSNKGAITGLMWGVVIA 26
Db      17 LVFPAEDVGSNKGAITGLMWGVVIA 42
```

```
RESULT 15
US-10-544-093-16
/ Sequence 16, Application US/10544093
/ Publication No. US20060188512A1
/ GENERAL INFORMATION:
/ APPLICANT: Yednock, Ted
/ APPLICANT: Vasquez, Nicki
/ APPLICANT: Bard, Frederique
/ APPLICANT: Seubert, Peter A.
/ TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
/ FILE REFERENCE: 15270J-009820US
/ CURRENT APPLICATION NUMBER: US/10/544,093
/ PRIOR FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
/ PRIOR FILING DATE: 2004-01-31
/ PRIOR APPLICATION NUMBER: US 60/444,150
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 16
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Padre-A-beta fragment fusion protein
/ NAME/KEY: MISC FEATURE
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (14)..(56)
/ OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
/ OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-16
```

```
Query Match          100.0%; Score 125; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3,1e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 LVFPAEDVGSNKGAITGLMWGVVIA 26
Db      30 LVFPAEDVGSNKGAITGLMWGVVIA 55
```

```
RESULT 16
US-10-544-093-19
/ Sequence 19, Application US/10544093
/ Publication No. US20060188512A1
/ GENERAL INFORMATION:
/ APPLICANT: Yednock, Ted
/ APPLICANT: Vasquez, Nicki
/ APPLICANT: Bard, Frederique
/ APPLICANT: Seubert, Peter A.
/ TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
/ FILE REFERENCE: 15270J-009820US
/ CURRENT APPLICATION NUMBER: US/10/544,093
/ PRIOR FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
/ PRIOR FILING DATE: 2004-01-31
/ PRIOR APPLICATION NUMBER: US 60/444,150
/ PRIOR FILING DATE: 2003-02-01
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(43)
/ OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
/ OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-19
```

```
Query Match          100.0%; Score 125; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3,1e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 LVFPAEDVGSNKGAITGLMWGVVIA 26
Db      17 LVFPAEDVGSNKGAITGLMWGVVIA 42
```

```
RESULT 17
US-10-515-919A-30
/ Sequence 30, Application US/10515919A
/ Publication No. US20060160146A1
/ GENERAL INFORMATION:
/ APPLICANT: Otsuka Pharmaceutical Co., Ltd.
/ TITLE OF INVENTION: METHOD OF SCREENING COMPOUND AFFECTING AMYLOID BETA PRODUCTION
/ FILE REFERENCE: 084952
/ CURRENT APPLICATION NUMBER: US/10/515,919A
/ PRIOR FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: PCT/JP03/06319
/ PRIOR FILING DATE: 2003-05-21
/ PRIOR APPLICATION NUMBER: JP 2002-159472
/ PRIOR FILING DATE: 2002-05-31
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 30
/ LENGTH: 58
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-515-919A-30
```

```
Query Match          100.0%; Score 125; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3,2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 33 LVFPAEDVGSNKGAIIGLMVGVVIA 58

RESULT 18
US-10-544-093-12
; Sequence 12, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Ted
; APPLICANT: Vasequez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-12

Query Match 100.0%; Score 125; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3,2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 17 LVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 19
US-10-544-093-14
; Sequence 14, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Ted
; APPLICANT: Vasequez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein

; OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-14

Query Match 100.0%; Score 125; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3,2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 17 LVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 20
US-10-544-093-27
; Sequence 27, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Ted
; APPLICANT: Vasequez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-27

Query Match 100.0%; Score 125; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 3,2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVVIA 26
DB 17 LVFPAEDVGSNKGAIIGLMVGVVIA 42

RESULT 21
US-09-731-899-1
; Sequence 1, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chaim, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 20555/120343-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3
SEQ ID NO 1
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
US-09-731-899-1

Query Match 100.0%; Score 125; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
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DB 21 LVFFADVGSNKGAITGLMWGVVIA 46

RESULT 22
US-10-544-093-20

Sequence 20, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31

PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2
SEQ ID NO 20

LENGTH: 60

TYPE: PRT

ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: Fusion protein

NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-20
Query Match 100.0%; Score 125; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
|||||
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 23
US-10-544-093-13

Sequence 13, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856

PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 13

LENGTH: 64
TYPE: PRT
ORGANISM: Artificial
FEATURE:

OTHER INFORMATION: A-beta fragment-tetanus toxoid fusion protein
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-13

Query Match 100.0%; Score 125; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
|||||
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 24
US-10-544-093-15

Sequence 15, Application US/10544093
Publication No. US20060188512A1
GENERAL INFORMATION:

APPLICANT: Vednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-009820US

CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31

PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2
SEQ ID NO 15

LENGTH: 79

TYPE: PRT

ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: A-beta fragment tetanus-toxoid fusion protein

NAME/KEY: MISC FEATURE

LOCATION: (1)..(43)

OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.

US-10-544-093-15
Query Match 100.0%; Score 125; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFFADVGSNKGAITGLMWGVVIA 26
|||||
DB 17 LVFFADVGSNKGAITGLMWGVVIA 42

RESULT 25
US-10-544-093-22
Sequence 22, Application US/10544093
Publication No. US20060188512A1

GENERAL INFORMATION:
APPLICANT: Vednock, Ted
APPLICANT: Vaequez, Nick
APPLICANT: Bard, Frederique
APPLICANT: Seibert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDGENIC DISEASE
FILE REFERENCE: 15370J-009820US
CURRENT APPLICATION NUMBER: US/10/544, 093
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
FEATURE:
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
NAME/KEY: MISC FEATURE
LOCATION: (57)..(99)
OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-22

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Query Match Similarity      100.0%; Score 125; DB 6; Length 99;
Best Local Alignment       Pred. No.5.6e-11;
Matches      26; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY          1 LVFFAEDVGSNKGAIIGLMVGGVIA 26
|||||
Db          17 LVFFAEDVGSNKGAIIGLMVGGVIA 42
|||||

RESULT 26
US-10-544-093-24
; Sequence 24, Application US/10544093
; Publication No. US20060185512A1
GENERAL INFORMATION:
APPLICANT: Yednock, Ted
APPLICANT: Vasquez, Nicki
APPLICANT: Bard, Frederique
APPLICANT: Seubert, Peter A.
TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
FILE REFERENCE: 15270J-0036200S
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
PRIOR FILING DATE: 2004-01-31
PRIOR APPLICATION NUMBER: US 60/444,150
PRIOR FILING DATE: 2003-02-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Fusion protein
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(43)
OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
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1 OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
2
3 FEATURES:
4 NAME/KEY: MISC FEATURE
5 LOCATION: (44)-(86)
6
7 OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present
8
9 OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
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Query Match	100.0%;	Score 125;	DB 6;	Length 99;
Best Local Similarity	100.0%;	Pred. No. 5.6e-11;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy 1 LVFPAEDVGSNKGAIIIGLMVGWVIA 26
| | | | | | | | | | | | | |
Db 17 LVFPAEDVGSNKGAIIGLMVGWVIA 42

```

RESULT 27
US-10-544-093-17
; Sequence 17, Application US/10544093
; Publication NO. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Vasequez, Ted
; APPLICANT: Yednock, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 152703-009820US
; CURRENT APPLICATION NUMBER: US/10/544,093
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17

```

```

1 ORGANISM: Artificial
2 FEATURE:
3 OTHER INFORMATION: A-beta-A-beta-Padre fusion protein
4 FEATURE:
5 NAME/KEY: MISC_FEATURE
6 LOCATION: (1)..(43)
7 OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
8 OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
9 FEATURE:
10 NAME/KEY: MISC_FEATURE
11 LOCATION: (44)..(86)
12 OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
13 OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
14 FEATURE:
15 NAME/KEY: MISC_FEATURE
16 LOCATION: (87)..(129)
17 OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
18 OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
19 FEATURE:
20 NAME/KEY: MISC_FEATURE
21 LOCATION: (132)..(132)
22 OTHER INFORMATION: X is cyclohexylalanine, tyrosine, or phenylalanine.
23
24 US-10-544-093-17

```

Query Match	100.0%;	Score 125;	DB 6;	Length 142;
Best Local Similarity	100.0%;	Pred. No. 8.3e-11;		
Matches	26;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

Dy 1 LVFFAEDVGSNKGAIIIGLMVGAVIA 26
|||
Dd 17 LVFFAEDVGSNKGAIIIGLMVGAVIA 42

```
RESULT 28
US-10-544-093-21
; Sequence 21, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(56)
; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (57)..(99)
; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(142)
; OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-21
Query Match          100.0%; Score 125; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 8,3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVFFADVGSNKGAIIGLMVGVVIA 26
        |||
DB      30 LVFFADVGSNKGAIIGLMVGVVIA 55

RESULT 29
US-10-544-093-23
; Sequence 23, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Bard, Frederique
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
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LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Only a contiguous fragment of residues 1-43 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (44)..(86)
; OTHER INFORMATION: Only a contiguous fragment of residues 44-86 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (87)..(129)
; OTHER INFORMATION: Only a contiguous fragment of residues 87-129 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-23
Query Match          100.0%; Score 125; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 8,3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVFFADVGSNKGAIIGLMVGVVIA 26
        |||
DB      17 LVFFADVGSNKGAIIGLMVGVVIA 42

RESULT 30
US-10-544-093-18
; Sequence 18, Application US/10544093
; Publication No. US20060188512A1
; GENERAL INFORMATION:
; APPLICANT: Yednock, Ted
; APPLICANT: Vasquez, Nicki
; APPLICANT: Seubert, Peter A.
; TITLE OF INVENTION: ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE
; FILE REFERENCE: 152703-00982005
; CURRENT APPLICATION NUMBER: US/10/544,093
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: WO PCT/US2004/002856
; PRIOR FILING DATE: 2004-01-31
; PRIOR APPLICATION NUMBER: US 60/444,150
; PRIOR FILING DATE: 2003-02-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Only a contiguous fragment of residues 3-3 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(56)
; OTHER INFORMATION: Only a contiguous fragment of residues 14-56 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; NAME/KEY: MISC FEATURE
; LOCATION: (57)..(99)
; OTHER INFORMATION: Only a contiguous fragment of residues 57-99 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC FEATURE
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; LOCATION: (100)..(142)
; OTHER INFORMATION: Only a contiguous fragment of residues 100-142 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (143)..(185)
; OTHER INFORMATION: Only a contiguous fragment of residues 143-185 are present.
; OTHER INFORMATION: Preferred fragments are 5-10 or 7-10 residues in length.
US-10-544-093-18

Query Match 100.0%; Score 125; DB 6; Length 185;
Best Local Similarity: 100.0%; Pred. No. 1.1e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVFPAEDVGSNKGAIIGLMVGVIA 26
|||
Db 30 LVFPAEDVGSNKGAIIGLMVGVIA 55

Search completed: September 28, 2006, 07:10:55
Job time : 10.1435 secs